Technical Support Document:

Upper Oyster Creek (Segment 1245) Bacteria TMDL

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ACRONYMS AND ABBREVIATIONS

ac-ft/m	Acre-feet per month
BMP	Best management practice
BRA	Brazos River Authority
BST	Bacterial Source Tracking
CAFO	Confined animal feeding operation
CFR	Code of Federal Regulations
CFU	Colony-forming unit
CI	Confidence interval
CWA	Clean Water Act
FM	Farm to market road
GCWA	Gulf Coast Water Authority
ID	Identification or identifier
IEH	Institute for Environmental Health, Inc.
LA	Load allocation
MGD	Million gallons per day
MOS	Margin of safety
MS4	Municipal separate storm sewer system
MUD	Municipal utility district
NLCD	National Land Cover Data
NWDLS	North Water District Laboratory Services, Inc.
PFGE	Pulsed Field Gel Electrophoresis
QA	Quality assurance
QAO	Quality assurance officer
QAPP	Quality assurance project plan
QC	Quality control
RFLP	Restricted fragment length polymorphism
rRNA	Ribosomal ribonucleic acid
SH	State highway
SOP	Standard operating procedure
SWMP	Stormwater management program
TCEQ	Texas Commission on Environmental Quality
TDCJ	Texas Department of Criminal Justice
TMDL	Total maximum daily load
UOC	Upper Oyster Creek
WWTP	Wastewater treatment plant

SECTION 1

INTRODUCTION

1.1 Purpose and Scope

Section 303(d) of the Clean Water Act (CWA) and U.S. Environmental Protection Agency (USEPA) Water Quality Planning and Management Regulations (40 Code of Federal Regulations [CFR] Part 130) require States to develop total maximum daily loads (TMDL) for water bodies not meeting designated uses where water quality-based controls are in place. TMDLs establish the allowable loadings of pollutants or other quantifiable parameters for a water body based on the relationship between pollution sources and in-stream water quality conditions, so States can implement water quality-based controls to reduce pollution from both point and nonpoint sources and restore and maintain the quality of its water resources (USEPA, 1991).

Texas Commission on Environmental Quality (TCEQ) is leading an effort to assess the water quality of classified Segment 1245 of Oyster Creek, known as “Upper Oyster Creek.” Segment 1245 was placed on the State of Texas 2002 303(d) list as impaired from the presence of fecal pathogen indicator bacteria and requires development of a TMDL for point and nonpoint sources of *Escherichia coli* (*E. coli)* bacteria. Segment 1245 is located within the Brazos River Basin, southwest of Houston, Texas in northern Fort Bend County (Figure 1-1 and 1-2). The segment begins at the Gulf Coast Water Authority (GCWA) Shannon Pump Station on the Brazos River and continues through Jones Creek to its confluence with Oyster Creek, through the City of Sugar Land to its confluence with Flat Bank Creek, through Flat Bank Creek to its confluence with the diversion canal, through the diversion canal to its confluence with Steep Bank Creek, and finally through Steep Bank Creek to its confluence with the Brazos River (Figure 1-2). Segment 1245 extends approximately 54 miles, and its watershed contains four incorporated areas: Fulshear, Sugar Land, Stafford, and Missouri City.

1.2 Water Quality Standards

Water quality standards (WQS) consist of designated beneficial uses, water quality criteria to protect the uses, and antidegradation policies. These standards serve dual purposes of establishing water quality goals for the nation’s water bodies and providing the regulatory basis for establishing certain treatment controls and strategies. The State of Texas WQSs applies to Upper Oyster Creek as described in the Texas Surface Water Quality Standards (TCEQ, 2000). Designated uses of Segment 1245 are intermediate aquatic life use, contact recreation, and public water supply. This report addresses only the contact recreation use.

Water quality criteria list specific constituent levels to be maintained to ensure that designated uses are met. To protect contact recreation use, water quality criteria are based on concentrations of fecal coliform and *E. coli* bacteria in water. Fecal coliform bacteria are a group of moderately heat-tolerant coliform bacteria abundant in the intestines of warm-blooded

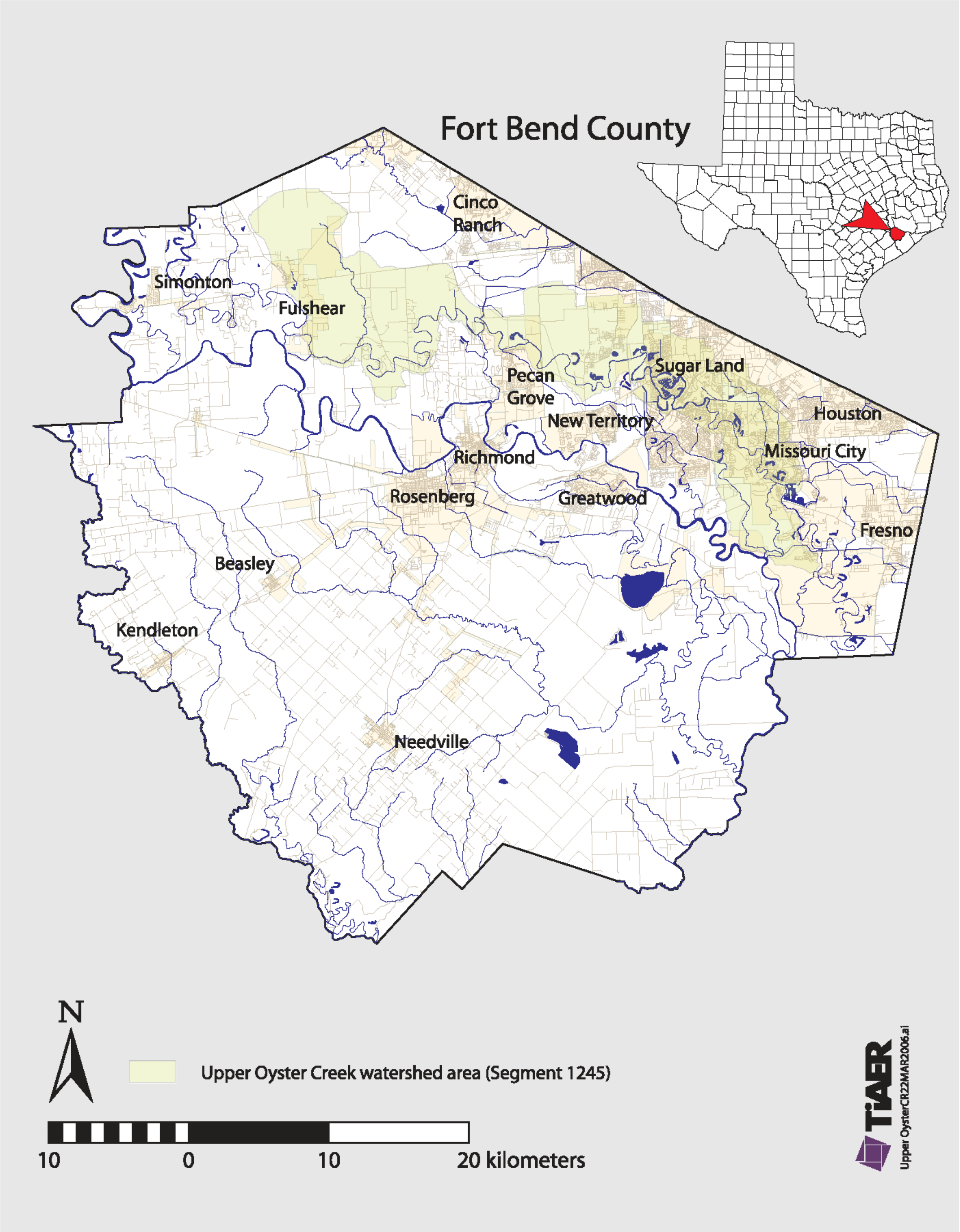

Figure 1-1 Location of Segment 1245 (Upper Oyster Creek), Fort Bend County, Texas

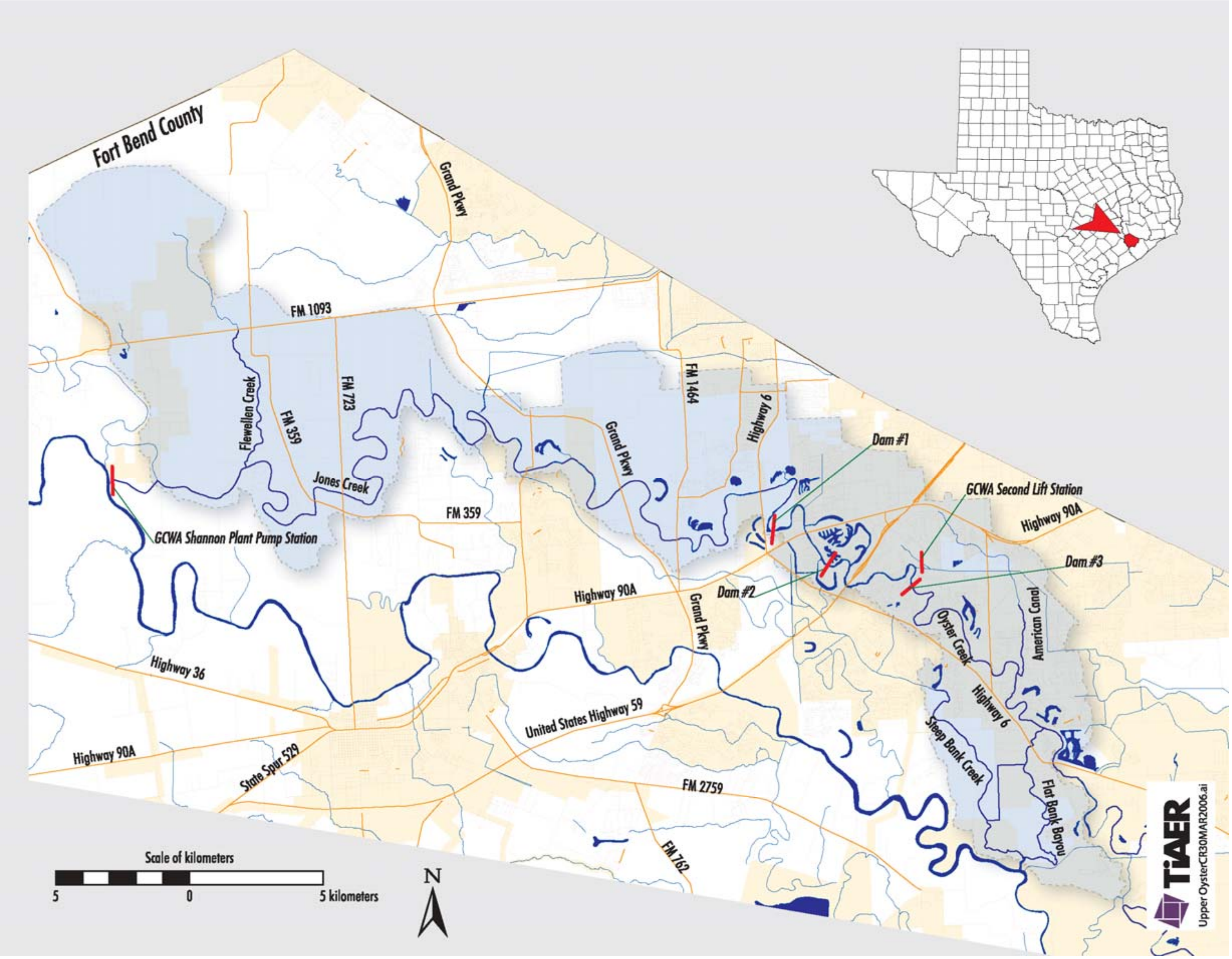

Figure 1-2 Relevant geographical references in Upper Oyster Creek

animals, but are not believed to survive in the environment long-term. Because they are relatively easy to measure in water, they are used as an indicator of the possible presence of fecal pathogenic microorganisms in water, including other bacteria, viruses, and harmful protozoans. Most fecal coliform bacteria are not pathogenic. It has been established that *E. coli* is more closely associated with fecal pollution than other fecal coliform bacteria, some of which may normally reside and multiply in the environment. *E. coli* is often the most abundant species of the fecal coliform group of bacteria, and a few strains of *E. coli*, notably strain O157:H7, are pathogenic.

Applicable water quality criteria for *E. coli* state that the geometric mean concentration (in colony-forming units [cfu] of bacteria per 100 milliliters [ml]) should not exceed 126/100 ml, and the single sample concentration should not exceed 394 per 100 ml. Water quality criteria for fecal coliform state that the geometric mean concentration should not exceed 200 per 100 ml, and the single sample concentration should not exceed 400 per 100 ml (TCEQ, 2000). The TCEQ prefers the use of *E. coli* as the fecal indicator organism rather than the fecal coliform, if sufficient data are available to allow assessment based on *E. coli*.

1.3 Report Purpose and Organization

The TCEQ contracted with the Texas Institute for Applied Environmental Research (TIAER) to conduct the appropriate studies to (1) acquire data and information necessary to identify pollutant sources and support modeling and assessment activities; (2) perform the assessment activities necessary to allocate the loadings of the constituent of concern; and (3) assist TCEQ in preparing a TMDL. The purpose of this report is to provide technical documentation for the bacteria TMDL of Upper Oyster Creek (segment 1245). The report contains information on historical data; watershed properties; bacteria monitoring to confirm the State of Texas 2002 Section 303(d) listing of impairment due to presence of indicator bacteria (*E. coli*); results of a bacterial source tracking (BST) study to identify broad categories of sources of *E. coli*; development of the load duration curve approach for the allocation process; and application of the load duration curve approach for the TMDL load allocation. TIAER was the technical lead entity for all studies and work provided in this report. For the bacterial source tracking study, TIAER's technical project team included Parsons Water & Infrastructure, Inc., who performed the majority of the field efforts associated with the work herein as well as taking the lead on writing the BST monitoring report (TIAER et al., 2005); North Water District Laboratory Services, Inc., who performed the *E. coli* concentration enumeration, and the Institute for Environmental Health, Inc. (IEH), who performed the molecular fingerprinting analyses.

SECTION 2

HISTORICAL DATA REVIEW AND WATERSHED PROPERTIES

2.1 Watershed Hydrology and Climate

An important factor in assessing water quality of a water body such as Segment 1245 is the hydrology of the system. There are two distinct hydrologic reaches within the Upper Oyster Creek segment. The upper reach extends from the GCWA Shannon Pump Station on the Brazos River to Dam #3 within the City of Sugar Land. The lower reach begins at Dam #3 and continues downstream through Steep Bank Creek to its confluence with the Brazos River.

Hydrology of the upper reach is highly variable and has been modified by seasonal pumping of water into the segment from the Brazos River. The GCWA uses the reach above Dam #3 as a section of its Canal System A, which supplies water for irrigation, industrial, and public drinking supply to areas southeast of the watershed, in addition to uses in the vicinity of the City of Sugar Land. Canal System A is operated by the GCWA in tandem with Canal System B, located south of the Upper Oyster Creek watershed. To serve as a conveyance for the pumped water, Jones Creek and the portion of Oyster Creek above Dam #3 have been dredged to provide adequate capacity. The hydrologic modifications also include a diversion structure that allows the water pumped from the Brazos River into Jones Creek to be diverted into Oyster Creek, and the presence of three small dams or retention structures operated by the GCWA.

The discussion of these small dams and their operation is taken from Kolbe (1992) and personal observations by TIAER staff. Each retention structure is constructed of concrete with slots for horizontally placed wooden boards, which may be added or removed to control water level. The dams form impoundments to maintain nearly constant water levels for industrial and recreational uses and off-channel lakes that create “lakefront” property with commensurate aesthetic and monetary value. Dam #2 stores water for industrial use and forms Brooks and Cleveland Lakes. Dam #3 retains water for Alkire, Eldridge, and Horseshoe Lakes, and also serves to retain water for the GCWA Second Lift Station where water is pumped into the American Canal for transport to the Texas City area.

Hydrology of the reach below Dam #3 is highly impacted by the presence of Dam #3 and the Second Lift Station. Small amounts of seepage do occur through Dam #3, and there is uncontrolled excess rainfall runoff over the dam into the lower reach. The Second Lift Station, however, operates under most wet-weather conditions to capture portions of the rainfall-runoff, which reduces the amount released below Dam #3. This reach, therefore, contains no retention structures, and is characterized by reduced flow composed of seepage from Dam #3, contributions from municipal dischargers, natural contributions from the drainage area below Dam #3, and excess rainfall runoff from the upper reach above Dam #3. The reach below Dam #3, however, is also hydrologically modified, though not for conveyance of water supplies and impoundment of water, but rather for flood prevention. These modifications result in

Oyster Creek being diverted into Flat Bank Creek and then into Steep Bank Creek via a diversion channel. These confluences and connections are not a result of natural stream conveyance and hydrologic conveyance patterns, but as stated previously, serve the utility of flood flow conveyance.

Data from GCWA Shannon Pump Station and the Second Lift Station were evaluated for trends and general characteristics for the period 1986 through 2000. The records for the Shannon Pump Station were used to indicate general conditions of water demands supplied through Canal System A. Records from the Second Lift Station were used to characterize monthly hydrologic conditions in the upper reach of Upper Oyster Creek, because some, though not all, rainfall runoff is captured and pumped from that station. The hydrologic conditions and pattern reflected in the records of the Second Lift Station provide more accurate estimates of flow conditions for the reach above Dam #3 than do the records of the Shannon Pump Station; therefore, those records will be used in comparison with water quality data.

Data for the Second Lift Station indicate that the pumped flow increases through the spring (between 1,000 to 3,000 acre-feet per month [ac-ft/m] on average) to a maximum in July. Pumped flow decreases through the fall and winter to its lowest average rate of 1,325 ac-ft/m in February. Average annual pumped flow through the segment is over 50,000 acre-feet per year. A minimum of 28,889 ac-ft per year were pumped in 1997, and a maximum of 69,670 ac-ft per year were pumped in 1995. Historical flow data from the U.S. Geological Survey (USGS) station 08112500 suggest similar characteristics and patterns of pumped flow, for a period from 1931 to 1973. Seasonal high flow was observed in the USGS data for the months of April through September while lower flow is noted in March and October. A period of reduced flow is indicative of the months of November through February.

The hydrology of the reach above Dam #3 may be impacted if Sugar Land, Missouri City, Fort Bend Water Control and Improvement District (WCID) No. 2, and the western portions of the City of Houston continue with plans to reduce their total reliance on ground water for public water supply and supplement demand with surface water from the Brazos River. In a study for the GCWA and Texas Water Development Board (TWDB), a feasibility study by Montgomery Watson America, Inc. (2000) for a regional surface water treatment plant for Brazoria, Fort Bend, and west Harris counties indicated a two-fold need to supplement groundwater with surface water. First, groundwater pumpage was causing subsidence, which can greatly increase flooding, and second, large population growth in the area may exceed reliable groundwater supplies. Discussions by TIAER staff with both GCWA and the City of Sugar Land in 2001 indicated that a facility to supply surface water from the Brazos River is still being considered, though the exact timeframe, size, and location of the facility are unknown. However, any plans for a facility to supply surface water from the Brazos River appear to have hydrologic implications to the upper reach of Upper Oyster Creek. The exact location of the water treatment plant would determine how much of the reach above Dam #3 would be directly impacted. The size of surface water treatment plant being considered could be as large as 150 million gallons per day (MGD) (maximum of 13,800 ac-ft/m), and conveyance would occur through Jones Creek and Oyster Creek, perhaps all the way to the Second Lift Station. Not only could the amount of additional flow in the upper reach of

Segment 1245 be substantial, the historical seasonal component would be modified because of the water needs of municipalities are more constant than agricultural needs.

In summary, the hydrology of Segment 1245 is anthropogenically modified. There is a seasonal pattern of pumping water from the Brazos River into the reach of Upper Oyster Creek above Dam #3. Peak pumping occurs in the summer and minimum pumping occurs in the winter, which reflects the water demands for irrigation purposes and the use of the upper reach as conveyance for these water demands. Increasing municipal demands from rapid urbanization in the entire region west and south of the City of Houston compounded by needs to supplement the present exclusive use of groundwater with surface water could, over time, change this seasonal water pumping pattern to one with a less pronounced seasonal pattern.

The Upper Oyster Creek watershed lies within a climatic region classified as subtropical humid, which is defined as having hot summers and dry winters. An average annual rainfall of 49.3 inches was measured at Sugar Land airport between 1970 and 2000 (NOAA, 2004). Over this same period, rainfall events of 0.1, 0.5, and 1 inch of rain were observed on average 64, 31, and 16 days per year, respectively. The Upper Oyster Creek watershed is within the upper portion of the Gulf Coast Prairies and Marshes ecoregion, an area characterized as containing nearly level, undissected plains with native vegetation types composed of tall grass prairie and post oak savanna. The elevation of the area is approximately 25 meters above mean sea level.

2.2 Review of Historical Fecal Coliform Monitoring Data

2.2.1 Data Acquisition

Investigations of historical water quality data, which involved evaluation of past and recent water quality data from Upper Oyster Creek, were performed. Data sources investigated included the TCEQ Texas Regulatory Activity and Compliance System (TRACS) database.

General assessment criteria methodologies established by TCEQ were used in data evaluations to determine the percentage of samples exceeding adopted criteria or screening levels for a water body.

2.2.2 Water Quality Assessment

Analyses of historical data were conducted by separating the data period 1988-2003 into two subsets, 1988-2001 and 2002-2003. For most monitoring stations, the majority of data was taken beginning in 1988 to the present, hence, the beginning date of 1988. More current data are discussed in the subset of 2002-2003.

2.2.3 Analysis of Bacteria Data

Nearly all fecal coliform bacteria data originate from three TCEQ stations– Station 12086, Oyster Creek at State Highway (SH) 6, Station 12083, Oyster Creek at Highway 90, and Station 12079, Oyster Creek at Highway 59. Refer to Figure 2-1 for specific station locations. Station 12083 is the only station for which data are available from 1970 to the

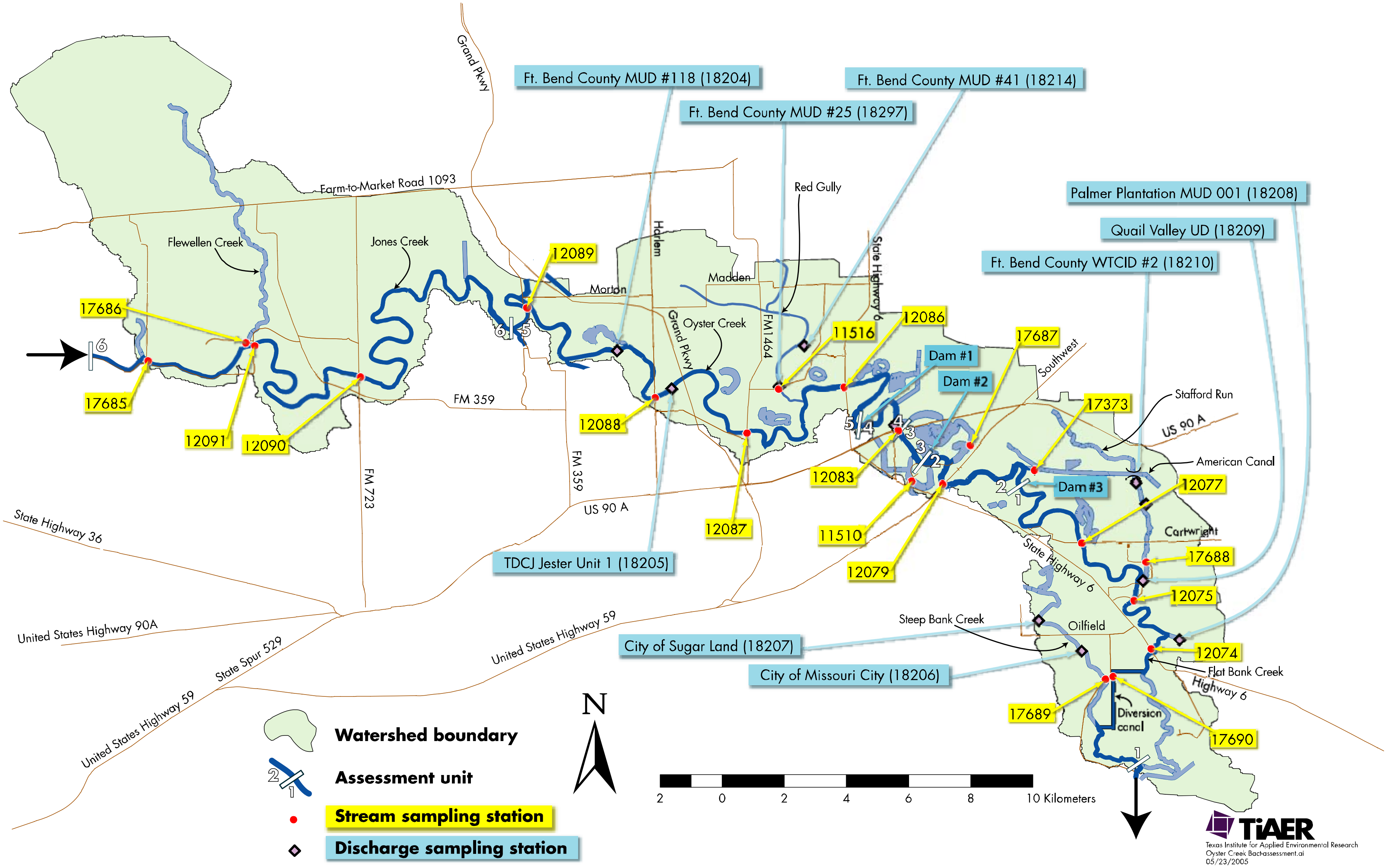

Figure 2-1 Upper Oyster Creek showing stations for bacteria sampling of Oct. 2002 – Aug. 2003 (Wastewater treatment plants operating during the time of monitoring are also shown on the map.)

present. There were occurrences of extremely high counts of bacteria at this station in the 1970s which have not occurred in the more recent data. The most downstream station, 12079, has less frequent excursions of fecal coliform above 400 cfu /100 ml; however, the data are also sparser at this station than at the other two stations.

Most of the fecal coliform data were collected in the impoundment area of Segment 1245. These bacterial data generally support the section 303(d) listing of the segment for nonsupport of the contact recreation use (Table 2-1), as fecal coliform concentrations above the criterion of 400 cfu/100 ml occurred at a frequency of greater than 25 percent at one site.

Table 2-1 Historical fecal coliform exceedances, 1988-2001

Oyster Creek (1988-2001)		
Station	**No. of Samples 1988-2001**	**% Exceedance Fecal coliform (cfu/100ml)**
12086	57	25%
12083	59	31%
12079	27	11%

The 2002 Texas Water Quality Inventory and 303(d) list indicated that the standard for the segment from Highway 90A to Dam #1, located 1.5 miles upstream of Harmon Street, was *not met* for contact recreational use. A *use concern* from Dam #1 to the confluence of Oyster Creek and Jones Creek was also listed. Table 2-2 lists the bacteria results for stations located in Segment 1245 as well as results from various tributaries and lakes for 12 survey events conducted during the time period of October 2002 to August 2003 (see Figure 2-1 for sampling station locations). In both groupings (mainstem, and tributary and lake) in Table 2-2, stations occur in an upstream to downstream direction. These survey events were performed by TIAER and were specifically designed to assist in assessment of the level of support of contact recreation use for Segment 1245. Appendix A contains the fecal coliform and *E. coli* data summarized in Table 2-2 for both mainstem Upper Oyster Creek and some major tributaries and lakes. The appendix also includes ancillary data collected with the bacteria data.

For the mainstem stations on Upper Oyster Creek, the geometric mean for fecal coliform should not exceed 200 cfu/100 ml. All stations exceeded the criteria during the time period from October 2002 to August 2003 except for Stations 17685, 12079, 17373, and 12077. The fecal coliform results for mainstem stations that exceeded the geometric mean criterion were between slightly over the exceedance criterion to 710 cfu/100 ml. The percent exceedance criteria is 42 percent (or the minimum number of samples in exceedance is 5) when the sample size is 12 as in this study (see assessment guidance TCEQ 2003a).[1] All stations on the mainstem ranged from 17 percent to 70 percent exceedance for fecal coliform. For the tributaries and lakes monitored, tributary Stations 17686, 17688, and 17689 exceeded the criteria for fecal coliform. For Stations 11516, 11510, and 17687, the geometric means for fecal coliform were 142, 83 and 66 cfu/100 ml, respectively. The percent exceedances for fecal coliform on the tributaries and lakes ranged from 17 percent to 82 percent.

Table 2-2 Historical fecal coliform and *E. coli* geometric mean concentration and percent exceedances, 2002-2003*

<table>
<tr><th colspan="5">Oyster Creek (2002-2003)</th></tr>
<tr><th>Station</th><th>Fecal coliform (cfu/100ml) geometric mean</th><th><i>E. coli</i> (cfu/100ml) geometric mean</th><th>% Exceedance Fecal coliform (cfu/100ml)</th><th>% Exceedance <i>E. Coli</i></th></tr>
<tr><td>17685, Jones Cr. at Bois D'Arc Ln.</td><td>102</td><td>75</td><td>17</td><td>8</td></tr>
<tr><td>12091, Jones Cr. at Winnerfoster Rd.</td><td>470</td><td>363</td><td>45</td><td>42</td></tr>
<tr><td>12090, Jones Creek at FM 723</td><td>452</td><td>427</td><td>33</td><td>58</td></tr>
<tr><td>12089, Oyster Cr. at Precinct Line Rd.</td><td>414</td><td>364</td><td>42</td><td>50</td></tr>
<tr><td>12088, Oyster Cr. at Harlem Road</td><td>454</td><td>293</td><td>42</td><td>42</td></tr>
<tr><td>12087, Oyster Cr. at FM 1464</td><td>427</td><td>301</td><td>50</td><td>50</td></tr>
<tr><td>12086, Oyster Cr. at Hwy 6</td><td>238</td><td>154</td><td>33</td><td>42</td></tr>
<tr><td>12083, Oyster Cr. at US Hwy 90A</td><td>560</td><td>333</td><td>33</td><td>33</td></tr>
<tr><td>12079, Oyster Cr. at US Hwy 59</td><td>80</td><td>65</td><td>17</td><td>18</td></tr>
<tr><td>17373, Oyster Cr. at Amer. Canal</td><td>79</td><td>58</td><td>18</td><td>8</td></tr>
<tr><td>12077, Oyster Cr. at Cartwright Rd.</td><td>160</td><td>104</td><td>36</td><td>25</td></tr>
<tr><td>12075, Oyster Cr. at Glen Lakes Dr.</td><td>710</td><td>948</td><td>44</td><td>58</td></tr>
<tr><td>12074, Flat Bank Cr. at Hwy 6</td><td>690</td><td>512</td><td>70</td><td>67</td></tr>
<tr><td>17690, Diversion Canal</td><td>423</td><td>417</td><td>50</td><td>50</td></tr>
<tr><th colspan="5">Tributaries and Lakes (2002-2003)</th></tr>
<tr><th>Station</th><th>Fecal coliform (cfu/100ml) geometric mean</th><th><i>E. coli</i> (cfu/100ml) Geometric mean</th><th>% Exceedance Fecal coliform</th><th>% Exceedance <i>E. Coli</i></th></tr>
<tr><td>17686, Flewellen Creek at Briscoe Rd.</td><td>1182</td><td>943</td><td>67</td><td>67</td></tr>
<tr><td>11516, Red Gully at Richmond-Gaines Rd.</td><td>142</td><td>98</td><td>42</td><td>42</td></tr>
<tr><td>11510, Brooks Lake at Fluor Daniel Dr.</td><td>83</td><td>59</td><td>25</td><td>17</td></tr>
<tr><td>17687, Alkire Lake at Alkire Lake Dr.</td><td>66</td><td>52</td><td>17</td><td>9</td></tr>
<tr><td>17688, Stafford Run at El Dorado Blvd.</td><td>1694</td><td>906</td><td>82</td><td>58</td></tr>
<tr><td>17689, Steep Bank Cr. At Thompson Ferry</td><td>819</td><td>522</td><td>73</td><td>58</td></tr>
</table>

*12 samples were collected at each station, though a few stations have less fecal coliform data (10 or 11 values).

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[1] The TCEQ applies the binomial method to establish the required number of exceedances to indicate nonsupport of contact recreation use. To determine nonsupport (i.e., greater than 25% of samples exceed the relevant criterion) and to keep the percent probability at less than 20% of inappropriately assessing a water body as not supporting when it is actually fully supporting, a minimum of 5 samples must be in exceedance for a sample size of 12; an exceedance of 42%.

For the mainstem stations on Upper Oyster Creek, the geometric mean for *E. coli* should not exceed 126 cfu/100 ml. All stations that exceeded the criteria for fecal coliform also exceeded the criteria for *E. coli* during the same time period. All other stations exceeded the criteria between slightly over the exceedances to 948 cfu/100 ml. The percent exceedances for all mainstem stations ranged from 8 percent to 67 percent. For the tributaries and lakes, Stations 17686, 17688, and 17689 exceeded the geometric mean criterion with concentrations of 943, 906, and 522, respectively. The *E. coli* geometric mean results for Stations 11516, 11510, and 17687 were between 98, 59, and 52 cfu/100 ml, respectively. The percent exceedances for the tributaries and lakes ranged from 9 to 67 percent for *E. coli.*

The findings of this data collection support the State of Texas 2002 303(d) listing of Upper Oyster Creek (Segment 1245) as impaired from the presence of fecal pathogen indicator bacteria and nonsupport of contact recreation use. Some stations would meet the pertinent bacteria criteria under dry weather conditions, though the very high *E. coli* levels observed under rainfall-runoff events combined with the frequency of rainfall in the watershed results in consistently high indicator bacteria levels. Typically, the highest *E. coli* levels were observed in several tributaries of Oyster Creek, including Stafford Run and Flewellen Creek. Red Gully exhibited very low *E. coli* levels under dry weather conditions, probably due to the discharge of chlorinated municipal WWTP effluent, and very high *E. coli* levels under runoff conditions. Generally low levels of *E. coli* were indicated in the waters pumped from the Brazos River as shown at the most upstream sampling station in Segment 1245 (Station 17685). *E. coli* levels tended to be lower in the broad-channeled impounded reaches of Oyster Creek (Stations 12079 and 17373), where the resulting low water velocities may permit settling of *E. coli* from the water column to sediments. In fact in the impounded reaches, fecal coliform and *E. coli* data indicated support of the contact recreation use except at the more upstream extremity of these reaches (i.e., Station 12083).

2.3 Potential Sources of Fecal Indicator Bacteria

2.3.1 Permitted Wastewater Discharges

Under the Texas Pollution Discharge Elimination System (TPDES), 15 facilities within Segment 1245 hold permits to discharge wastewater (Table 2-3). Two additional facilities hold permits without provisions that allow discharge of wastewater—the Texas Department of Criminal Justice (TDCJ) holds a permit for a confined animal feeding operation (CAFO) with land application of solid and liquid waste and Bono Brothers, Inc. holds a permit for beneficial land application of sewage sludge and domestic septage. For completeness these two facilities are also included in Table 2-3. Finally, Hines Horticulture, in addition to holding a permit for discharge of a small amount of treated human waste, also holds a permit to discharge storm/irrigation waters. All entities holding active TPDES discharge permits are domestic wastewater (sewage) treatment facilities. From approximately 2000 to mid-2004, the reported average daily domestic wastewater discharge to Upper Oyster Creek was 11.9 MGD, which is well below the permitted daily flow of 31.9 MGD. A number of facilities have become operational since 2004 and no monitored discharge information is provided for these facilities. Increasing discharge limits for some municipal permittees within the segment and adding new

Table 2-3 Permitted operations in Upper Oyster Creek watershed

TPDES Permit No.	Facility	Dates Monitored	Monthly Average Discharge (MGD)	Final Permitted Discharge (MGD)	Selected Permit Requirements on Final Permitted Discharge	
					Report Fecal Coliform Bacteria	Disinfection Requirement[6]
WQ003742	Bono Brother's Inc. (Sludge)[1]	NA	NA	NA	NA	NA
WQ0013873-001	City of Missouri City	12/31/99-6/30/04	0.69	3.0	Yes (includes effluent limits)	Chlorination & Dechlorination
WQ0012833-002	City of Sugar Land	1/31/00-6/30/04	4.61	10.0	No	Chlorination & Dechlorination
WQ0012003-001	Fort Bend County MUD # 25	9/30/99-7/31/04	0.42	1.6	Yes	Chlorination & Dechlorination
WQ0012475-001	Fort Bend County MUD # 41	11/30/99-5/31/04	0.25	0.86	No	Chlorination
WQ0013951-001	Fort Bend County MUD # 118	8/31/00-5/31/04	0.064	1.2	No	Chlorination & Dechlorination
WQ0014715-001	Fort Bend County MUD # 134[2]	NA[3]	—	0.30	No	Chlorination
WQ0014408-001	Fort Bend County MUD # 142	NA[3]	—	1.2	No	Chlorination & Dechlorination
WQ0014692-001	Fort Bend County MUD # 182	NA[3]	—	0.8	No	Chlorination
WQ0010086-001	Fort Bend County WCID #2	1/31/00-7/31/04	3.52	6.0	No	Chlorination & Dechlorination
WQ003015-000	Hines Nurseries Inc.[4]	NA[3]	—	0.0035	No	None
WQ0012937-001	Palmer Plantation MUD 001	11/30/99-6/30/04	0.29	0.60	No	Chlorination
WQ0011046-001	Quail Valley UD	1/31/00-7/31/04	1.77	4.0	No	Chlorination & Dechlorination
WQ0014100-001	Sienna Plantation MUD # 1	NA[3]	—	0.902	No	Chlorination
WQ0014064-001	Stafford Mobile Home Park, Inc.	NA[3]	—	0.10	No	Chlorination
WQ0011475-001	TDCJ Jester Unit # 1 – WWTF	5/31/01-2/29/04	0.27	0.315	No	Chlorination
TXG920522[5]	TDCJ Jester (Swine CAFO) [1]	NA	NA	NA	NA	NA
Total			11.9	31.9		

Notes: [1] Permit does not contain a discharge provision

[2] Pending permit as of Oct. 2, 2006 (Ft. Bend Co. MUD # 134)

[3] New permit or not operational during period of dates monitored (1999-2004)

[4] Permit also includes storm water discharge not to exceed 1.0 MGD

[5] Concentrated Animal Feeding Operation (CAFO) general permit number

[6] An equivalent method of disinfection may be substituted with approval from TCEQ and only chlorination (no dechlorination) is required for facilities operating under a capacity of 1 MGD

NA = Not applicable; MGD = million gallons per day discharge permits in recent years indicate a steadily increasing wastewater input into the segment commensurate with the rapid urbanization of the watershed.

The City of Sugar Land and Fort Bend County WCID #2 permits allow the largest discharge of the wastewater facilities at over 5 MGD each. The other wastewater facilities with permitted wastewater discharges of greater than 1 MGD are Quail Valley Utility District, Missouri City, and Fort Bend County MUDs #s 25, 118, and 142. Most of the wastewater permits do not include specific limits and monitoring requirements for fecal coliform concentrations in their effluents. With the exception of Hines Nurseries, all permitted facilities are required to disinfect their effluents (Table 2).

In 2001 TIAER staff reviewed the TPDES permit files to identify enforcement actions or other persistent problems with permitted discharge facilities within Segment 1245. This review was updated in 2005 by reviewing the discharge monitoring reports (DMR) from the Permit Compliance System (PCS) downloaded from the USEPA Envirofacts Data Warehouse (USEPA, 2005). No enforcement actions were uncovered in the screening; however, some self-reporting, operation, and administration violations were noted in the files. The TDCJ facility has had some minor violations regarding uncertified personnel, operational requirements, and final effluent limitations; however, these violations surfaced during an annual inspection and were completely resolved within the required time frame. The TDCJ facility underwent a $4.5 million expansion during 2001-2002. Imperial Sugar Corporation resolved a recurring violation on the annual certification of accuracy for pumping capacity used to measure flow, which was observed on biannual inspections in 1996 and 1998, though this facility has ceased operation and discharge since late in 2003. Of potential relevance to this study was a violation of the fecal coliform bacteria daily maximum, 7-day average, and daily average criteria by Missouri City in August 2000. The problem occurred due to an off line aerator that had accumulated a large amount of settled solids. Solids were redistributed throughout the plant when the unit was restarted, causing poor effluent quality. The problem was resolved immediately, and subsequent fecal readings indicated no long-term concerns. No other fecal coliform effluent quality violations were reported since that time.

Because efforts to improve water quality problems have a long history in Upper Oyster Creek, a number of significant changes and improvements have occurred with likely results of improved water quality. Kolbe (1992) reports 1) the City of Sugar Land wastewater treatment plant (WWTP) discharge was moved to its present location in 1975; 2) the Hines Horticulture direct discharge was removed in 1990 and reduced to stormwater overflow releases; and 3) wastewater treatment of the TDCJ units has improved and feedlot runoff is better managed. After June 1996, Imperial Sugar's major discharges were delivered to the Brazos River Authority (BRA) regional WWTP for treatment and subsequent discharge outside the watershed and, as previously mentioned, has totally ceased any discharge into Oyster Creek since 2003. Kolbe (1992) states that from 1987 through 1990, Imperial Sugar discharged an average of 17 to 21 MGD of wastewater at elevated temperature, which was allowed in their permits.

The National Pollutant Discharge Elimination System Phase II rule, promulgated in 1999, requires small municipalities in urban areas to obtain permits for their stormwater systems.

These permits, known as Municipal Separate Storm Sewer System (MS4) permits, require cities to reduce discharges of pollutants in stormwater to the "maximum extent practicable" by developing and implementing a Stormwater Management Program (SWMP). The SWMPs require specification of BMPs for six minimum control measures:

- Public education and outreach;
- Public participation/involvement;
- Illicit discharge detection and elimination;
- Construction site runoff control;
- Post-construction runoff control; and
- Pollution prevention/good housekeeping.

Most of the eastern half of the Upper Oyster Creek watershed would be covered under these permits, including the cities of Missouri City, Stafford, and Sugar Land. The cities and any other affected parties will likely obtain coverage during 2007 under a General Permit for stormwater discharges, once the permit is promulgated by TCEQ. This program may positively impact water quality in Upper Oyster Creek.

2.3.2 Land Use

The Upper Oyster Creek watershed covers approximately 110 square miles, approximately 12.5 percent, of the area of Fort Bend County. Based on 1996-97 Landsat Thematic Mapper imagery identification performed by Baylor University much of the watershed is in pasture lands, though the residential and urban land uses comprised 24 percent at that time (Table 2-4; Baylor University 1997). Undoubtedly because of rapid population growth, an even greater percentage of the watershed is in residential and urban land use in 2006 than roughly 10 years ago.

Table 2-4 Land use in Upper Oyster Creek watershed in 1996-97 (Baylor, 1997)

Land use	Area (%)
Forest	7.2
Pasture	56.1
Range land	9.5
Residential	10.7
Urban (Mixed)	13.3
Water	3.2

2.3.3 Population Density: Humans and Pets

The population of the Upper Oyster Creek watershed in 2000 was estimated to be 96,273 (31,573 households) with an overall average population density of 877 persons per square mile (U.S. Census Bureau, 2000). The population of Fort Bend County is estimated by the U.S. Census Bureau to have increased approximately 6 percent per year since the 2000 census, so the current (2005) population may exceed 125,000. Approximately 28,000 cats and 25,000 dogs are also estimated to reside with households within the watershed, based on the 2000 census data along with national averages of pets per household from the American Veterinary Medical Association (2002).

Fort Bend County is expected to increase in population by approximately 78 percent from 2000 to 2020, according to the TWDB (TWDB, 2006). As a result, the county expects significant increases in water demand for municipal purposes (65% increase). Smaller increases are expected for manufacturing (17%), mining (8%), and steam electric (10%) uses. Table 2-5 sets out TWDB population growth estimates for selected cities within Fort Bend County from 2000 to 2020.

The population estimates for Sugar Land are held constant after the year 2010 because the city is expected to be completely built-out by this date. Conversations with TWDB staff confirmed that previous TWDB estimates were made in error and did not account for the built-out issue. However, TWDB estimates may not account for future annexations that could occur. Annexations were used to drive population growth in the 1990s. The 2000 census figures indicate a 158 percent increase in the population of Sugar Land since 1990.

Table 2-5 Fort Bend County population and projected increases by city, 2000 to 2020

City	2000 Census Population	2010 Population	2020 Population	Growth Rate (2000-2020)
Fulshear	716	883	1,056	47%
Missouri City	47,419	76,768	96,601	104%
Stafford	15,371	23,026	30,959	101%
Sugar Land	63,328	72,500	72,500	14%

Source: TWDB (2006).

2.3.4 Sewered and Non-Sewered Areas

The method of sewage disposal for housing units in the Upper Oyster Creek watershed was estimated from the 1990 federal census at the block group level because these data were not collected in the 2000 census (U.S. Census Bureau, 1990). Because of rapid urbanization in the watershed, estimates based on those data may no longer be accurate. At that time, approximately 6 percent of households in the watershed utilized septic tanks for sanitary waste disposal, while 93 percent were connected to a sanitary sewer system. Approximately 1,400 housing units in the watershed were reportedly not connected to a sanitary sewer system. The more rural western half of the watershed was primarily served by septic tanks; however, the highest density of septic tanks was in two areas: the Fifth Street area, bounded roughly by Cartwright Road on the south, American Canal on the north and east, and farm-to-market (FM) Road 1092 on the west, and the Four Corners area northwest of Sugar Land, bounded by SH 6 on the east, Old Richmond Road on the west, Voss Road on the south, and Boss-Gaston Road on the north. The density of septic tanks in these two areas ranged from approximately 0.2 to 0.3 per acre.

2.3.5 Livestock Populations

The smallest unit for which livestock census data are available is the whole of Fort Bend County, which indicate beef cattle to be the dominant livestock species in the watershed (Table 2-6). Other livestock species present in the watershed include horses, goats, chickens, and hogs. Livestock populations were estimated from the 2002 agricultural census of the National Agricultural Statistics Service of the U.S. Department of Agriculture, or from more recent estimates of the Texas Agricultural Statistics Service, when available.

Table 2-6 Estimated potential source populations in Fort Bend County

Category	Livestock	Fort Bend County	Estimated Watershed Population
Human	Census	—	128,000[#]
Pets	Cats	—	28,000*
Pets	Dogs	—	25,000*
Livestock	Cattle & Calves-All	51,000 [†]	6,375
Livestock	Beef cows	35,000 [†]	4,375
Livestock	Milk cows	0 [‡]	0
Livestock	Horses	3,400 [‡]	425
Livestock	Mules, burros, & donkeys	116 [‡]	14
Livestock	Hogs & Pigs	1,367 [‡]	171§
Livestock	Goats-all	1,400 [†]	175
Livestock	Sheep & Lambs	622 [‡]	78
Livestock	Rabbits	311[‡]	39
Livestock	Bison	27 [‡]	3
Livestock	Domestic Deer	82 [‡]	10
Livestock	Chickens	2,226 [‡]	278
Livestock	Ducks-Domestic	172 [‡]	22
Livestock	Geese-Domestic	390 [‡]	49
Livestock	Turkeys-Domestic	49 [‡]	6
Livestock	Pheasants-Domestic	220 [‡]	28
Livestock	Quail-Domestic	1,382 [‡]	173
Livestock	Emus	47 [‡]	6
Livestock	Other poultry*	200 [‡]	25

[#] projected based on 2000 federal census and annual growth rate of 6%
* From *2002 U.S. Pet Ownership & Demographics Sourcebook*, American Veterinary Medical Association
[†] As of January 1, 2004 Texas Agricultural Statistics Service
[‡] 2002 Agricultural Census, USDA
[§] Probably an underestimate, based on observed population at prison farm

2.4 Summary of Sanitary Survey Observations

A sanitary survey to identify potential bacteria sources within the Upper Oyster Creek watershed was performed from May 3 to 5, 2004 by the Parsons sampling team. Fecal sampling was also performed as part of the survey when scat samples were observed.

The most evident feces observed adjacent to water bodies in urban areas were from waterfowl, specifically ducks and geese. A large number of Muscovy ducks were observed in central portions of the watershed, particularly in the many residential lake areas. This species is a non-native resident, often domesticated, and frequently white or white and black with a red bulbous bill. Duck fecal matter was very dense along the banks of impounded Oyster Creek at the Fluor-Daniel Road. Black-Bellied Whistling Ducks were also observed to defecate at this same location. Fecal samples of each were collected.

Pigeons and swallows were observed to be nesting on bridges over Oyster Creek at a number of locations, and perching on utility lines over the creek. Their dried fecal matter caked portions of the bridges. The swallows were only observed during the summer months. Other common birds in and near the creeks included several species of herons and egrets.

In rural areas, cattle and raccoon feces were observed the most. Cattle feces were more widespread and more abundant than others. Cattle were observed to be numerous in the western half of the watershed. Brangus and Limousine appeared to be the most abundant cattle breeds. Abundant raccoon feces were observed adjacent to smaller more sheltered waterways. It was observed during the March fecal sampling event that the raccoon diet appeared to consist mostly of blackberries, but crayfish parts littered the banks of these smaller water bodies as well. Road kill indicated the expected fauna of southeast Texas, including skunks, raccoons, armadillos, and opossum.

The Fifth Street and Four Corners areas of the watershed have mobile homes and other homes with poor-quality septic systems. At the time of the sanitary survey, no failing septic systems were observed; however, communications with various local entities confirmed that some problematic areas exist in both areas. Approximately two dozen chickens were observed throughout the neighborhoods within these areas.

Hog waste at the Jester Unit of the TDCJ was managed in three consecutive passive treatment lagoons. The pig housing was very clean at the time of the site visit, making sample collection difficult, but successful. No connection was noted between the lagoons and the adjacent Oyster Creek. The land on which the farm was located sloped away from the creek, but drained into a swale that appeared to curve around the hog area to the north and back of the creek.

SECTION 3

BACTERIAL SOURCE TRACKING STUDY

3.1 Objectives and Methods

3.1.1 Fundamentals of Bacterial Source Tracking and Ribotyping

The BST method is based on two principles. The first is that the bacterial population genetic structure is clonal, a well-established element of microbial genetics. Bacteria reproduce by binary fission, or dividing in half, and the two daughter cells generated as a result of this cell division are virtually identical in all aspects. All descendents of a common ancestral cell are genetically related to each other. Over time, members of a given clone may accumulate genetic changes which will cause them to diverge from the main lineage and form one or several new clonal groups. BST makes use of the clonal population structure of bacteria to classify organisms into groups of clonal descent based on their genetic fingerprints.

The second principle of BST methodology is the assumption that within a given species of bacteria, various members have adapted to living/environmental conditions in specific hosts/environments. As a result, there is a high degree of host specificity among bacterial strains that are seen in the environment. A bacterial strain that has adapted to a particular environment or host (*e.g.*, animal intestinal tract) is capable of colonizing that environment and competing favorably with members of the hosts' indigenous flora. Such a bacterial strain is called a resident strain. Resident strains are usually shed from their host over a long period of time, thus providing a reliable, characteristic signature of their source. A transient strain is a bacterial strain that is introduced into a new environment or host but cannot colonize and persist in that environment. If a host is sampled over time for a given species of bacteria, a few resident strains are consistently being shed while a large number of transient strains are shed for brief lengths of time. A study conducted by Hartl and Dykhuizen (1984) illustrates this point. Over a period of 11 months, 22 fecal samples were taken from a single individual. A total of 550 *E. coli* isolates were characterized, of which two were considered to be resident strains, appearing 252 times. Data show that using this subtyping method (rRNA typing using two restriction enzyme reactions), more than 96 percent of *E. coli* strains are seen in only one host species (or group of related species) (Mazengia 1998). Thus, it appears that only about 4 percent of the *E. coli* strains are transient and not attributable to one specific source.

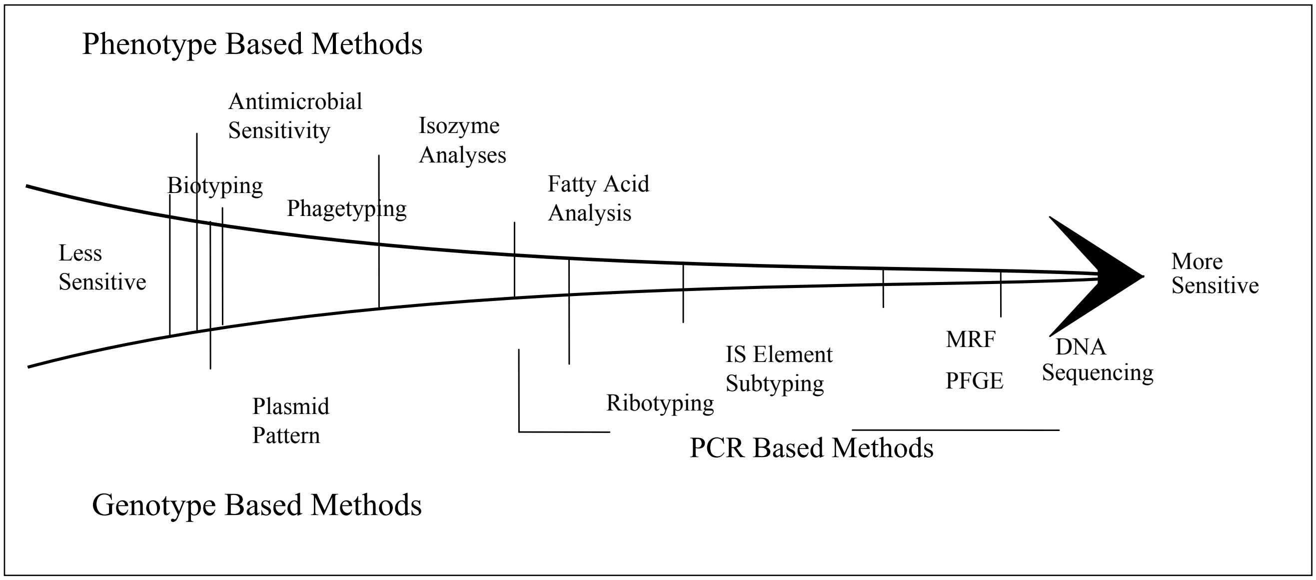
The key methodological problem in tracing sources of microbial contamination in the environment has been the lack of a universal single-reagent typing scheme for bacteria. This was overcome by the work of several investigators in the fields of population genetics, molecular systematics, and molecular epidemiology. In 1986, Grimont *et al*. showed that DNA probes corresponding to specific regions of the rRNA operon could be used to speciate bacteria. Stull *et al*. (1988) and Lipuma *et al*. (1988) used the rRNA operon to study the molecular epidemiology of several species of bacteria. To trace the indicator bacterium, *E. coli*, from water to its specific source, the bacterial strain must first be uniquely identified. Populations of *E. coli*, like other bacteria, are composed essentially of a mixture of strains of clonal descent. Due to the relatively low rates of recombination, these clones remain more or less independent (Selander *et al.* 1987). These clones, or strains of bacteria, are uniquely adapted to their own specific environments. As a result, the *E. coli* strain that inhabits the intestines of one species is genetically different from the strain that might inhabit another.

Ribosomal ribonucleic acids, which are integral to the machinery of all living cells and tend to be very highly conserved, make an ideal choice of target in interstrain differentiation. Since the *E. coli* chromosome contains seven copies of the rRNA operon, a ribosomal nucleic acid probe can be used as a definitive taxonomic tool (Grimont *et al.* 1986). That is, when digested with restriction enzymes, resolved by agarose gel electrophoresis, transferred to a membrane and hybridized with an rRNA probe, an *E. coli* chromosome will produce several bands to create a specific restriction fragment length polymorphism (RFLP) pattern that can be used to uniquely identify the bacterial strain.

The pattern of DNA fragments corresponding to the rRNA operon is referred to as the ribotype. Ribotyping has been useful in many studies to differentiate between bacterial strains that would have otherwise been difficult or impossible to distinguish. Fisher *et al.* (1993) followed the transmission of *Pseudomonas cepacia* from environmental sources to and between cystic fibrosis patients and discovered the majority of cases contracted cystic fibrosis from one of two treatment centers. Moyer *et al.* (1992) used rRNA typing to identify the Aeromonad strains responsible for several waterborne gastroenteritis episodes in a community and was able to trace the contamination to specific locations in water treatment and distribution systems. Barloga and Harlander (1991) compared several typing methods for distinguishing between strains of *Listeria monocytogenes* implicated in a food-borne illness and found that ribotyping was the preferred method due to its precision and reproducibility. Atlas *et al.* (1992) described the technology of ribotyping as applicable to the tracking of genetically engineered microorganisms (GEM) in the environment.

Dr. Samadpour's BST method, which was employed in this study, was developed on the basis of the principles of microbiology, epidemiology, molecular epidemiology, microbial population genetics, sanitary engineering, and hydrology. In any watershed, there are multiple contributing animal sources of microbial pollution, each of which has its own unique clones of bacteria that constitute their normal flora. Ribotyping is applied as part of a BST study in the following steps. First, collections of isolates from appropriate bacterial species are compiled from the polluted sites and the suspected animal sources of pollution, which are identified through a sanitary survey of the region surrounding the polluted site. Second, using an appropriate molecular subtyping method, all bacteria in the collection can be subtyped. Finally, the genetic fingerprints of the bacterial isolates from the polluted site are compared to those of the bacteria from the suspected animal sources. When a strain of bacteria with an identical genetic fingerprint is isolated from both a water sample and a suspected animal source, the animal is implicated as a contributor of that specific strain of the bacteria to the polluted site. The relative contributions of various sources are quantified based on the fraction of isolates from a representative set of ambient water samples that match ribotypes of resident strains from that source (human or nonhuman).

Figure 3-1 displays a conceptual sensitivity continuum of some of the widely used subtyping methods. Phenotypic based methods (methods based on the expression of phenotypes) are at the less sensitive domain of the continuum while genotypic based methods constitute the more sensitive end of the spectrum. The level of sensitivity depends on the choice of gene(s) and the size of fragment(s) sequenced.



Source: Samadpour 2001.

Figure 3-1 Microbial source tracking methods

Ribotyping was selected as the BST method for this project because it balances high source specificity with moderate requirements for library size. Pulse Field Gel Electrophoresis (PFGE), while excellent at resolving different source species, also requires a very large and expensive library due to the high variation in PFGE profiles. There is substantial uncertainty over the efficacy of antibiotic resistance analysis at distinguishing bacterial sources.

All bacterial source tracking methods, including the ribotyping used herein, are predicated on proper statistical sampling of the water body. Almost countless numbers of *E. coli* occur in the waters of Oyster Creek at any given time, and it is resource prohibitive to use ribotyping for source identification on but a few of those bacteria during any one sampling event. Through proper sampling design, however, statistically meaningful inferences can be made concerning identified sources within the watershed. Caution must be exercised so that the findings are not extended beyond their statistical validity, where, for instance, the findings for a sampling station during a single event may be misleading, but aggregation of data across multiple events or all events provides increasingly more reliable findings.

3.1.2 Study Design and Data Quality Objectives

The purpose of this study was to estimate the relative magnitude of fecal sources contributing to the observed high *E. coli* levels on the main stem and tributary stations of the Upper Oyster Creek drainageway. This project had two general objectives: (1) to assess the water quality in Upper Oyster Creek with regard to the relative contributions of fecal bacteria from human, avian, livestock, and other animal contributions, to the water bodies; and (2) to develop local genetic libraries that can be used in determining the animal or human nonpoint fecal source contamination of surface water.

This project involved several steps:

- A sanitary survey of the watershed to identify potential contributing sources of fecal microbes that needed to be considered.
- Development of libraries of ribotypes of *E. coli* isolated from fecal matter collected from known sources in the Upper Oyster Creek watershed.
- Collection and culturing of a representative set of *E. coli* isolates from Upper Oyster Creek.
- Determination of the ribotypes of these *E. coli* isolates from Upper Oyster Creek, followed by matching to those from the known source library to identify the sources of each *E. coli* isolate.
- Quantification of the accuracy and precision of the ribotyping source determinations.
- Estimation of the relative source contributions of *E. coli* in the Upper Oyster Creek watershed, and the confidence of these estimates, based on the above measurements.

3.1.2.1 Ambient Water Sampling

Ambient water sampling was performed to collect *E. coli* isolates from Upper Oyster Creek. These ambient water sampling events included 12 events, spaced approximately 3 weeks apart, beginning in March 2004 and ending in late November 2004. Originally, the monitoring plan included collecting samples for *E. coli* analysis at six stations dispersed throughout the main stem of the Upper Oyster Creek watershed and one tributary to the watershed. An amendment to the monitoring plan added three supplemental monitoring stations for the last four sampling events, beginning in September 2004, for a total of nine monitoring stations.

3.1.2.2 Monitoring Station Descriptions

Stations were selected with the objective of identifying the sources contributing to violations of water quality criteria for *E. coli* in Upper Oyster Creek. The sources contributing to *E. coli* violations were expected to vary from station to station. Given that Oyster Creek is somewhat hydrologically divided by dams and diversions into multiple reaches, most of these stations were assigned to adequately characterize various reaches and to isolate, whenever possible, major contributing areas. Stations within each reach were selected where high bacterial levels were indicated from the 2002-2003 sampling results. The lower portion of Upper Oyster Creek below Dam #3 provided challenges in station selection because of access issues in the extreme lower portion (Steep Bank and Diversion Canal portions) and the presence of Dam #3, which reduced bacteria concentrations along the portion of the sub-segment immediately below the dam. Consequently, the station selection process necessitated inclusion of a tributary station (Station 17688 on Stafford Run) in addition to a main-stem station (12074). These two stations are listed in Table 3-1 with the four other selected stations, and set out in Figure 3-2.

Three additional stations were added to the project in September 2004. These three stations were chosen to provide important supplemental data to the six core stations and to assist in the determination of the spatial distribution of *E. coli* sources. Two of the new stations were located on major tributaries to Segment 1245, while the third is located on Jones Creek, which is designated as a main stem of Segment 1245. The two tributary stations were selected and designed to be used in characterizing potential bacterial sources to the Upper Oyster Creek. The station on Jones Creek, near the Shannon Pump Station, assisted in determining sources associated with the transfer of water via pumping that occurs from the Brazos River into the Upper Oyster Creek. The station descriptions for the three additional sites are listed below the original six stations in Table 3-1. Photographs of the six main BST stations and three additional stations are provided in Appendix B. Station descriptions follow.

Table 3-1 Ambient water sampling stations

Water Body	Station ID
Jones Creek at FM 723	12090
Upper Oyster Creek at FM 1464	12087
Upper Oyster Creek at Highway 6	12086
Upper Oyster Creek at US 90A	12083
Stafford Run at El Dorado Boulevard	17688
Flat Bank Creek at Highway 6	12074
Red Gully at Richmond-Gaines Road	11516
Jones Creek at Bois D'Arc Lane	17685
Flewellen Creek at Briscoe Road	17686

* Shaded stations were added for events 9 – 12.

Station 12090 is located on Jones Creek at FM 723, 5.5 miles north of the City of Rosenberg. The station is in the upper portion of Segment 1245. The station was selected to represent bacterial sources from Flewellen Creek and water pumped from the Brazos River at the Shannon Pump Station.

Station 12087 is located on Upper Oyster Creek at FM 1464 west of Sugar Land. The station is in the middle portion of Segment 1245 and downstream from Station 12090. The station was selected to represent bacterial sources downstream of the TDCJ wastewater discharge, a CAFO, upstream of Fort Bend County municipal utility district (MUD) #21 and the confluence with Red Gully, a tributary with high bacteria concentrations during storm events.

Station 12086 is located on the Upper Oyster Creek at SH 6 near Hull Airport in Sugar Land. This station has been the focus of significant monitoring, including routine and special studies, occurring in Upper Oyster Creek since 1989. The station is in the middle portion of Segment 1245 and downstream from Station 12087. The station was selected to represent

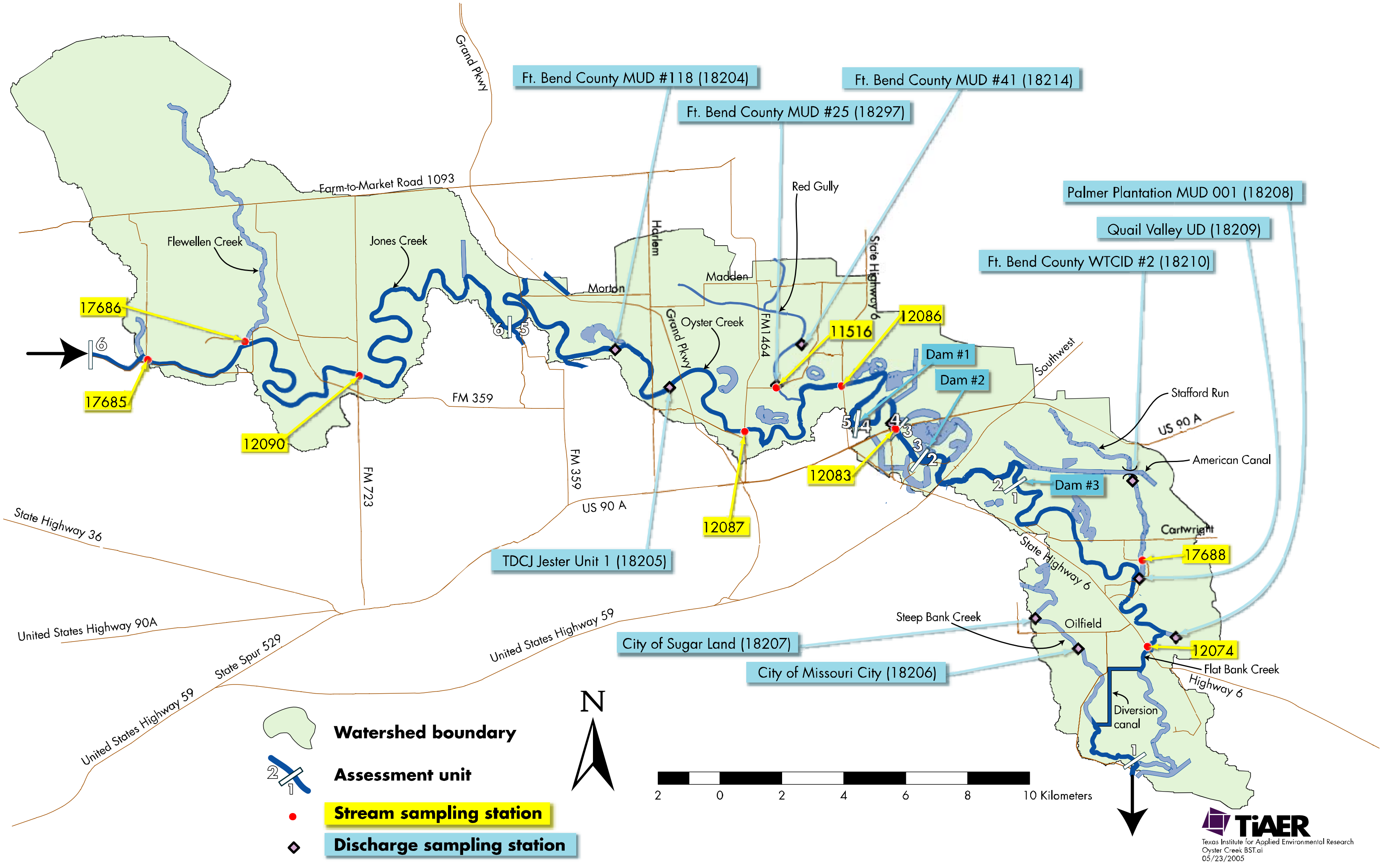


Figure 3-2 Upper Oyster Creek showing BST stations (Wastewater treatment plants operating during the time of monitoring are also shown on the map.)

bacterial sources and characterize water quality upstream of Fort Bend County MUD #25 wastewater discharge and Dam #1, below the confluence with Red Gully.

Station 12083 is located on Upper Oyster Creek at Highway 90A in Sugar Land. This station has historically been the focus of water quality monitoring in Upper Oyster Creek. Beginning in 1970, monitoring has occurred at varying frequencies at this station in support of both special studies and routine monitoring efforts. The station is in the middle portion of Segment 1245 and downstream from Station 12086. The station was selected to characterize water quality below Dam #1 and above Dam #2, as well as potential impacts from the significant number of waterfowl that frequent this stretch of river from fall to spring.

Station 17688 is located on Stafford Run at El Dorado Boulevard in Missouri City. The station was selected to characterize water quality in Stafford Run, a major tributary on the lower portion of Segment 1245. The station is in the lower portion of Upper Oyster Creek and downstream from Station 12083.

Station 12074 is located on Flat Bank Creek at SH 6 near Dewalt. The station is in the lower portion of Upper Oyster Creek and downstream from Station 17688. The station was selected to characterize bacteria sources and water quality downstream of Palmer Plantation MUD #001 in the reach of Segment 1245 below Dam # 3.

Station 11516 is located on Red Gully at Richmond-Gaines Road, 2.4 miles northwest of Sugar Land. The station is in the middle portion of Segment 1245. This supplementary station was selected to characterize water quality in Red Gully, including the impact of septic systems and two small WWTPs. Ft. Bend MUD #25 and MUD #41 are upstream of this station. Observed *E. coli* concentrations have been very high following runoff.

Station 17685 is located on Jones Creek at Bois D'Arc Lane, 3.5 miles south of Fulshear. The station is in the upper portion of Segment 1245. This supplementary station was selected to represent bacteria sources to water pumped from the Brazos River into the segment by the GCWA Shannon Pump Station and to characterize water quality above the Jones Creek confluence with Flewellen Creek.

Station 17686 is located on Flewellen Creek at Briscoe Road, one quarter mile upstream of Jones Creek. The station is in the upper portion of Segment 1245. This supplementary station was selected to characterize bacteria sources from Flewellen Creek, which is a major tributary to Segment 1245. Flewellen Creek is the largest tributary to the Upper Oyster Creek watershed. It is largely rural and has many ranches. Cattle are often in or near the water at sampling stations in the vicinity.

3.1.2.3 Ambient Water Sample Collection and Analysis

Because *E. coli* populations have been found to vary on fine spatial and temporal scales, sampling representativeness was increased by collecting five independent water samples per station, 1-2 minutes and 3-10 feet apart, at each event. Typically, this was done by sampling five points evenly spaced around each station. Because six stations were sampled in the first eight events, and nine stations were sampled in the last four events, a total of 420 water samples were collected.

Typically, water samples were collected directly from the stream (approximately 1 foot below the surface) into sterile wide-mouthed polypropylene bottles supplied by the culturing laboratory. Care was exercised to avoid the surface microlayer of water, which may be enriched with bacteria and not representative of the water column. In cases where, for safety reasons, it was inadvisable to enter the stream bed, or access was not practical, staff used a long handled dipper to collect samples from the stream, and poured the water into the sample bottles. The dipper was thoroughly rinsed and sanitized with bleach between stations. At the time of water sample collection, field observations for current weather, flow severity, water conditions and days since last significant precipitation were made based on standard operating procedures (SOP) in *TCEQ's Surface Water Quality Monitoring Procedures Volume 1: Physical and Chemical Monitoring Methods for Water, Sediment and Tissue* (TCEQ, 2003b).

After collection, all water samples were placed on ice in a cooler and transported to North Water District Laboratory Services (NWDLS) for *E. coli* culturing and enumeration via the membrane filter modified mTEC method. A 6-hour holding time was adhered to for sample delivery to the laboratory.

Following the 24-hour incubation and enumeration, the *E. coli* cultures were shipped overnight at a temperature of 1-4^{o}C to the ribotyping lab for *E. coli* colony isolation and confirmation, archiving, and ribotyping analysis. The ribotyping lab selected at least two isolates from each culture for processing and analysis.

3.1.2.4 BST Ribotyping Procedure

The ribotyping was performed at the Seattle, Washington laboratories of Institute for Environmental Health, Inc. (IEH). The detailed ribotyping protocol is found in Appendix C.

3.1.3 Known Source Ribotype Library Development

3.1.3.1 Sanitary Survey

A key component of the monitoring plan was preparation of a sanitary survey for the Upper Oyster Creek watershed. Through the sanitary survey, potential sources and general categories of fecal contamination within the watershed were identified and listed. These included assessment of wildlife, livestock, concentrated waterfowl areas, bird rookeries or bat colonies, dogs, cats, and other domestic animals, and utilization of waterways by wildlife. Human influences were also identified, including malfunctioning septic systems, municipal WWTPs, and sewer overflows. Based on information derived from the sanitary survey, a field collection strategy was defined for collecting known fecal source samples from throughout the watershed.

A sanitary survey of source regions, as well as information about land use, population density, wastewater and storm water infrastructure, agricultural practices, and wildlife provided information to assist in identifying the sources of fecal pollutants within the Upper Oyster Creek watershed study area. This was important for two reasons.

- First, identification of the possible sources throughout the watershed ensured that analysis of resident *E. coli* strains from each contributing source was accomplished.
- Second, this information provides TCEQ with information not only on the specific animal source of fecal contamination, but also assisted in pinpointing the sources geographically.

The Project Team reviewed available literature, data, and information germane to describing the contributions and defining sources of bacterial loading in the watersheds. Data analyses included discussion of temporal (inter-annual, seasonal) and spatial trends in water quality, an evaluation of potential sources, and an identification of data gaps. Special emphasis was placed on acquiring land use/land cover and human and agricultural census data. These data were integral in assisting in the planning and execution of the project. Several other types of existing data and information were useful in the sanitary survey, described in Section 2. These data included:

- Reported wastewater permit information, including permit limits, self-reported effluent quality data, violations, and inspection reports;
- Hydrologic and meteorological data;
- Land use, population density, and the extent to which on-site sewerage systems are used (septic tanks) in the watershed;
- Livestock density and agricultural practices in the watershed from the most recent county-level agricultural census, as well as the abundance and type of CAFOs;
- Estimated populations of domestic pets; and
- Special studies and published reports for the study area.

3.1.3.2 Known Source Library Sample Collection

Based on the sanitary survey, a list of targets for the known source library was compiled (Table 3-2). The original planned size of the library included 400 fecal and sewage samples from known sources. This local library supplemented the much larger IEH library of many thousand *E. coli* from known sources collected throughout the United States over several years. A complete list of library samples is included in Appendix D.

Sample collection for library development was targeted at 400 *E. coli* isolates, although 500 isolates were actually collected. The species collected included: hogs, horses, cattle, goats,

Table 3-2 Summary of fecal source sampling for library development

Upper Oyster Creek Segment 1245		**Target No. Samples to Collect**	**TotalSamples Collected**	**Sample % of Target**
Major Category	Minor Category			
Human/Sewage	human - raw sewage	35	55	
	Human septage	35	15	
Human/Sewage Total		70	70	100%
Pets	cat	20	14	
	dog	40	51	
	other	10	5	
Pets Total		70	70	100%
Livestock	cattle, dairy	0	1	
	cattle, beef	35	54	
	chicken	10	16	
	turkey	0	4	
	horses/ponies	16	41	
	goat	5	23	
	sheep	5	0	
	donkeys	10	7	
	hog (domestic)	15	37	
	Guinea fowl	0	4	
Livestock Total		96	187	195%
Wildlife-mammals	raccon	10	20	
	deer	10	0	
	hog (feral)	3	10	
	mouse	5	0	
	rat	5	0	
	rabbit	3	0	
	opossum	5	1	
	squirrel	5	1	
	armadillo	3	0	
	coyote	1	9	
	fox	1	0	
	beaver	1	0	
	nutria	1	0	
	skunk	3	0	
	other	5	1	
Wildlife-avian	ducks/geese	35	80	
	swallow	20	3	
	pigeon	20	0	
	heron	3	7	
	grackle	5	2	
	egret	3	16	
	martin	5	0	
	sparrow	2	0	
	dove	5	3	
	other (birds)	5	1	
	mockingbird	0	1	

Upper Oyster Creek Segment 1245		Target No. Samples to Collect	TotalSamples Collected	Sample % of Target
	starling	0	13	
	killdeer	0	4	
	crow	0	1	
Wildlife Total		164	173	104%
Other	compost	0	1	
	Grand Total	**400**	**501**	**125%**

dogs, cats, raccoon, feral hogs, coyotes, waterfowl, and other birds. Samples of sewage and septage were also collected throughout the Upper Oyster Creek watershed.

Fresh animal fecal samples were collected aseptically into sterile test tubes, capped, and sealed. To the extent possible, known source samples were collected directly from the source. An exception was human samples, which were collected from septic tanks, sewer lines, and WWTPs. In some cases, wildlife samples were collected indirectly, from “found” fecal samples. The sources of these “found” wildlife fecal samples were identified to the lowest practical taxonomic level by experienced field biologists. Following sample collection, samples were shipped on ice in coolers via overnight courier to IEH. All sample containers were labeled with the following information: sample type, host species, sample date and time, sample location, and sampler’s initials. All the sample information was logged into a field log.

3.1.4 Quality Assurance/Quality Control

This project provides an estimate of the relative contributions from various fecal sources in the watershed to the observed *E. coli* levels in Upper Oyster Creek; however, it is important to understand the level of uncertainty that accompanied those estimates. Precision, accuracy, sensitivity, completeness, and representativeness are critical data quality issues affecting uncertainty. Representativeness must be controlled by developing an environmental monitoring program characteristic of actual environmental conditions. Accuracy, precision, sensitivity, and completeness can be similarly controlled through careful planning, but also should be quantified via quality control (QC) measures. These QC measures include analysis of replicate laboratory duplicate samples performed by the culture lab, and known standards for BST (samples of known origin).

3.1.4.1 Completeness

Completeness of the data is a measure of how much of the data are available for use compared to the total potential data. Ideally, 100 percent of the data should be available. However, the possibility of unavailable data due to accidents, insufficient sample volume, broken or lost samples, *etc.* is to be expected. Therefore, it was a general goal of the project(s) that 90 percent data completion be achieved.

An additional element of completeness is involved with BST. The sources of *E. coli* isolates which do not match those from a library of known sources cannot be identified. In all

BST studies, a source cannot be identified with acceptable confidence for a portion of the *E. coli* isolates. This inability to identify some isolates is a function of 1) the size of the library relative to the true diversity of *E. coli* in the watershed; 2) ability of the method to distinguish sources with acceptable confidence; and 3) abundance of *E. coli* strains that colonize multiple sources, and thus cannot be used to uniquely identify a source. The project team developed a library of approximately 500 isolates collected from fecal sources within the Upper Oyster Creek watershed. This local library was supplemented by a much larger library previously developed by IEH. It was a general goal of this project to identify the sources of 70 percent of the *E. coli* strains isolated from water.

3.1.4.2 Quantification of Accuracy and Precision in Ribotyping Source Determinations

BST does not lend itself easily to the same QC methods as chemical quantification. Blank samples may be irrelevant, and replicate water samples may often yield different *E. coli* strains. The method accuracy and precision was quantified through a special QC study with "double-blind" safeguards, as practiced in epidemiological QC.

The IEH prepared triplicate cultures of 40 *E. coli* isolates from known sources collected in the Upper Oyster Creek watersheds as part of this study. These isolates were selected from a variety of species. The 120 (40x3) cultures were placed in 120 identical culture tubes, each with a removable label indicating their source and the isolate number. These tubes were mailed to the Parsons Quality Assurance Officer (QAO). The Parsons QAO prepared and sent a list of the 40 isolate sources to the TIAER QAO, who selected from the list 20 isolates to be blind QC test samples. (By selecting a subset of only 50 percent of the prepared tubes, the laboratory had no basis for anticipating the identity of the unmarked blind samples when received.) The Parsons QAO identified the 60 culture tubes associated with those 20 isolates, replaced each label with a new label, numbered them from 1 to 60 in random fashion, and recorded those numbers on a key with the isolate number and source. The Parsons QAO sent those 60 culture tubes back to the IEH after verifying that there was no way for their source to be identified. Parsons sent the key to the TIAER QAO. The samples were processed through the ribotyping procedures in a blind fashion; that is, the laboratory did not know the sources. The IEH sent the results to the Parsons QAO, who made a copy of the key and results and provided it to the IEH and TIAER QAO. The Parsons QAO evaluated and prepared a brief report on the accuracy and precision of the methods, the results of which are found in Section 4.

In ribotyping, with the inherent high precision and accuracy of the rRNA methods, data completeness was most affected by the number of ribotypes found that match ribotypes in the known source library. Thus, a large library was important.

3.1.5 Sampling Event Summary

The intent of this section is to provide general information about the condition of the water bodies and observable weather at the time of water sampling. Rainfall occurring over the region at least 1 week prior to the sampling events was also noted. The maximum allowed holding times for water samples analyzed for *E. coli* was 6 hours. All samples were transferred to the lab and processed within the required holding time.

Fecal sampling occurred as sample material was identified during water sampling events, as well as during sampling events specific for fecal collection. In addition to water and fecal sampling events, a sanitary survey was conducted which is described in Section 2. The sanitary survey included potential bacteria source identification as well as fecal sampling.

Event 1

The first water sampling event took place on March 15, 2004. The event included five bacteria water samples collected at each of the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074 and 17688). The weather was overcast and 1.42 inches of rain fell the day before sampling. The flow at all stations was strong and the water was brown and turbid. Swallows and pigeons were observed under bridges at the downstream segments. This event was considered a run-off event.

Event 2

The second sampling event took place on April 6, 2004. The event included five bacteria water samples collected at each of the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074 and 17688). The weather was cloudy and humid. It had been 3 days since the prior significant rain event, but rain storms moved into the area during sampling. The flow at all stations was strong and the water was brown and turbid. Swallows and pigeons were observed under bridges at the downstream segments.

Heavy rain started at 11:20 am. Samples at Station 12090 were collected after rain had been falling for approximately 35 minutes; therefore; only Station 12090 was considered a runoff-influenced event.

Event 3

The third sampling event took place on May 4, 2004. The event included five bacteria water samples collected at each of the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074 and 17688). This sampling event was observed by both TCEQ and TIAER personnel. No significant weather was noted, with clear skies, a light southwesterly breeze, and 80°F temperature. Almost three inches of rain fell on May 1. The flow at all stations was slightly above normal and the water was brown and turbid with storm debris along the banks.

A fecal sampling event was scheduled to coincide with the water event occurring on May 5, 2004. Parsons and TIAER personnel met with personnel from GCWA who provided access to privately owned land along Oyster and Flewellen Creeks. Wild and domestic animal scat was collected with help from the GCWA personnel. The TDCJ, Jester Unit was also visited by Parsons and TIAER personnel. Dog, hog and wild egret scat was collected during the visit.

Event 4

The fourth sampling event took place on May 25, 2004. The event included five bacteria water samples collected at each of the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074 and 17688). No significant weather was noted. The previous significant rain fell on May 14, eleven days prior to the sampling event. The flow at all stations was normal or below normal and the water was brown and turbid.

Event 5

The fifth sampling event took place on June 22, 2004. The event included five bacteria water samples collected at each of the original six sampling locations (12090, 12087, 12086, 12083, 12074 and 17688). The weather was hot, cloudy and humid with rain moving into the area. Rain fell over the sampling area five days prior to the sampling event. The flow at all stations was normal and the water was brown and turbid at Stations 12074 and 12083; clear and greenish at Station 17688; and tan with a little turbidity at Stations 12086 and 12087. Rain started to fall as sampling was completed. A definite odor of pigeon and swallow feces was noted under the bridge at Station 12074. Samples at the last station 12090 were collected after rain had been falling, therefore; only station 12090 was considered a run-off event.

Event 6

The sixth sampling event took place on July 13, 2004. The event included five bacteria water samples collected at each of the original six sampling locations (12090, 12087, 12086, 12083, 12074 and 17688). No significant weather was noted. An inch and a half of rain fell over the sampling area two days prior to the sampling event. The flow at all stations was normal and the water was brown and slightly turbid at all stations except 12074, where it was tan and slightly turbid, and 17688 where the water was greenish with low turbidity. As a result of recent storms, a debris line approximately 20 inches over the ordinary high water mark was observed.

Dedicated fecal sampling occurred on July 14th and the 26th -29th. The fecal samples were placed on ice and transferred to the ribotyping lab. Wastewater treatment plant influent samples were collected at Sugarland WWTP and the Missouri City WWTP. The WWTP samples were placed on media plates and incubated at 35°C for 2 hours after which the temperature was increased to 44.5°C for 24 hours.

Event 7

The seventh sampling event took place on August 10, 2004. The event included five bacteria water samples collected at each of the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074 and 17688). The weather was hot, clear and calm. The previous significant rainfall had fallen eight days before the sampling event. The flow at all stations was normal or lower than normal and the water was greenish-tan and had low turbidity.

Event 8

The eighth sampling event took place on August 24, 2004. The event included five bacteria water samples collected at each of the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074 and 17688). The weather was hot, clear and calm. The previous significant rainfall (0.56") had fallen 3 days before the sampling event; however 0.24 inches of rain had fallen just a day before. The flow at all stations was normal and the water was greenish-tan with low turbidity.

Event 9

The ninth sampling event took place on September 28, 2004. Water and fecal sampling initially occurred on September 14, but the lab was not prepared to handle the water samples. Re-sampling took place on September 28, 2004. The event included five bacteria water samples collected at each of the three new sampling sites, in addition to the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074, 17688, 11516, 12086, 17685 and 17688). The weather was warm, clear and calm. Significant rain (0.38 inches) fell over the sampling area three days prior to the sampling event. The flow at all stations was normal and the water was greenish-tan with low turbidity.

Event 10

The tenth sampling event took place on October 12, 2004. The event included five bacteria water samples collected at each of the three new sampling sites, in addition to the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074, 17688, 11516, 12086, 17685 and 17688). The weather was warm, clear, and calm. An inch of rain had fallen five days prior to the sampling event. The flow at all stations was normal and the water was greenish-tan and turbid.

Event 11

The eleventh sampling event took place during a large rain event on November 2, 2004. The event included five bacteria water samples collected at each of the three new sampling sites, in addition to the original six sampling locations (Stations 12090, 12087, 12086, 12083, 12074, 17688, 11516, 12086, 17685 and 17688). The weather was cool and cloudy with a slight breeze. A substantial amount of rain (2.83 inches) fell on November 1, with another 0.8 inch on the sampling day. The flow at all stations was very high and the water was brown and turbid. This event was considered a run-off event.

Event 12

The twelfth and last water sampling event took place on November 23, 2004. The event included five bacteria water samples collected at each of the three new sampling sites, in addition to the original six sampling locations (Station 12090, 12087, 12086, 12083, 12074, 17688, 11516, 12086, 17685 and 17688). The weather was cloudy, cool, humid, and calm with skies starting to clear. Heavy rain had fallen over the sampling area for several days until approximately six hours prior to the sampling event. The total rainfall for the four-day rain event was 5.8 inches, with more than one-half inch each day. The flow at all stations was very high and the water was brown with high turbidity. This event was considered a run-off event.

Fecal samples were collected on November 22nd. Additional fecal sampling occurred on December 8 and 9, 2004 that included additional trips to private property on a ranch, the GCWA pump station property, and the TDCJ, Jester Unit. Wastewater treatment plant influent samples were collected at Sugarland WWTP and the Missouri City WWTP. A sample of composted planting soil was collected from Houston Nurseries. City of Rosenberg and Fort Bend County Animal Shelters were also visited for domestic animal fecal samples. The WWTP samples were placed on media plates and incubated at 35°C for 2 hours after which the temperature was increased to 44.5°C for 24 hours.

3.2 Results and Discussions

Ambient water sampling for this project lasted approximately 9 months and consisted of 12 sampling events beginning March 15, 2004 and ending November 23, 2004. The ambient water sampling sites included six core sites that were sampled 12 times, and three supplementary sites that were sampled during the last four events, beginning September 28, 2004.

Rainfall runoff washes fecal material from the land surface into water, and typically causes a pronounced increase in fecal bacteria levels. The objective of this sampling was to obtain representative sampling of Upper Oyster Creek under both runoff and non-runoff conditions, with the ratio of runoff to non-runoff samples typical of the natural frequencies of these conditions. A sampling event was considered to be influenced by runoff if more than one-quarter inch of rain was measured at the Hull (Sugar Land) Airport on the day of sampling (before the sample was collected) or on the previous day. From March through November 2004, one-quarter inch or more of rain fell on 45 days. Considering days of consecutive rainfall of one-quarter inch or more and the above definition of a runoff-influenced sampling event, 76 days out of 276 days (or 28 percent) would be considered runoff influenced. Thus, Upper Oyster Creek was expected to be influenced by runoff on one of every three or four days, on average.

Overall, 30 percent of the water samples were considered runoff-influenced, in general agreement with the natural frequency of this condition. However, this frequency was not uniform for all sites. For the three monitoring stations added in September 2004, samples were runoff-influenced on two of the four sampling dates. Thunderstorms began during two sampling events, and only the last samples collected on those dates were considered to be influenced by runoff. Thus, five of the 12 sampling events at Station 12090 were runoff-influenced. For the other five stations, three of 12 samples were considered to be runoff-influenced.

3.2.1 Quality Assurance/Quality Control Results

QA/QC measures utilized by NWDLS in the culturing and enumeration of *E. coli* from water samples, and by IEH in the ribotyping of *E. coli* are described separately below.

3.2.1.1 Culturing and Enumeration of *E. coli*

Method blanks were run by the laboratory with each group of samples delivered to the laboratory. Method blanks were sterile buffered dilution water free of *E. coli,* and were carried through the entire analytical process. All method blanks were negative for *E. coli*, reflecting a lack of contamination in the analytical procedure, including media, filters, dilution and rinse water, and glassware and equipment.

Positive and negative control cultures were also run with each group of ambient water samples. Positive controls were known *E. coli* cultures to ensure that the media supported growth of *E. coli*. Negative controls were cultures of bacteria species other than *E. coli* to ensure that other types of bacteria did not grow on the media under the incubation conditions. All positive controls were positive, and all negative controls were negative.

Laboratory duplicate samples were analyzed at a rate of just under one in 10 samples. These samples were collected by analysis of two separate aliquots of an ambient water sample delivered to the laboratory. Laboratory duplicate samples were used to quantify variation in the analytical procedure. The relative percent deviation of the log-transformed *E. coli* concentrations of laboratory duplicates averaged less than 2 percent, did not exceed 7 percent, and remained within the control limits specified in the Quality Assurance Project Plan (QAPP) indicating that very little variation was introduced during analysis.

3.2.1.2 Ribotyping and Source Identification

Ribotyping was extremely precise and repeatable. As described in Section 3, IEH analyzed 60 unknown *E. coli* cultures. These 60 cultures represented three copies each of 20 different *E. coli* isolates selected randomly by the TIAER QAO from a group of 120 (three copies each of 40 different *E. coli* isolates) cultures provided by IEH to the Parsons QAO from the IEH known source library of *E. coli* isolates. These included isolates from seagulls, humans, and cattle. Labels on the slant tubes containing the isolates were randomly changed by the Parsons QAO before being returned to IEH, so IEH could not identify the cultures except through ribotyping. For each of the 60 unknown *E. coli* cultures tested, IEH assigned the same ribotype identification (ID) to each of the three copies of a given isolate. In other words, with repeated analysis the method produced the same ribotype result each time; thus, precision of the method was judged to be 100 percent. Accuracy was judged by the ability of the lab to assign the correct ribotype ID to the unknown cultures. IEH assigned the correct ID to 57 of the 60 unknown cultures, for a correct rate of 95 percent. It should be noted that though the ribotype ID was incorrectly identified for one isolate (three cultures); the source species identified was actually correct. In other words, the correct source species was identified for 100 percent of the cultures. These precision and accuracy rates met the 90 percent accuracy and precision data quality objectives of the project.

3.2.2 *E. coli* Levels in Water

Measured *E. coli* levels were summarized by event, by site, and with measured concentration, and are provided in Appendix E. The overall geometric mean *E. coli* level at each site, including both runoff-influenced and non-runoff event samples can be compared to the geometric mean water quality criterion of 126 cfu /100 ml. However, it is more appropriate to make inter-comparisons between sites based on levels under either runoff or non-runoff conditions, but not the aggregate, as the frequency of runoff influence varied from site to site.

Table 3-3 summarizes the observed *E. coli* concentration under runoff and non-runoff conditions. The geometric mean *E. coli* levels exceed the 126 cfu/100 ml water quality criterion at all sites except Station 12083, Upper Oyster Creek at Highway 90A in Sugar Land. Additionally, the measured *E. coli* levels exceeded the single sample maximum water quality criterion (394 cfu/100 ml) in more than 25 percent of the samples at all sites. These levels indicate general non-attainment of water quality criteria protecting contact recreation throughout the system.

Table 3-4 summarizes the much lower *E. coli* levels observed under non-runoff conditions. Only three stations, Stafford Run, Flat Bank Creek, and Jones Creek at FM 273, exceeded water quality criteria. Repeated exceedances of the water quality criteria under non-runoff conditions may indicate disinfection problems with point source wastewater discharges, livestock in the stream, or localized wildlife impacts such as birds residing under the bridge at the monitoring station. The highest levels were observed at Stafford Run. Excluding the supplementary stations which were sampled only twice under non-runoff conditions, the lowest *E. coli* levels were observed in Upper Oyster Creek in and just upstream of Sugar Land (Stations 12083 and 12086).

Table 3-3 Measured *E. coli* levels under all conditions

Site Description	Station Number	Number of Events	*E. coli* Concentration (cfu/100 mL) Min	Max	Geometric Mean	% Samples Exceeding 394 / 100 ml
Jones Creek at FM 273	12090	12	13	>20,000	563	52%
Upper Oyster Creek at FM 1464	12087	12	17	7,500	268	38%
Upper Oyster Creek at Hwy 6	12086	12	20	7,600	227	33%
Upper Oyster Creek at US 90A	12083	12	<1	5,400	114	33%
Stafford Run at El Dorado Blvd	17688	12	63	16,900	788	57%
Flat Bank Creek at Hwy 6	12074	12	<1	10,300	341	52%
Red Gully at Richmond-Gaines Rd	11516	4	<1	19,000	219	50%
Jones Creek at Bois D'Arc Lane	17685	4	11	18,000	358	50%
Flewellen Creek at Briscoe Road	17686	4	62	>20,000	972	50%

Table 3-4 Measured *E. coli* levels under non-runoff conditions

Site Description	Station Number	Number of Events	*E. coli* Concentration (cfu/100 mL) Min	Max	Geometric Mean	% Samples Exceeding 394 / 100 ml
Jones Creek at FM 273	12090	7	13	880	135	17%
Upper Oyster Creek at FM 1464	12087	9	17	1080	121	18%
Upper Oyster Creek at Hwy 6	12086	9	20	630	75	11%
Upper Oyster Creek at US 90A	12083	9	<1	680	41	11%
Stafford Run at El Dorado Blvd	17688	9	63	7500	356	42%
Flat Bank Creek at Hwy 6	12074	9	<1	2900	157	36%
Red Gully at Richmond-Gaines Rd	11516	2	<1	18	4	0%
Jones Creek at Bois D'Arc Lane	17685	2	11	77	33	0%
Flewellen Creek at Briscoe Road	17686	2	62	95	76	0%

Table 3-5 summarizes the high *E. coli* levels observed under runoff conditions. Some measurements exceeded 20,000 cfu/100 ml. On average, the highest levels were observed in Flewellen Creek, Red Gully, and Stafford Run, and the lowest levels were observed in Oyster Creek at Highway 90A in Sugar Land.

Table 3-5 Measured *E. coli* levels under runoff conditions

Site Description	Station Number	Number of Events	*E. coli* Concentration (cfu/100 ml)			% Samples Exceeding 394/100 ml
			Min	Max	Geometric Mean	
Jones Creek at FM 273	12090	5	690	>20,000	4,165	100%
Upper Oyster Creek at FM 1464	12087	3	1,000	7,500	3,392	100%
Upper Oyster Creek at Hwy 6	12086	3	4,800	7,600	6,265	100%
Upper Oyster Creek at US 90A	12083	3	650	5,400	2,355	100%
Stafford Run at El Dorado Blvd	17688	3	3,400	16,900	8,565	100%
Flat Bank Creek at Hwy 6	12074	3	1,570	10,300	3,509	100%
Red Gully at Richmond-Gaines Rd	11516	2	5,900	19,000	10,871	100%
Jones Creek at Bois D'Arc Lane	17685	2	850	18,000	3,913	100%
Flewellen Creek at Briscoe Road	17686	2	7,100	>20,000	12,411	100%

Some general conclusions can be reached based on the observed *E. coli* levels. First, it does not appear that water entering the system by pumping from the Brazos River represents a major source of the observed *E. coli* levels. With its high bacteria levels, Stafford Run may exert a major influence on observed *E. coli* levels in the lower reaches of the segment. *E. coli* levels in the middle reaches of Upper Oyster Creek may be reduced by the dams and impoundments, where the resulting lower water velocities permit bacteria to settle out of the water column. Finally, the profound influence of runoff on *E. coli* levels must be noted. The persistence of high *E. coli* levels following runoff is not well-quantified in this system, and may require further examination. Very high *E. coli* levels were observed during sampling event #1 (March 15), 1 day after a 1.4-inch rainfall event. Sampling event #6 (July 13) occurred 2 days after a 1.5-inch rain, and *E. coli* levels ranged between 130 cfu and 680 cfu/100 ml, higher than but in the same range of magnitude as most other non-runoff-influenced events. While the influence of runoff does not persist too long, the frequency of rainfall in this area indicates that it may be difficult to meet water quality standards.

3.2.3 Identified Bacterial Sources Based on BST Technology

Overall, 1,136 *E. coli* isolates from ambient water samples were ribotyped, substantially exceeding the stated project objective of ribotyping 840 isolates (120 per site for the six original stations plus 40 per site for the supplemental stations). Table 3-6 provides a summary of the isolates ribotyped by site. Data completeness met or exceeded 100 percent at all sites.

Table 3-6 Count of *E. coli* ribotype characterization by site and runoff condition

Site Description	Station Number	Count of *E. coli* Isolates Ribotyped		
		Non-runoff	Runoff	Total
Jones Creek at FM 273	12090	99	70	169
Upper Oyster Creek at FM 1464	12087	110	47	157
Upper Oyster Creek at Hwy 6	12086	130	49	179
Upper Oyster Creek at US 90A	12083	92	47	139
Stafford Run at El Dorado Blvd	17688	135	48	183
Flat Bank Creek at Hwy 6	12074	119	49	168
Red Gully at Richmond-Gaines Rd	11516	20	20	40
Jones Creek at Bois D'Arc Lane	17685	25	23	48
Flewellen Creek at Briscoe Road	17686	29	24	53
All Sites Combined		759	377	1136

To interpret results of BST methodology, and summarize the fraction of fecal coliform in ambient water from specific sources, it is important to note that the relative weighting of individual water samples in the source summary is not equal. There are many reasons for this unequal weighting related to the sampling and analytical process. The primary reasons include:

- The number of water samples collected from each site was variable, considering that the three supplementary sites were sampled only four times;
- the number of discrete fecal coliform colonies that could be harvested by IEH from a plate was in some cases limited due to low *E. coli* counts or laboratory dilutions. In some cases, no *E. coli* were observed in a sample.
- the fraction of fecal coliform colonies harvested from a plate that, upon purification and testing, were verified to be *E. coli* and ribotyped, was variable; and
- discretion of the laboratory staff. (In some cases, fecal coliform filter were re-sampled to harvest additional colonies.)

To achieve an overall average of two isolates ribotyped from each water sample, IEH often selected as many as five or six isolates from an individual filter. The number of satisfactory ribotypes obtained from a single water grab sample ranged from zero to six. Thus, when reporting and interpreting the data, the reader must understand that when computing summary statistics regarding source identification, one site, sampling event, or individual water sample may have more influence on the summary results than another. Attempts to normalize the results to reduce this disparate influence could be made, but because many factors control the sample influence, there are as many different possible ways to normalize. For this reason, raw data in Appendix F will be provided to allow the user to interpret data according to their needs.

3.2.3.1 Source Categorization

The subjective grouping of ribotypes into source categories merits discussion. The categorization is based to some extent on the basis of biological similarity, but it is also influenced by co-occurrence of species. For example, cattle and guinea fowl are not biologically similar, but these categories can be grouped from a management viewpoint as livestock that tend to occur on farms and ranches.

E. coli strains that have been observed in more than one source type are considered transient strains. Because they cannot be used to identify a source, the source of *E. coli* is identified as "unknown." *E. coli* isolated from water samples that do not match any *E. coli* in the known source library are also identified as "unknown" sources.

When *E. coli* are observed in multiple species, but the species are closely related, they are not identified as transient strains, but the source category description is expanded. For example, strains that have been seen in dogs and coyotes will be assigned to the category "canine," and strains observed in bison and cattle will be assigned to the category "bovine." There is a biological basis for this grouping, because conditions in the gut of closely related species are expected to be similar, and gut conditions are believed to be the primary factor influencing which *E. coli* strains are abundant.

Strains of *E. coli* are often observed to occur in many different species of birds, but not in mammals. Thus, even when an *E. coli* isolate has been observed from only one type of bird, it is assumed that it may also occur in other species and is assigned to the generic "avian" source category, unless numerous observations confirm that its occurrence is specific to a particular type of bird. An exception is waterfowl, which appear to host some strains of *E. coli* that do not occur in other types of birds. These *E. coli* were assigned to the category "waterfowl," a subset of the avian category.

The category "human" is assigned to *E. coli* that have only been observed in raw sewage. Sewage, septage, and sewage sludge are assumed to consist primarily of human waste, but also include fecal matter from other species. When source categories are grouped into "super-categories," sewage, septage, and sludge were grouped together with human sources.

Dogs, cats, and other non-native, non-livestock animals are grouped into the super-category "pets." All the native wild mammals, including rodents, coyotes, deer, *etc*., are grouped into the super-category "non-avian wildlife." When categories include both wild and domestic species, they are included in the respective domestic super-category totals because it is believed that abundance of the domestic species typically exceeds that of the wild species. For example, *E. coli* from the "canine" source category, which includes strains found in both dogs and coyotes, are included in the super-category "pets" rather than "non-avian wildlife." This may be a poor assumption in some cases, such as the porcine category, because wild hogs were observed to be abundant in the Upper Oyster Creek watershed, likely outnumbering their domestic cousins.

3.2.3.2 *E. coli* Source Contribution

In this section, *E. coli* source contributions are estimated for the Upper Oyster Creek watershed as a whole and for individual sampling sites. Source contributions are calculated as the sum of isolates matching a particular source category or super-category, divided by the total number of *E. coli* for which sources are identified. Confidence intervals around the source contribution estimates were calculated from the following formula:

$$\overline{p} \pm z_{\alpha/2}\sqrt{\frac{p(1-p)}{n}}$$

where p is the estimated proportion of the *E. coli* from a given source, n is the total number of isolates, and $z_{\alpha/2}$ is the value of the standard normal distribution at confidence interval α.

3.2.3.3 All Sites Combined

In this section, results for all nine monitoring stations were pooled to estimate bacteria sources to Upper Oyster Creek as a whole. Table 3-7 and Figure 3-3 summarize the identified sources of *E. coli* from all 12 events, including both runoff and non-runoff conditions. Wildlife represented the largest source of *E. coli*, accounting for 43 percent of the total observed in the stream. Among the wildlife, birds (23.2%) were a slightly more significant source than mammals (19.5%). Among birds, the *E. coli* specific to waterfowl accounted for approximately 7 percent of the total. Among mammals, rodents, including squirrels, were the major source, accounting for 11.4 percent of the total. Raccoons were also a significant (>4%) source of *E. coli*, in agreement with the observations of their abundance during the sanitary survey and subsequent sampling. Pets, primarily dogs, accounted for just fewer than 10 percent of the total *E. coli* observed. Cats were not a significant source. Livestock represented 19 percent of the total *E. coli* observed. Livestock contributions were primarily from bovine (7%, assumed to be cattle), swine (5.7%, hogs and pigs, including both feral and domestic), and horses (5%). Goats and poultry were very minor sources. As stated earlier, the BST methodology does not distinguish wild from domestic hogs. Since wild hogs were observed to be abundant in the watershed, this source may more appropriately be assigned to the wildlife super-category. The source of approximately 15 percent of *E. coli* isolates could not be identified, either because there were no matching ribotypes in the known source library or because the matching isolates were transients, *i.e.*, they are not host-specific having been observed in multiple types of host species.

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Table 3-7 *E. coli* source characterization of Upper Oyster Creek under all conditions

Super-category	Category	Source	Isolates	% Contribution	95% Confidence Interval
Human/sewage	human	human	18	1.6%	0.9-2.3%
Human/sewage	sewage	sewage	143	12.6%	10.7-14.5%
Human/sewage	subtotal		161	14.2%	12.1-16.2%
Livestock		bovine	79	7.0%	5.5-8.4%
Livestock		horse	57	5.0%	3.7-6.3%
Livestock		poultry	9	0.8%	0.3-1.3%
Livestock		Guinea fowl	1	0.1%	0.0-0.3%
Livestock		donkey	1	0.1%	0.0-0.3%
Livestock		goat	3	0.3%	0.0-0.6%
Livestock		porcine	65	5.7%	4.4-7.1%
Livestock	subtotal		215	18.9%	16.6-21.2%
Pets	canine	canine	85	7.5%	6.0-9.0%
Pets	canine	dog	17	1.5%	0.8-2.2%
Pets	feline	feline	5	0.4%	0.1-0.8%
Pets	subtotal		107	9.4%	7.7-11.1%
Wildlife	mammal	coyote	9	0.8%	0.3-1.3%
Wildlife	mammal	deer	20	1.8%	1.0-2.5%
Wildlife	mammal	rabbit	1	0.1%	0-0.3%
Wildlife	mammal	raccoon	47	4.1%	3.0-5.3%
Wildlife	mammal	rodent	128	11.3%	9.4-13.1%
Wildlife	mammal	opossum	14	1.2%	0.6-1.9%
Wildlife	mammal	skunk	1	0.1%	0.0-0.3%
Wildlife	mammal	squirrel	1	0.1%	0.0-0.3%
Wildlife	mammal	subtotal	221	19.5%	17.2-21.8%
Wildlife	avian	waterfowl	76	6.7%	5.2-8.1%
Wildlife	avian	avian	187	16.5%	14.3-18.6%
Wildlife	avian	subtotal	263	23.2%	20.7-25.6%
Wildlife	subtotal		484	42.6%	39.7-45.5%
Unknown		unknown	169	14.9%	12.8-16.9%
Grand Total			1136	100.0%	

Figure 3-3 *E. coli* source characterization of Upper Oyster Creek under all conditions

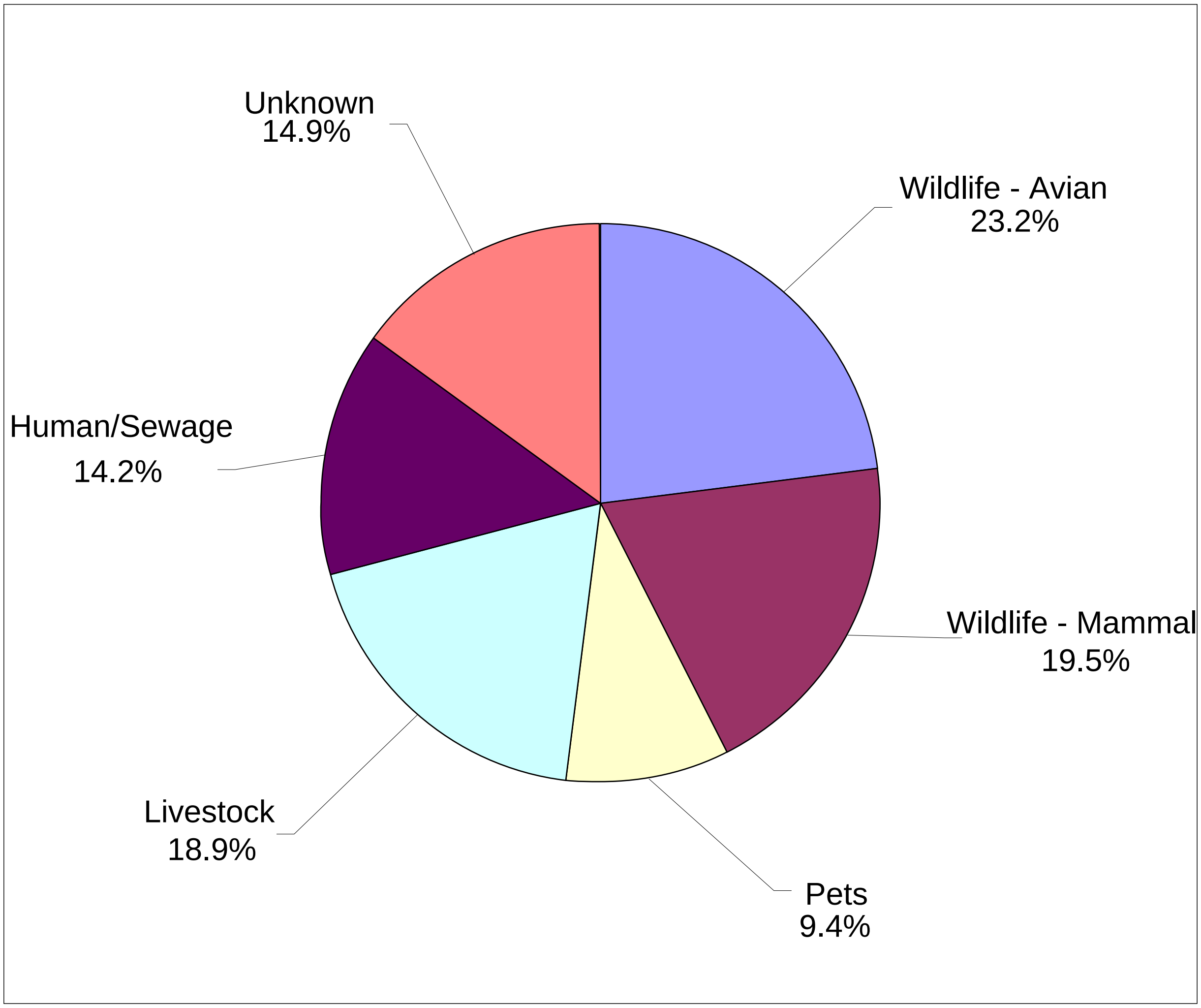


Table 3-8 summarizes and compares the sources of *E. coli* from all sites under runoff and non-runoff conditions. No statistically significant (α=0.05) differences in sources were observed between runoff and non-runoff conditions. While somewhat counter-intuitive, this result has been frequently observed in other BST projects.

Table 3-8 Comparison of *E. coli* sources from all sites under runoff and non-runoff conditions

			Non-runoff			**Runoff**		
Super-Category	**Category**	**Source**	**Isolates**	**% Contribution**	**95% CI**	**Isolates**	**% Contribution**	**95% CI**
Human	Human	Human	11	1.4	0.6-2.3	7	1.9	0.5-3.2
Human	sewage	sewage	100	13.2	10.8-15.6	43	11.4	8.2-14.6
			111	14.6	12.1-17.1	50	13.3	9.8-16.7
Livestock		bovine	53	7.0	5.2-8.8	26	6.9	4.3-9.5
Livestock		horse	33	4.3	2.9-5.8	24	6.4	3.9-8.8
Livestock		poultry	7	0.9	0.2-1.6	2	0.5	0.0-1.3
Livestock		Guinea fowl	0	0.0		1	0.3	0.0-0.8
Livestock		donkey	1	0.1	0.0-0.4	0	0.0	
Livestock		goat	3	0.4	0.0-0.8	0	0.0	
Livestock		porcine	42	5.5	3.9-7.2	23	6.1	3.7-8.5
Livestock	subtotal		139	18.3	15.6-21.1	76	20.2	16.1-24.2%
Pets	canine	canine	57	7.5	5.6-9.4	28	7.4	4.8-10.1
Pets	canine	dog	14	1.8	0.9-2.8	3	0.8	0.0-1.7
Pets	feline	feline	5	0.7	0.1-1.2	0	0.0	
Pets	subtotal		76	10.0	7.9-12.1	31	8.2	5.4-11.0
Wildlife	mammal	coyote	6	0.8	0.2-1.4	3	0.8	0.0-1.7
Wildlife	mammal	deer	16	2.1	1.1-3.1	4	1.1	0.0-2.1
Wildlife	mammal	rabbit	1	0.1	0.0-0.4	0	0.0	
Wildlife	mammal	raccoon	38	5.0	3.5-6.6	9	2.4	0.8-3.9
Wildlife	mammal	rodent	81	10.7	8.5-12.9	47	12.5	9.1-15.8
Wildlife	mammal	opossum	9	1.2	0.4-2.0	5	1.3	0.2-2.5
Wildlife	mammal	skunk	0	0.0		1	0.3	0.0-0.8
Wildlife	mammal	squirrel	1	0.1	0.0-0.4	0	0.0	
Wildlife	mammal	subtotal	152	20.0	17.2-22.9	69	18.3	14.4-22.2
Wildlife	avian	waterfowl	50	6.6	4.8-8.4	26	6.9	4.3-9.5
Wildlife	avian	avian	118	15.5	13.0-18.1	69	18.3	14.4-22.2
Wildlife	avian	subtotal	168	22.1	19.2-25.1	95	25.2	20.8-29.6
Wildlife	subtotal		320	42.2	38.6-45.7	164	43.5	38.5-48.5
Unknown		unknown	113	14.9	12.4-17.4	56	14.9	11.3-18.4
Grand Total			759	100.0		377	100.0	

As noted earlier, it is possible to normalize results to reduce potential bias introduced in the source characterization by the unequal number of *E. coli* ribotyped for each site and sampling event. This normalization was performed by calculating the source contribution at each site for each sampling event, then averaging those results by site, and finally calculating an overall average source contribution percentage for all sites. Table 3-9 provides results for this normalization for all sites and events combined. Table 3-9 can be compared to the non-normalized results in Table 3-7. All differences are very minor, and none are statistically significant at the 95 percent confidence level.

Table 3-9 Normalized *E. coli* source characterization of Upper Oyster Creek under all conditions

Super-category	Category	Source	% Contribution	95% Confidence Interval
Human/sewage	human	Human	2.5%	1.6-3.4%
Human/sewage	sewage	Sewage	11.4%	9.6-13.3%
Human/sewage	subtotal		13.9%	11.9-15.9%
Livestock		Bovine	6.4%	5.0-7.9%
Livestock		Horse	6.1%	4.7-7.5%
Livestock		Poultry	0.6%	0.1-1.0%
Livestock		Guinea fowl	0.1%	0.0-0.2%
Livestock		Donkey	0.1%	0.0-0.3%
Livestock		Goat	0.1%	0.0-0.3%
Livestock		Porcine	4.3%	3.1-5.5%
Livestock	Subtotal		17.7%	15.5-20.0%
Pets	Canine	canine	8.6%	7.0-10.2%
Pets	Canine	dog	1.6%	0.9-2.4%
Pets	Feline	feline	0.8%	0.3-1.3%
Pets	Subtotal		11.0%	9.2-12.8%
Wildlife	Mammal	coyote	0.7%	0.2-1.2%
Wildlife	Mammal	deer	1.2%	0.5-1.8%
Wildlife	Mammal	rabbit	0.1%	0.0-0.2%
Wildlife	Mammal	raccoon	3.4%	2.3-4.4%
Wildlife	Mammal	rodent	11.7%	9.8-13.55
Wildlife	Mammal	opossum	0.9%	0.3-1.4%
Wildlife	Mammal	skunk	0.1%	0.0-0.3%
Wildlife	Mammal	squirrel	0.1%	0.0-0.2%
Wildlife	Mammal	subtotal	18.0%	15.8-20.2%
Wildlife	Avian	waterfowl	5.6%	4.3-7.0%
Wildlife	Avian	avian	17.6%	15.4-19.8%
Wildlife	Avian	subtotal	23.2%	20.8-25.7%
Wildlife	Subtotal		41.2%	38.3-44.1%
Unknown		unknown	16.1%	14.0-18.3%

Neither the raw nor normalized source characterizations presented to this point in this report reflect the observed variations in *E. coli* concentrations in Upper Oyster Creek. Typically, two to four *E. coli* were ribotyped from each water sample, regardless of whether there were 20 or 20,000 *E. coli* in the water sample. Thus, sources that contribute large numbers of *E. coli* under runoff conditions when *E. coli* concentrations in water are high may be minimized by the unweighted methodology. Table 3 - 10 summarizes the source

Table 3-10 Concentration-weighted *E. coli* source characterization of Upper Oyster Creek under all conditions

Super-category	Category	Source	% Contribution	95% Confidence Interval
Human/sewage	Human	human	1.6%	0.8-2.3%
Human/sewage	Sewage	sewage	12.8%	10.8-14.7%
Human/sewage	Subtotal		14.3%	12.3-16.4%
Livestock		bovine	6.9%	5.4-8.3%
Livestock		horse	5.2%	3.9-6.5%
Livestock		poultry	0.8%	0.3-1.3%
Livestock		Guinea fowl	0.1%	0.0-0.3%
Livestock		donkey	0.1%	0.0-0.3%
Livestock		goat	0.3%	0.0-0.5%
Livestock		porcine	5.8%	4.4-7.2%
Livestock	Subtotal		19.1%	16.8-21.4%
Pets	Canine	canine	7.2%	5.7-8.7%
Pets	Canine	dog	1.5%	0.8-2.2%
Pets	Feline	feline	0.3%	0.0-0.7%
Pets	Subtotal		9.0%	7.4-10.7%
Wildlife	Mammal	coyote	0.8%	0.3-1.3%
Wildlife	Mammal	deer	1.6%	0.8-2.3%
Wildlife	Mammal	rabbit	0.1%	0.0-0.2%
Wildlife	Mammal	raccoon	4.1%	2.9-5.2%
Wildlife	Mammal	rodent	11.2%	9.4-13.0%
Wildlife	Mammal	opossum	1.2%	0.6-1.9%
Wildlife	Mammal	skunk	0.1%	0.0-0.3%
Wildlife	Mammal	squirrel	0.1%	0.0-0.2%
Wildlife	Mammal	subtotal	19.2%	16.9-21.5%
Wildlife	Avian	waterfowl	6.6%	5.2-8.1%
Wildlife	Avian	avian	16.6%	14.4-18.8%
Wildlife	Avian	subtotal	23.2%	20.8-25.7%
Wildlife	Subtotal		42.4%	39.5-45.3%
Unknown		unknown	15.1%	13.1-17.2%
Grand Total			100.0%	

characterization that results from weighting sources by the *E. coli* concentration in each water sample from which it was harvested. Table 3-10 can be compared to the non-normalized results in Table 3-7. All differences are very minor, and none are statistically significant at the 95 percent confidence level.

3.2.3.4 Station 12090 Jones Creek at FM 273

In this section, results for Station 12090 are described individually. This source characterization is based on 99 isolates collected in seven non-runoff events and 70 isolates collected in five runoff events. Table 3-11 and Figure 3-4 summarize the identified sources of *E. coli* from all 12 events, including both runoff and non-runoff conditions. A detailed characterization of sources is provided in Appendix G, Table G-1. The human and sewage source contribution was 13 percent overall, similar to that of the watershed as a whole, and did not vary significantly under runoff versus non-runoff conditions. The livestock source contributions were higher at this site than for the watershed as a whole, which was expected considering the rural nature of the western watershed. The source of approximately 14 percent of the *E. coli* isolates could not be identified.

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, unweighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

3.2.3.5 Station 12087 Upper Oyster Creek at FM 1464

In this section, results for Station 12087 are described individually. This source characterization is based on 110 isolates collected in nine non-runoff events and 47 isolates collected in three runoff events. Table 3-12 and Figure 3-5 summarize the identified sources of *E. coli* from all 12 events, including both runoff and non-runoff conditions. The human and sewage source contribution was only 3.2 percent overall, significantly less than that of the watershed as a whole, and was not observed at this site under runoff conditions. Livestock source contributions were high at this site due to the porcine contributions of almost 15 percent. The porcine contribution was particularly high under runoff conditions at 19 percent (see Appendix G, Table G-2 for contribution by individual sources, such as porcine). This high porcine contribution may reflect the influence of the hog farm on TDCJ property at the Jester Unit, a short distance upstream of this station. The source of approximately 14 percent of the *E. coli* isolates could not be identified.

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, unweighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

Table 3-11 *E. coli* source characterization of Station 12090

Super - category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	14.1%	7.3-21.0%	11.4%	4.0-18.9%	13.0%	7.9-18.1%
Livestock	—	22.2%	14.0-30.4%	31.4%	20.6-42.3%	26.0%	19.4-32.7%
Pets	—	11.1%	4.9-17.3%	4.3%	0.0-9.0%	8.3%	4.1-12.4%
Wildlife	mammal	19.2%	11.4-26.9%	20.0%	10.6-29.4%	19.5%	13.6-25.5%
Wildlife	Avian	23.2%	14.9-31.6%	14.3%	6.1-22.5%	19.5%	13.6-25.5%
Wildlife	subtotal	42.4%	32.7-52.2%	34.3%	23.2-45.4%	39.1%	31.7-46.4%
Unknown	—	10.1%	4.2-16.0%	18.6%	9.5-27.7%	13.6%	8.4-18.8%

Figure 3-4 *E. coli* source characterization of Station 12090 under all conditions

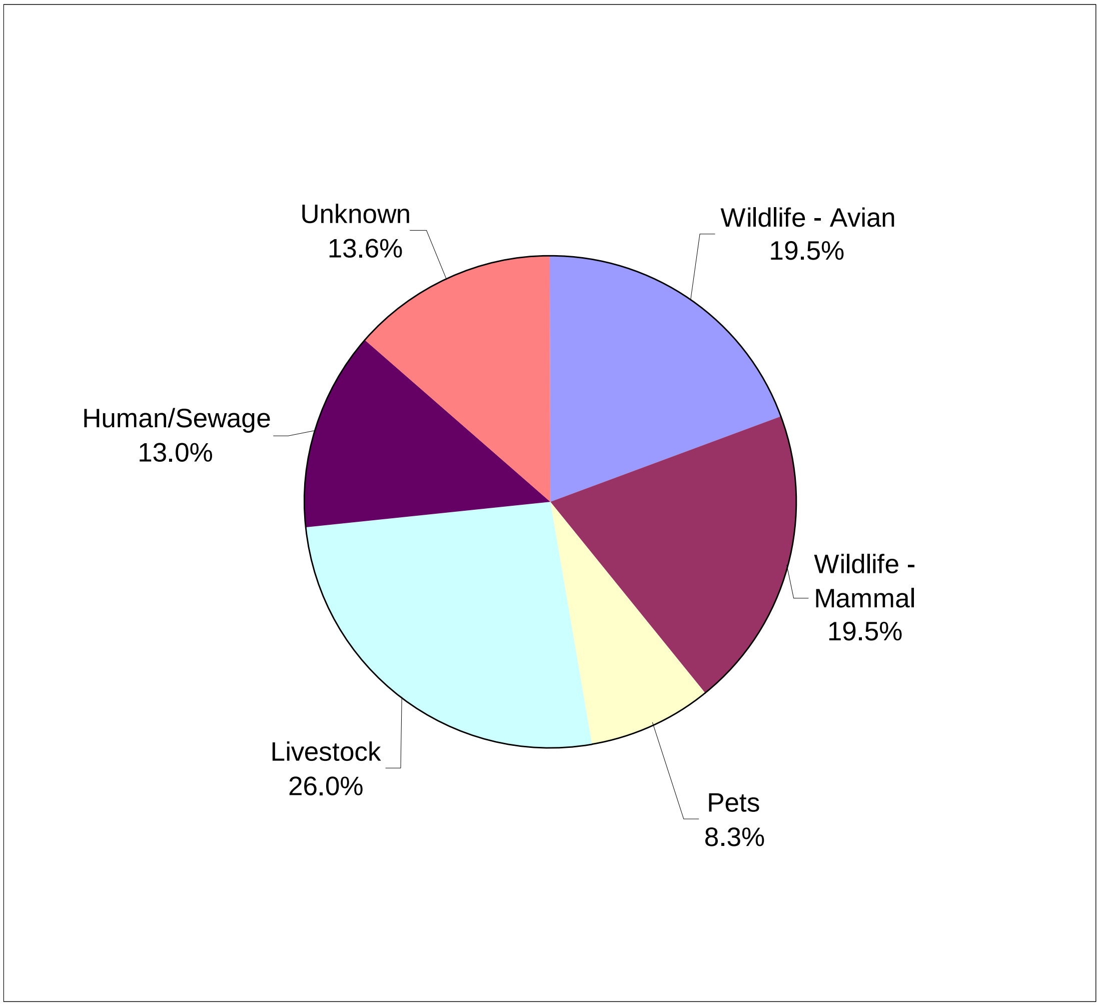
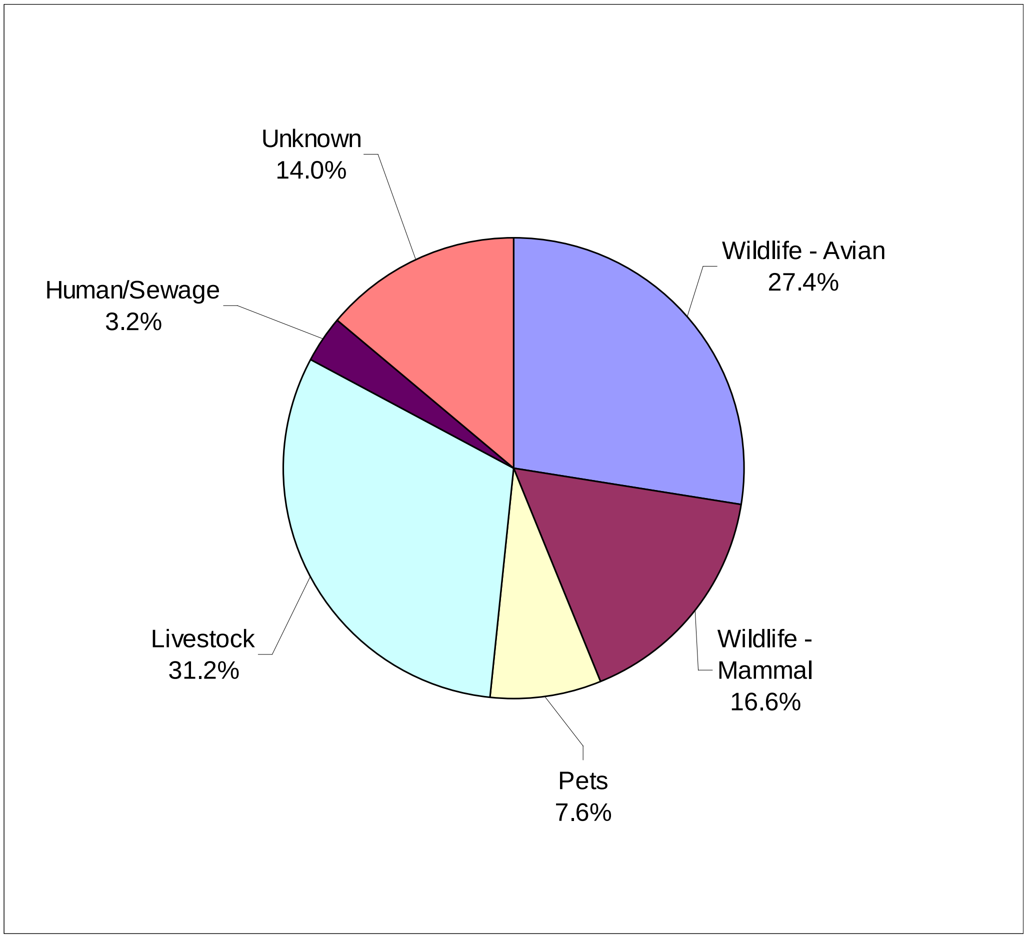


Table 3-12 *E. coli* source characterization of Station 12087

Super - category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	4.5%	0.7-8.4%	0.0%	0.0-0.0%	3.2%	0.4-5.9%
Livestock	—	29.1%	20.6-37.6%	36.2%	22.4-49.9%	31.2%	24.0-38.5%
Pets	—	8.2%	3.1-13.3%	6.4%	0.0-13.4%	7.6%	3.5-11.8%
Wildlife	Mammal	12.7%	6.5-19.0%	25.5%	13.1-38.0%	16.6%	10.7-22.4%
Wildlife	Avian	28.2%	19.8-36.6%	25.5%	13.1-38.0%	27.4%	20.4-34.4%
Wildlife	Subtotal	40.9%	31.7-50.1%	51.1%	36.8-65.4%	43.9%	36.2-51.7%
Unknown	—	17.3%	10.2-24.3%	6.4%	0.0-13.4%	14.0%	8.6-19.4%

Figure 3-5 *E. coli* source characterization of Station 12087 under all conditions



3.2.3.6 Station 12086 Upper Oyster Creek at SH 6

In this section, results for Station 12086 are described individually. This source characterization is based on 130 isolates collected in nine non-runoff events, and 49 isolates collected in three runoff events. Table 3-13 and Figure 3-6 summarize the identified sources of *E. coli* from all 12 events, including both runoff and non-runoff conditions. The human and sewage source contribution was 15.6 percent overall, slightly higher than that of the watershed as a whole. Horses represented only 2.2 percent of the *E. coli* sources and rodents were a major source at this site, representing over 17 percent of the *E. coli* typed (see Appendix G, Table G-3 for contribution by individual sources, such as rodent). In general *E. coli* sources at this station closely resembled those of the watershed as a whole.

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, un-weighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

3.2.3.7 Station 12083 Upper Oyster Creek at Highway 90A in Sugar Land

In this section, results for Station 12083 are described individually. This source characterization is based on 92 isolates collected in nine non-runoff events and 47 isolates collected in three runoff events. Table 3-14 and Figure 3-7 summarize the identified sources of *E. coli* from all 12 events, including both runoff and non-runoff conditions. A more detailed summary of sources is provided in Appendix G, Table G-4. The human and sewage source contribution was 20.9 percent overall, substantially higher than that of the watershed as a whole. Livestock contributions were minor at this site. These observations agree with the urbanized nature at this station. The source of approximately 14 percent of the *E. coli* isolates could not be identified.

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, un-weighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

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Table 3-13 *E. coli* source characterization of Station 12086

Super - category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	16.9%	10.5-23.4%	12.2%	3.1-21.4%	15.6%	10.3-21.0%
Livestock	—	15.4%	9.2-21.6%	16.3%	6.0-26.7%	15.6%	10.3-21.0%
Pets	—	9.2%	4.3-14.2%	4.1%	0.0-9.6%	7.8%	3.9-11.8%
Wildlife	mammal	26.2%	18.6-33.7%	26.5%	14.2-38.9%	26.3%	19.8-32.7%
Wildlife	Avian	22.3%	15.2-29.5%	28.6%	15.9-41.2%	24.0%	17.8-30.3%
Wildlife	subtotal	48.5%	39.9-57.1%	55.1%	41.2-69.0%	50.3%	43.0-57.6%
Unknown	—	10.0%	4.8-15.2%	12.2%	3.1-21.4%	10.6%	6.1-15.1%

Figure 3-6 *E. coli* source characterization of Station 12086 under all conditions

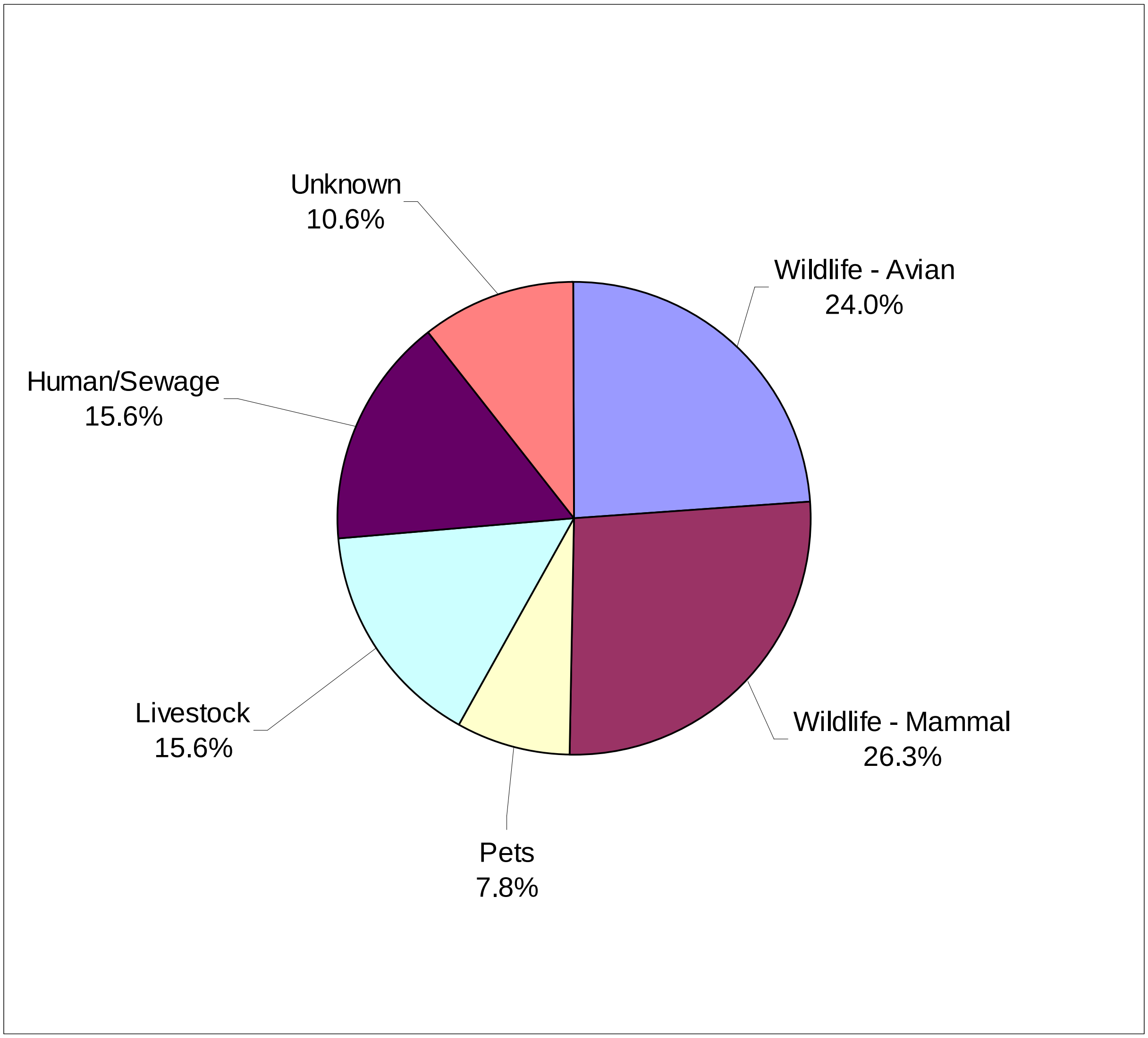
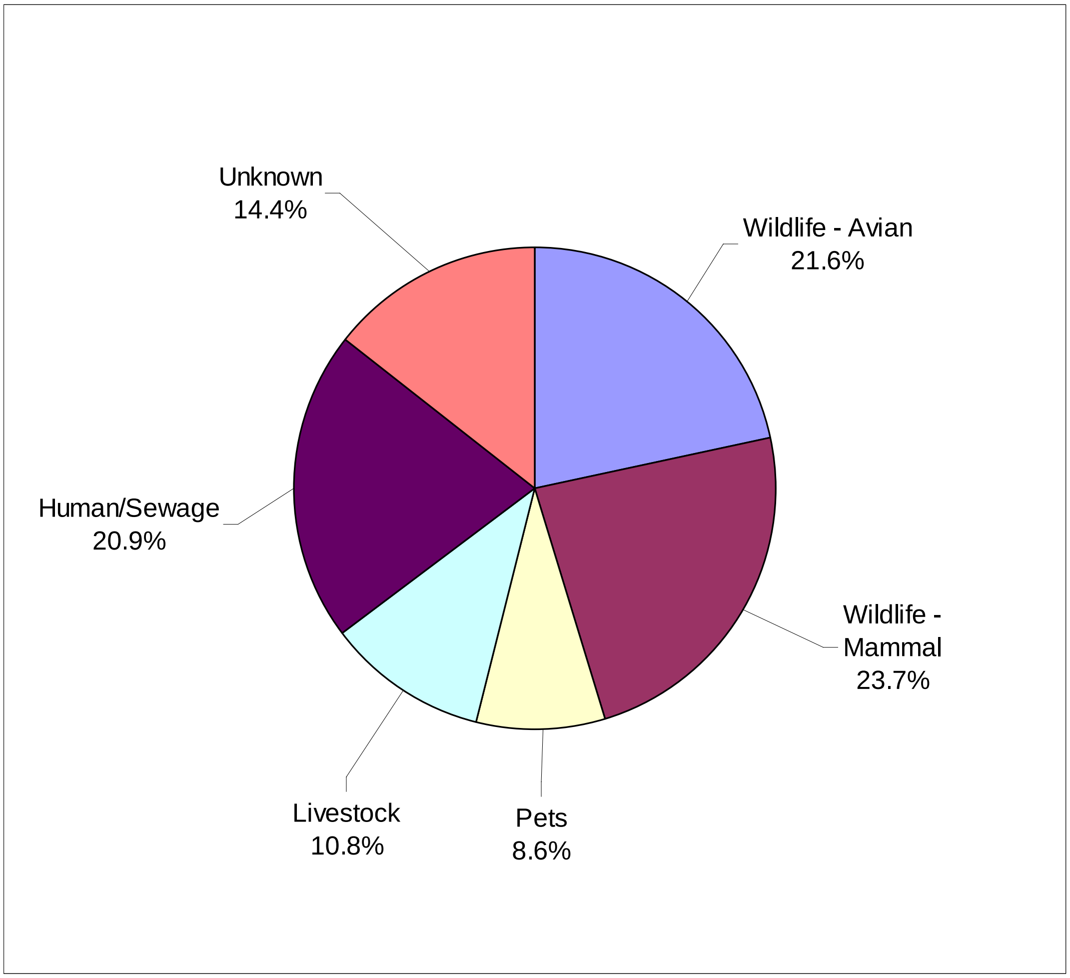


Table 3-14 *E. coli* source characterization of Station 12083

Super - category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	17.4%	9.6-25.1%	27.7%	14.9-40.4%	20.9%	14.1-27.6%
Livestock	—	10.9%	4.5-17.2%	10.6%	1.8-19.5%	10.8%	5.6-15.9%
Pets	—	9.8%	3.7-15.9%	6.4%	0.0-13.4%	8.6%	4.0-13.3%
Wildlife	mammal	28.3%	19.1-37.5%	14.9%	4.7-25.1%	23.7%	16.7-30.8%
Wildlife	Avian	17.4%	9.6-25.1%	29.8%	16.7-42.9%	21.6%	14.7-28.4%
Wildlife	subtotal	45.7%	35.5-55.8%	44.7%	30.5-58.9%	45.3%	37.0-53.6%
Unknown	—	16.3%	8.8-23.9%	10.6%	1.8-19.5%	14.4%	8.6-20.2%

Figure 3-7 *E. coli* source characterization of Station 12083 under all conditions



3.2.3.8 Station 17688 Stafford Run at El Dorado Boulevard

In this section, the results for Station 17688 are described individually. This source characterization is based on 135 isolates collected in nine non-runoff events and 48 isolates collected in three runoff events. Table 3-15 and Figure 3-8 summarize the identified sources of *E. coli* from all 12 events, including both runoff and non-runoff conditions. A more detailed summary of sources is provided in Appendix G, Table G-5. In most respects, the source contributions at this site mirrored that of the watershed as a whole. Perhaps the only significant difference was that the source of approximately 22 percent of the *E. coli* isolates could not be identified, and one third of those collected under runoff conditions could not be identified.

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, un-weighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

3.2.3.9 Station 12074 Flat Bank Creek at SH 6

In this section, results for Station 12074 are described individually. This source characterization is based on 119 isolates collected in nine non-runoff events and 49 isolates collected in three runoff events. Table 3-16 and Figure 3-9 summarize the identified sources of *E. coli* from all 12 events, including both runoff and non-runoff conditions. The sewage contribution at this site was 21.4 percent, higher than that of the watershed as a whole. The porcine contribution was also relatively high under both runoff and non-runoff conditions (see Appendix G, Table G-6 for contribution by individual sources, such as porcine).

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, un-weighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

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Table 3-15 *E. coli* source characterization of Station 17688

Super – category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	16.3%	10.1-22.5%	12.5%	3.1-21.9%	15.3%	10.1-20.5%
Livestock	—	14.8%	8.8-20.8%	8.3%	0.5-16.2%	13.1%	8.2-18.0%
Pets	—	11.9%	6.4-17.3%	4.2%	0.0-9.8%	9.8%	5.5-14.2%
Wildlife	mammal	19.3%	12.6-25.9%	8.3%	0.5-16.2%	16.4%	11.0-21.8%
Wildlife	Avian	18.5%	12.0-25.1%	35.4%	21.9-48.9%	23.0%	16.9-29.0%
Wildlife	subtotal	37.8%	29.6-46.0%	43.8%	29.7-57.8%	39.3%	32.3-46.4%
Unknown	—	19.3%	12.6-25.9%	31.3%	18.1-44.4%	22.4%	16.4-28.4%

Figure 3-8 *E. coli* source characterization of Station 17688 under all conditions

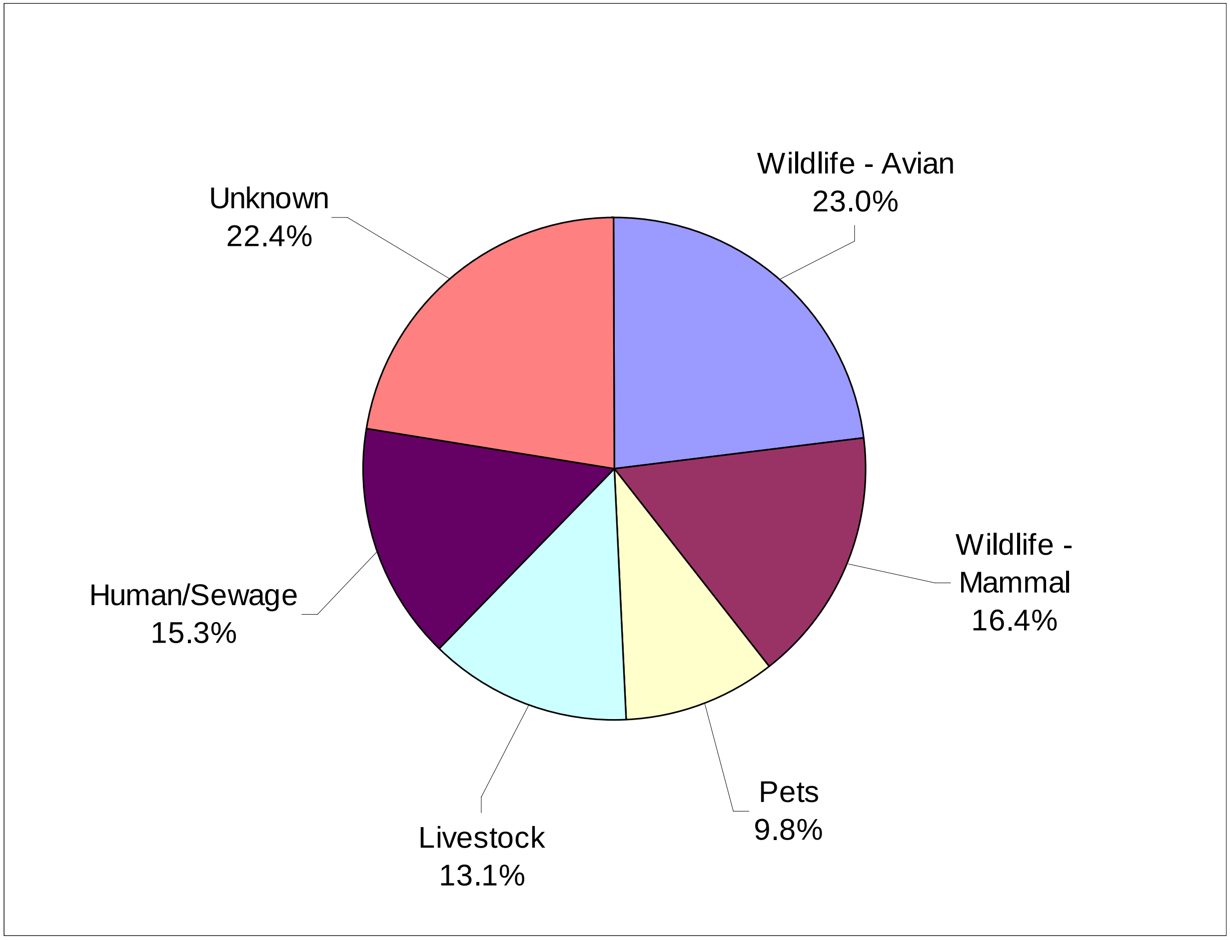
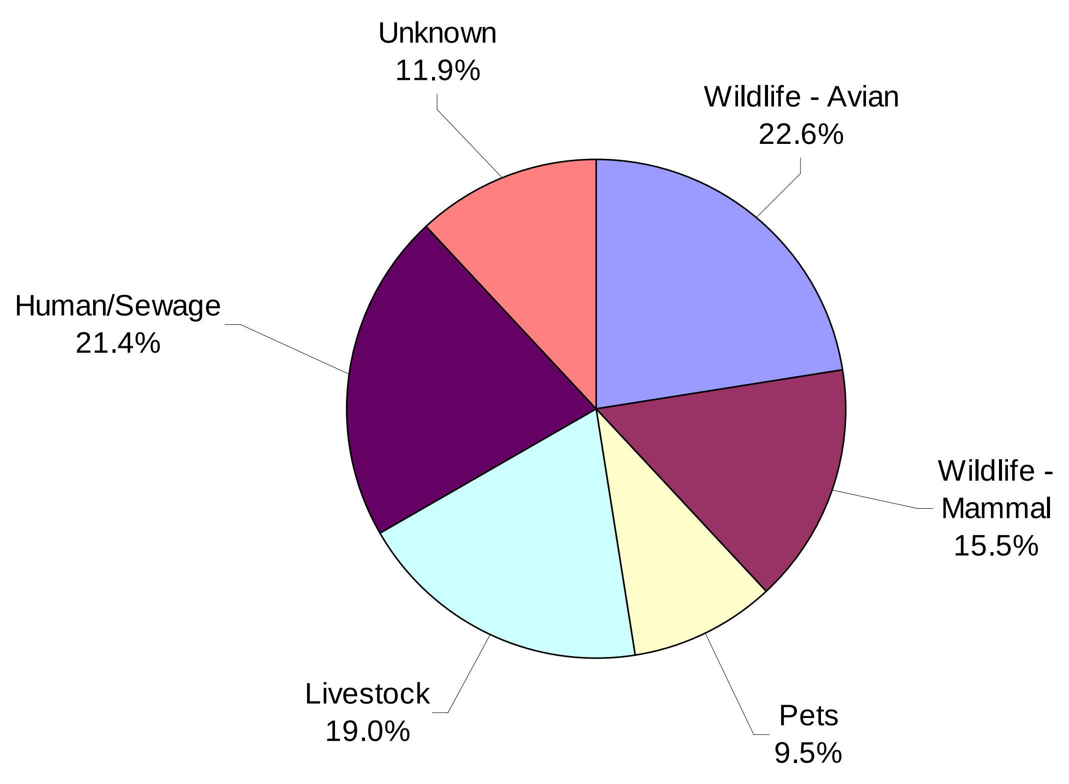


Table 3-16 *E. coli* source characterization of Station 12074

Super - category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	21.8%	14.4-29.3%	20.4%	9.1-31.7%	21.4%	15.2-27.6%
Livestock	—	20.2%	13.0-27.4%	16.3%	6.0-26.7%	19.0%	13.1-25.0%
Pets	—	7.6%	2.8-12.3%	14.3%	4.5-24.1%	9.5%	5.1-14.0%
Wildlife	mammal	12.6%	6.6-18.6%	22.4%	10.8-34.1%	15.5%	10.0-20.9%
Wildlife	Avian	24.4%	16.7-32.1%	18.4%	7.5-29.2%	22.6%	16.3-28.9%
Wildlife	subtotal	37.0%	28.3-45.6%	40.8%	27.1-54.6%	38.1%	30.8-45.4%
Unknown	—	13.4%	7.3-19.6%	8.2%	0.5-15.8%	11.9%	7.0-16.8%

Figure 3-9 *E. coli* source characterization of Station 12074 under all conditions



3.2.3.10 Station 11516 Red Gully at Richmond-Gaines Road

In this section, results for supplemental Station 11516 are described individually. This source characterization is based on 20 isolates collected in two non-runoff events and 20 isolates collected in two runoff events. Due to the relatively small number of isolates, the confidence intervals around the source estimates are broad. With the qualification that the source estimates are based on only 40 isolates, canines and birds were well-represented among those, while the human/sewage category was not. Table 3-17 and Figure 3-10 summarize the identified sources of *E. coli* from all four events, including both runoff and non-runoff conditions. A more detailed summary of sources is provided in Appendix G, Table G-7.

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, un-weighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

3.2.3.11 Station 17685 Jones Creek at Bois D’Arc Lane

In this section, results for supplemental Station 17685 are described individually. This source characterization is based on 25 isolates collected in two non-runoff events and 23 isolates collected in two runoff events. Due to the relatively small number of isolates, the confidence intervals around the source estimates are broad. Table 3-18 and Figure 3-11 summarize the identified sources of *E. coli* from all four events, including both runoff and non-runoff conditions. A more detailed summary of sources is provided in Appendix G, Table G-8. Few isolates at this site were from human and sewage sources, which is expected given the rural nature of this western area of the watershed; otherwise the sources were similar to the watershed as a whole. Because of downstream proximity of this station to the Shannon Pump Station, the sources characterized here also reflect conditions in the Brazos River at the pump station during the four sampled events.

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, un-weighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

Table 3-17 *E. coli* source characterization of Station 11516

Super - category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	10.0%	0.0-23.1%	0.0%		5.0%	0.0-11.8%
Livestock	—	0.0%		25.0%	6.0-44.0%	12.5%	2.3-22.7%
Pets	—	25.0%	6.0-44.0%	15.0%	0.0-30.6%	20.0%	7.6-32.4%
Wildlife	mammal	5.0%	0.0-14.6%	15.0%	0.0-30.6%	10.0%	0.7-19.3%
Wildlife	Avian	40.0%	18.5-61.5%	30.0%	9.9-50.1%	35.0%	20.2-49.8%
Wildlife	subtotal	45.0%	23.2-66.8%	45.0%	23.2-66.8%	45.0%	29.6-60.4%
Unknown	—	20.0%	2.5-37.5%	15.0%	0.0-30.6%	17.5%	5.7-29.3%

Figure 3-10 *E. coli* source characterization of Station 11516 under all conditions

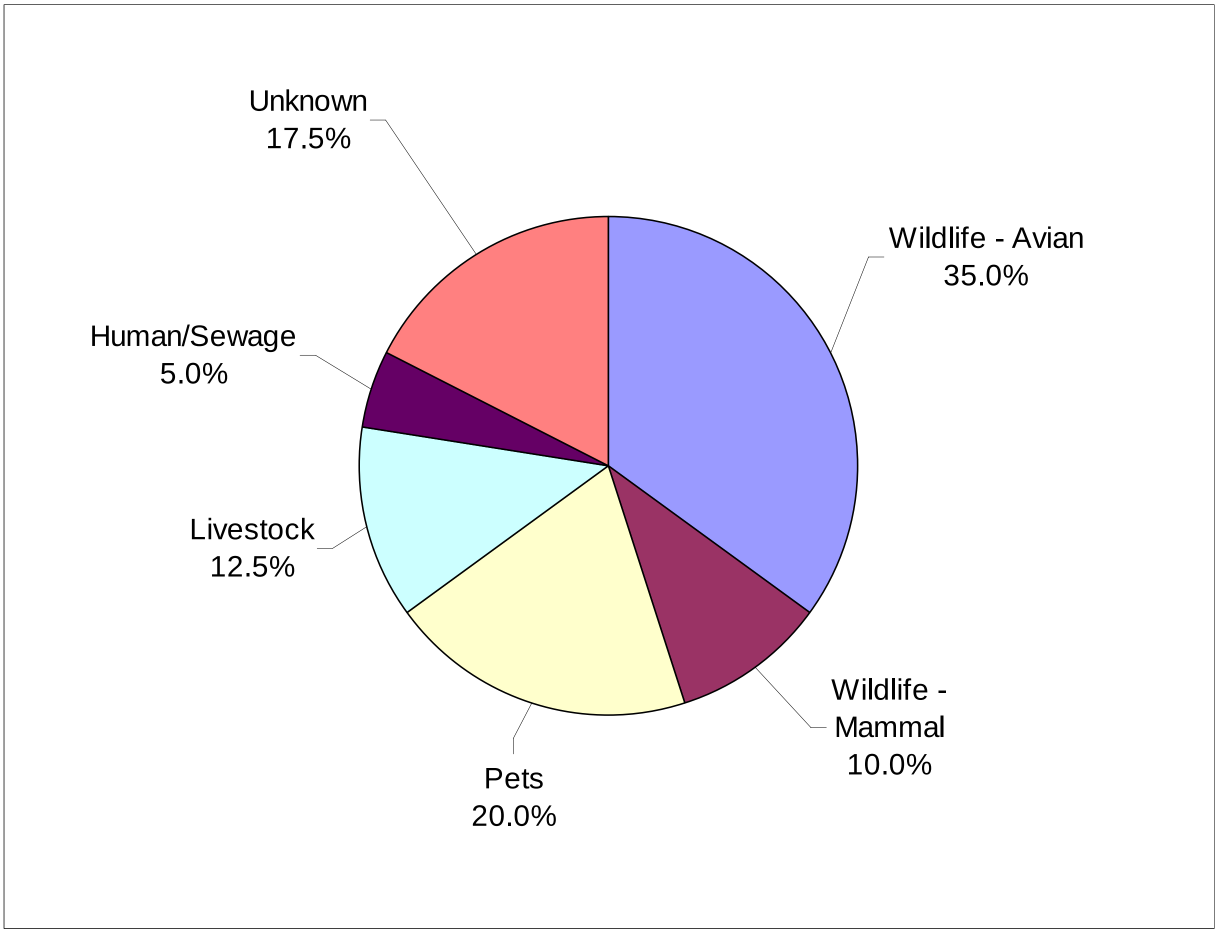
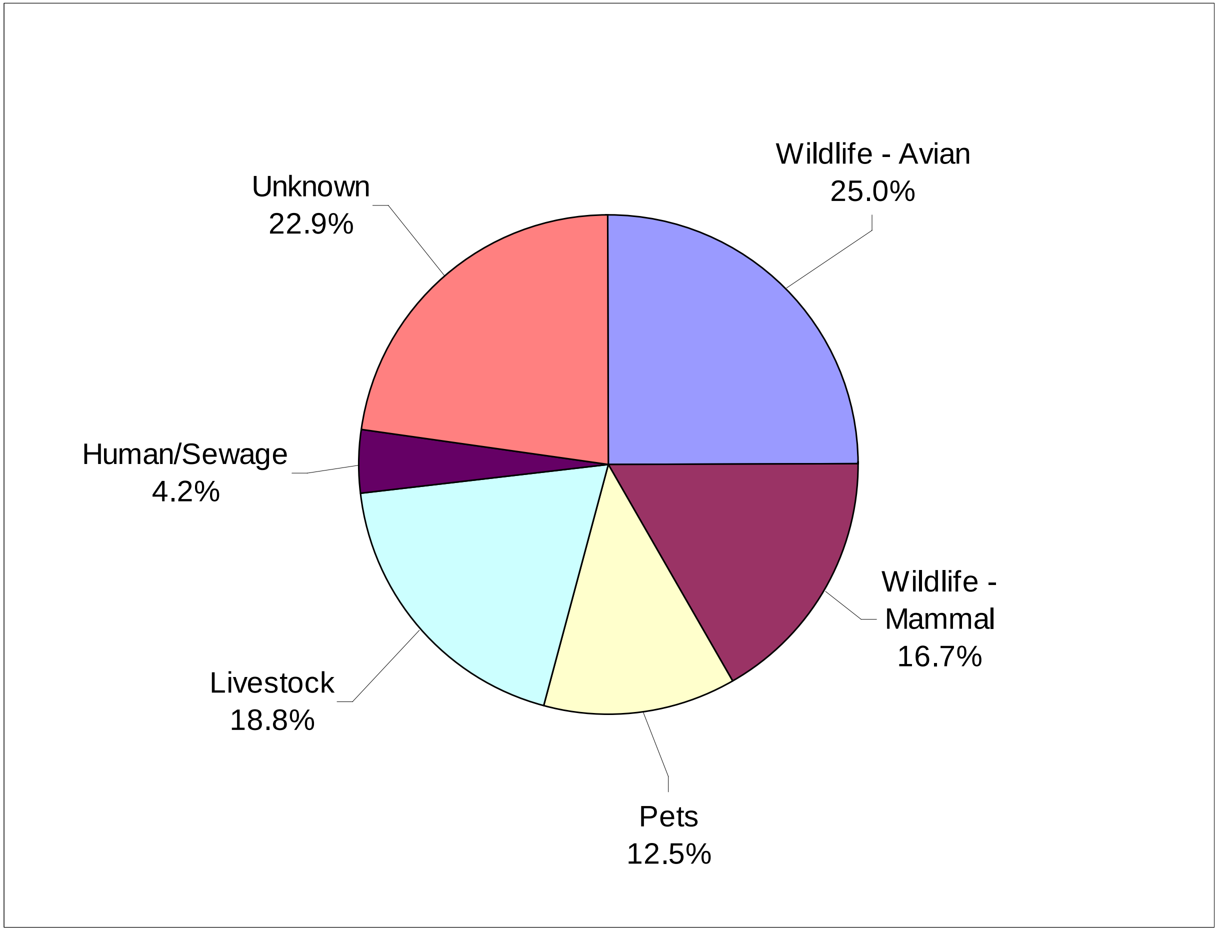


Table 3-18 *E. coli* source characterization of Station 17685

Super - category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	4.0%	0.0-11.7%	4.3%	0.0-12.7%	4.2%	0.0-9.8%
Livestock	—	20.0%	4.3-35.7%	17.4%	1.9-32.9%	18.8%	7.7-29.8%
Pets	—	4.0%	0.0-11.7%	21.7%	4.9-38.6%	12.5%	3.1-21.9%
Wildlife	Mammal	32.0%	13.7-50.3%	0.0%		16.7%	6.1-27.2%
Wildlife	Avian	12.0%	0.0-24.7%	39.1%	19.2-59.1%	25.0%	12.8-37.3%
Wildlife	Subtotal	44.0%	24.5-63.5%	39.1%	19.2-59.1%	41.7%	27.7-55.6%
Unknown	—	28.0%	10.4-45.6%	17.4%	1.9-32.9%	22.9%	11.0-34.8%

Figure 3-11 *E. coli* source characterization of Station 17685 under all conditions



3.2.3.12 Station 17686 Flewellen Creek at Briscoe Road

In this section, results for supplemental Station 17686 are described individually. This source characterization is based on 29 isolates collected in two non-runoff events and 24 isolates collected in two runoff events. Due to the relatively small number of isolates, the confidence intervals around the source estimates are broad. Table 3-19 and Figure 3-12 summarize the identified sources of *E. coli* from all four events, including both runoff and non-runoff conditions. A more detailed summary of sources is provided in Appendix G, Table G-9. The large number of sewage isolates at this site under runoff conditions was somewhat surprising, given the rural nature of this western area of the watershed.

The event normalizations and concentration-weighted source characterizations are not presented for this site because there were no significant differences from the non-normalized, un-weighted results. Also, there were no statistically significant differences in source contributions under runoff versus non-runoff conditions.

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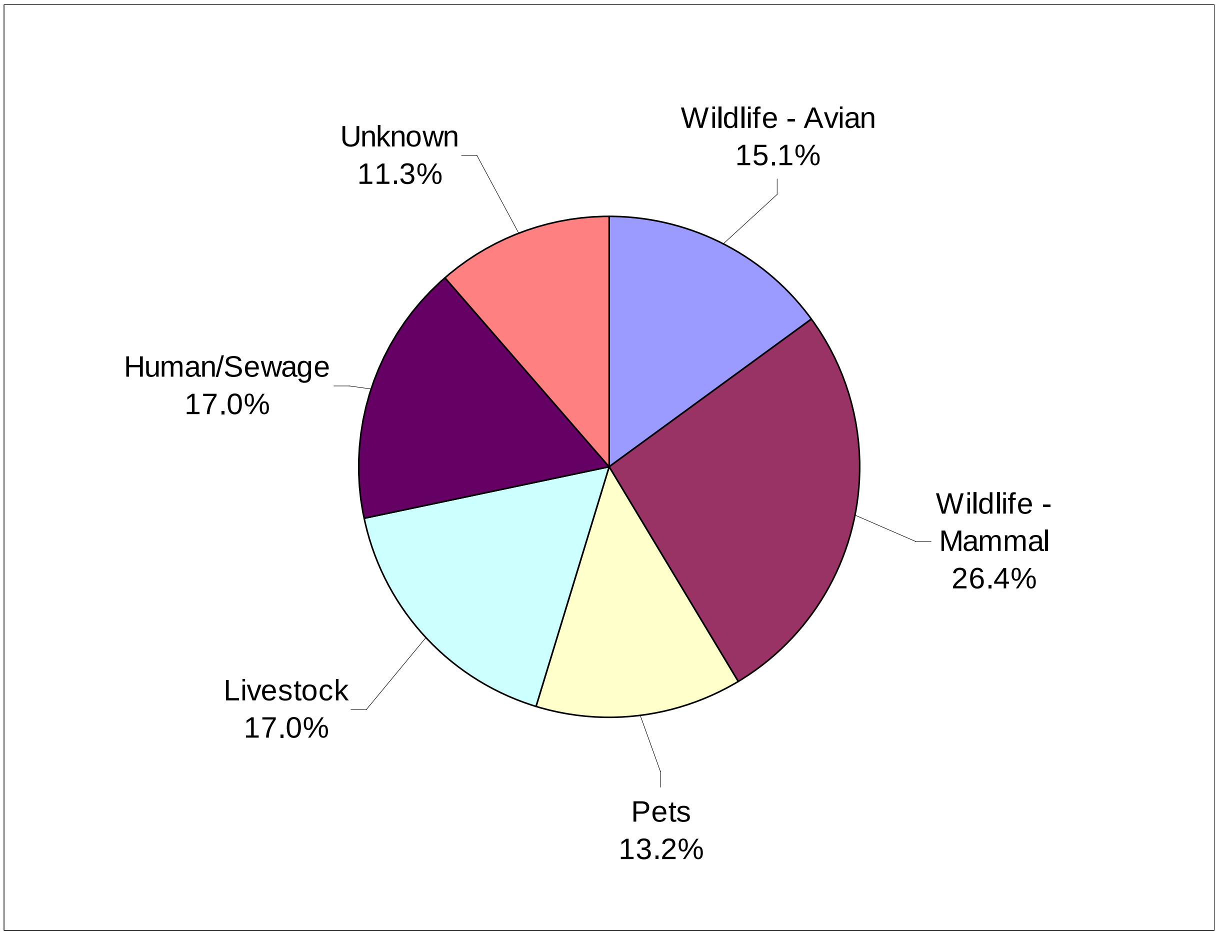
Table 3-19 *E. coli* source characterization of Station 17686

Super – category	Category	Non-runoff		Runoff		All Conditions	
		% Contribution	95% CI	% Contribution	95% CI	% Contribution	95% CI
Human	—	10.3%	0.0-21.4%	25.0%	7.7-42.3%	17.0%	6.9-27.1%
Livestock	—	20.7%	5.9-35.4%	12.5%	0.0-25.7%	17.0%	6.9-27.1%
Pets	—	13.8%	1.2-26.3%	12.5%	0.0-25.7%	13.2%	4.1-22.3%
Wildlife	mammal	31.0%	14.2-47.9%	20.8%	4.6-37.1%	26.4%	14.5-38.3%
Wildlife	Avian	13.8%	1.2-26.3%	16.7%	1.8-31.6%	15.1%	5.5-24.7%
Wildlife	subtotal	44.8%	26.7-62.9%	37.5%	18.1-56.9%	41.5%	28.2-54.8%
Unknown	—	10.3%	0.0-21.4%	12.5%	0.0-25.7%	11.3%	2.8-19.9%

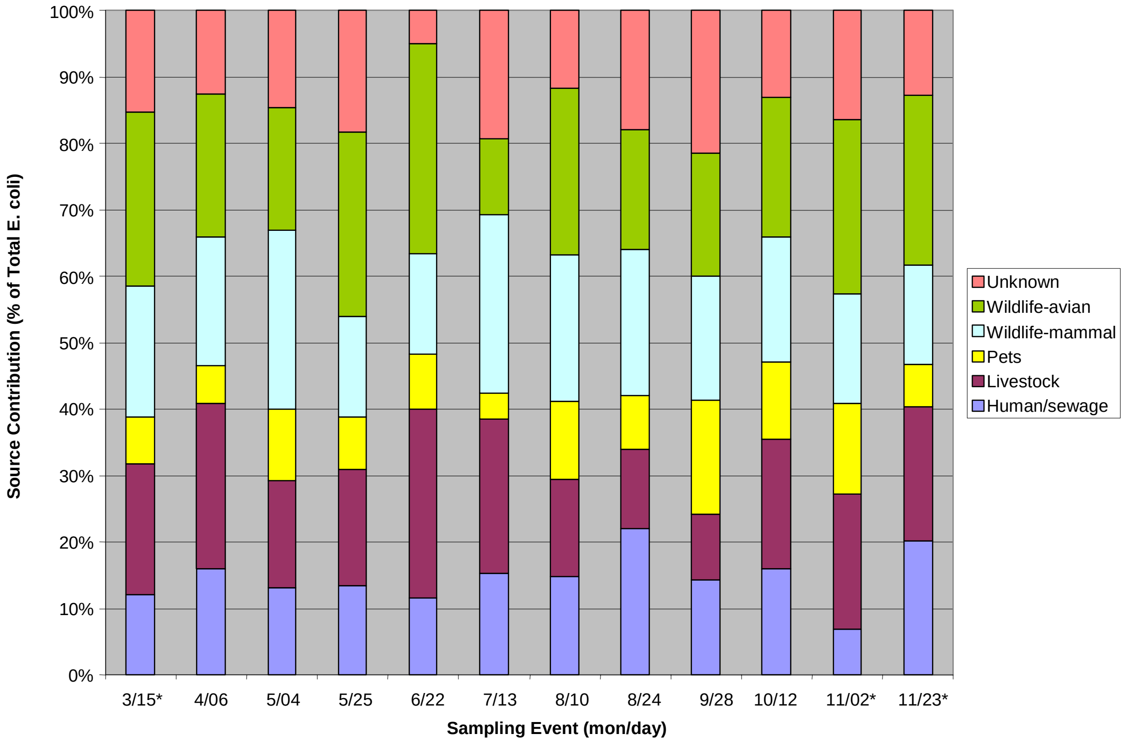
Figure 3-12 *E. coli* source characterization of Station 17686 under all conditions



3.2.3.13 Seasonality of *E. coli* Sources

An analysis of the source contributions for each sampling event was performed to identify changes in source composition from season to season. Figure 3-13 does not indicate a pronounced or systematic variation in the relative magnitude of major source categories from event to event. This figure includes data from all sites. Note that events one, eleven and twelve were runoff events.

Figure 3-13 Seasonal *E. coli* source characterization.



*Runoff influenced event

3.2.4 Summary and Conclusions

To determine sources of the *E. coli* in Oyster Creek ribotyping was selected as the bacterial source tracking (BST) method. Six core water sampling stations were established where high bacteria levels were identified from the 2002-2003 sampling. These core stations were sampled during 12 events from March through November 2004. Three supplemental stations were added in September 2004 to provide additional information on the spatial distribution of sources. Overall 1,136 *E. coli* isolates from ambient water samples were ribotyped. At all six core stations, the project objective of 120 ribotyped isolates was exceeded, sometimes substantially.

A mixture of sources contributing to observed *E. coli* levels was identified by BST. No single source category comprised the dominant source of *E. coli* at any station. Wildlife were the source of approximately 43% of the *E. coli* when data from all stations were combined, and the wildlife sources were roughly evenly split between avian and mammals. Major wildlife contributors included rodents (11%), waterfowl (7%), and raccoons (4%). Livestock (primarily cattle, horses, and hogs) accounted for approximately 19% of the observed *E. coli*. Dogs accounted for approximately 9% of the *E. coli*. Human and sewage accounted for approximately 14% of the *E. coli*. The source of approximately 15% of the *E. coli* could not be identified, either because there were no matching ribotypes in the known source library or because the matching isolates were transients, i.e., they are not host-specific having been observed in multiple types of host species.

There were no statistically significant differences in sources under rainfall-runoff versus non-runoff conditions when the data were evaluated either collectively or station-by-station. Similarly, event normalizations and concentration-weighted source characterizations did not result in any significant differences from the non-normalized, unweighted results for any station. No significant patterns of seasonal variation in source contribution were observed when the data were evaluated collectively. Seasonality on a station-by-station basis was not performed, because insufficient *E. coli* isolates were ribotyped for any one event by station to allow statistically valid evaluations at this spatial and temporal level.

In general, source identification results for individual sites did not depart significantly from the results of the combined data set (Table 3-20). The station-to-station differences in source composition that were observed could in some instances be related to watershed characteristics. For example, the human and sewage influence was less apparent and the livestock influence more apparent in the more rural western portions of the watershed. Also, the porcine influence, though not shown in Table 3-20, was highest at station 12087, which is just downstream of the TDCJ Jester Unit hog farm. Even at this station, porcine only constituted approximately 15% of the *E. coli*, and at the next downstream station, 12086, the porcine contribution was back to the average across all stations.

As shown in Table 3-20 a diversity of sources contributed to the observed *E. coli* at each station, and no source dominated contribution at any station. As examples, human and sewage never comprised over a quarter of the contribution at any station, and livestock never comprised over a third of the contribution at any station. The combination of mammal and avian wildlife categories comprised the largest percent contribution and the percent is generally in the 40% range. The wide spectrum of *E. coli* sources and the absence of dominance by any particular source indicate that approaches to reduce *E. coli* in Upper Oyster Creek will need to be broad and consider a wide variety of control measures.

Table 3-20 *E. coli* source characterization summarization for Upper Oyster Creek

Station	Human & Sewage	Livestock	Pets	Wildlife (mammal)	Wildlife (avian)	Unknown
All	14.2%	18.9%	9.4%	19.5%	23.2%	14.9%
12090	13.0%	26.0%	8.3%	19.5%	19.5%	13.6%
12087	3.2%	31.2%	7.6%	16.6%	27.4%	14.0%
12086	15.6%	15.6%	7.8%	26.3%	24.0%	10.6%
12083	20.9%	10.8%	8.6%	23.7%	21.6%	14.4%
17688	15.3%	13.1%	9.8%	16.4%	23.0%	22.4%
12074	21.4%	19.0%	9.5%	15.5%	22.6%	11.9%
11516*	5.0%	12.5%	20.0%	10.0%	35.0%	17.5%
17685*	4.2%	18.8%	12.5%	16.7%	25.0%	22.9%
17686*	17.0%	17.0%	13.2%	26.4%	15.1%	11.3%

*Stations added for events 9-12.

SECTION 4

BACTERIA ALLOCATION TOOL DEVELOPMENT

This report section provides the basis for the bacteria allocation tool used to assist in developing the TMDL allocation. First the reason will be discussed for selecting a hybrid tool that combines an empirical based approach with the necessary streamflow data provided by a mechanistic hydrologic model. Provided next is the development and calibration of the hydrologic model. The section ends with development of the bacteria load duration curves as the tool for allocation.

4.1 Model Selection

The TMDL allocation process for bacteria involves assigning bacteria, e.g., *E. coli*, loads to their sources such that the total loads do not violate the pertinent numeric criteria protecting contact recreation use. To perform the allocation process, a tool must be developed to assist in allocating bacteria loads. Selection of the appropriate bacteria allocation tool for Upper Oyster Creek considered availability of data and other information necessary for supportable application of the selected tool. Generally one of two basic approaches is in common usage for bacteria TMDLs—mechanistic computer models and an empirical approach referred to as the load duration curve.

The preferred allocation tool is often a mechanistic computer model. These models provide analytical abstractions of the real or prototype system—for this situation Upper Oyster Creek. Mechanistic models, also referred to as process models, are based on theoretical principles that provide for representation of governing processes that determine the response of certain state variables, such as streamflow and bacteria concentration. Under circumstances where the governing processes are acceptably quantifiable, the mechanistic model provides understanding of the important biological, chemical, and physical processes of the prototype system and reasonable predictive capabilities to evaluate alternative allocations of pollutant load sources.

The load duration curve approach has found relatively broad acceptance among the regulatory community, because of the simplicity of the approach and ease of application. Whether implicitly or explicitly a consideration of the regulatory community, the approach further recognizes the frequent data limitations with bacteria TMDLs that constrain use of the more powerful mechanistic models. The load duration curve approach has no capabilities to allow evaluation of alternative allocation approaches to reach TMDL goals, but it does provide a means to estimate the amount of bacteria reduction required and indications of the broad origins of the bacteria, i.e., point source and nonpoint source.

4.1.1 Situational Limitations of Mechanistic Modeling

Because the present surface water bacteria standards for Upper Oyster Creek, as most Texas waters, do not distinguish under what streamflow conditions the criteria should be met, the allocation process must consider all streamflow conditions ranging from low flows to high flows.[2] The allocation tool, therefore, must be capable of characterizing streamflows and bacteria loads at desired locations under a wide variety of environmental conditions as experienced in Upper Oyster Creek. If a mechanistic modeling tool is applied, it must be capable of simulating response of Upper Oyster Creek bacterial loadings to hydrologic (streamflow) conditions during base flow as well as during times of response to rainfall runoff and those intermediate conditions between well-defined base flow and strong rainfall-runoff response. The type of mechanistic tool with capabilities to simulate all these complexities is often referred to as a combined watershed loading and hydrologic/water quality model. These models simulate the hydrologic response of the watershed to rainfall, route runoff water through the conveyance channels of the watershed, add in point source contributions, and typically include other hydrologic processes such as interaction of surface waters with shallow ground water.

The bacteria component of the model is in many ways even more complex than the hydrologic component and typically must include many different processes. Point sources and nonpoint sources of bacteria need to be defined and simulated by the model. Movement or washoff of bacteria from the various landscapes (e.g., urban yards, roads, pastures, wooded areas, areas of animal concentration), potential illegal connections of sewage lines to stormwater lines, broken sewer lines, and sewer overflows in response to rainfall are only some of the sources possibly needing to be represented in the model. Transport of the bacteria in Upper Oyster Creek by streamflow and the response of the bacteria while in transport to settling, die-off, resuspension, regrowth in the water column, regrowth in the sediment, etc. need to be defined with adequate certainty to allow proper model representation for each of these physical and biological processes.

While admittedly the hydrologic processes requiring simulation are complex, these processes are generally better understood and more readily simulated within needed levels of confidence by a mechanistic model than the bacterial processes. The hydrologic processes regarding response of the landscape to rainfall are well studied over many decades because of implications on transport of waterborne constituents, of which bacteria is only one of many. But even more importantly, these hydrologic processes are well investigated because of needs to design reservoirs and flood-control structures, define floodplains, and design the myriad of other structures required to direct and retain stormwater in both urban and rural situations. While each watershed is unique, the experienced hydrologist is able to readily and successfully apply these mechanistic

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[2] Present State of Texas surface water quality standards do not require that the criteria to protect contact recreation use be met when streamflow conditions are below the 7-day, 2-year low-flow.

models, often though not preferably, with minimal or no streamflow data from the prototype system to validate model predictions.

Mechanistic bacteria modeling has evolved over the last several decades beginning in the late 1960s to early 1970s as increasing computer resources have made such endeavors possible. Regrettably for the application of mechanistic bacteria models, while the numerical equations to represent many pertinent processes exist and are incorporated in readily available models, these processes are appreciably more watershed specific than hydrologic processes. As one simple example, whether or not there are failed on-site treatment systems, such as septic systems, in a watershed rarely makes measurable differences to streamflow, but can dramatically impact *E. coli* concentrations present in the same streamflow. In the vast majority of circumstances, and Upper Oyster Creek is no exception, only very limited watershed-specific information is available on many of the physical and biological processes that affect bacteria concentrations and loadings. Consequentially, the operator of the mechanistic model must specify, in many circumstances, numerous input parameters governing bacteria processes for which actual numeric values can not be known within a reasonable range of certainty. Compounding the problems is that the bacteria concentrations and loadings predicted by the model, which potentially contain high uncertainty, will of necessity be used in direct comparison to the relevant numeric criteria.

4.1.2 Upper Oyster Creek Data Resources

Streamflow and *E. coli* data availability were used to provide guidance in the allocation tool selection process. As already mentioned, the necessary information and data are largely unavailable for Upper Oyster Creek to allow adequate definition of most of the physical and biological processes influencing in-stream bacteria concentrations, and this limitation became an important consideration in the allocation tool selection process.

Recent monitoring associated with the present Segment 1245 bacteria TMDL does provide a moderate amount of *E. coli* data collected under a variety of hydrologic conditions with some stations having as many as 24 data points obtained during the period from October 2002 through November 2004 (TIAER et al., 2005). Though more limited than the *E. coli* data, streamflow data from physical measurement as opposed to streamflow gauging station data are available at selected locations within Upper Oyster Creek watershed. No continuous streamflow (e.g., daily) data on Upper Oyster Creek are available for recent years, though daily records are available for the two pumping stations operated by the Gulf Coast Water Authority (GCWA).[3]

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[3] Historical streamflow data are available for the period from 1931 through 1973 at U.S. Geological Survey station 08112500.

4.1.3 Allocation Tool Selection

Based on limitations of data availability, the decision was to use a hybrid allocation tool composed of the load duration curve approach and a mechanistic hydrologic model. The load duration curve approach involves:

- definition of a streamflow duration curve at desired points requiring daily streamflow data over a period of at least several years,
- development of allowable bacteria load duration curve at the same points based on the relevant criteria and the data from the streamflow duration curve,
- superposing of historical bacteria data, in this situation *E. coli* data from 2002–2004, on the allowable bacteria load duration curve, and
- interpretation of the superposed bacteria data in the context of both the bacterial source tracking findings and the allowable bacteria load duration curve, which allows informed and data supported decisions regarding allocation of loads among sources.

Because of information limitations mentioned in the preceding paragraphs, the strengths of the mechanistic bacteria model become its weakness, and the degree of uncertainty surrounding the predictions of the model, if truly ascertained, negate any advantages of this approach over the simpler empirical approach. Under circumstances of limited information on bacteria processes in Upper Oyster Creek, the greater resource commitment to develop and apply a mechanistic model was considered unwarranted when compared to the reduced resource commitment for the load duration curve approach.

However, streamflow data limitations posed a challenge to use of the load duration curve approach to Segment 1245. The approach requires an adequate amount of streamflow data, typically multiple years of daily data, which in many watersheds may be readily obtained from U.S. Geological Survey (USGS) gauging stations. When such data are not available for desired locations, various accepted procedures, such as interpolation of intermediate locations between USGS gauging stations and simple drainage area ratios, may be used to construct the necessary data record. Upper Oyster Creek's hydrology, however, contains several complications that make the absence of watershed-specific data an important complexity. The pumping of water from the Brazos River into the watershed's conveyance system and the removal of this water by additional pumping is one complexity. The presence of several relatively large municipal wastewater treatment plant (WWTP) discharges is another. Various diversions of stormwater flows out of the watershed to limit or prevent flooding in urban areas is yet another. As a result of these hydrologic complexities and in the absence of pertinent historical hydrologic data, the decision was reached to apply the hydrologic components of a watershed loading, mechanistic model in order to provide the necessary daily streamflow data for the load duration curve approach.

Fortunately, the use of streamflow data generated from a mechanistic model does not carry the same implications as predictions of bacteria. First, hydrologic predictions in this situation need to only be relatively correct in magnitude in order to distinguish low, moderate, and high flow, since they are not to be used in comparison to absolute numeric criteria. Second, as stated above, mechanistic hydrologic model capabilities are generally much more robust and transferable from one watershed to next than mechanistic model capabilities for bacteria resulting in a greater likelihood of obtaining sufficiently accurate model predictions for the intended use.

4.2 Hydrologic Model Information

A mechanistic watershed-scale model called SWAT (Soil and Water Assessment Tool) was used to simulate streamflow in the Upper Oyster Creek (UOC) watershed (Arnold et al., 1998). SWAT is a conceptual, continuous time model that was developed in the early 1990s to assist water resource managers in assessing the impact of management and climate on water supplies and nonpoint source pollution in watersheds and large river basins. SWAT was developed and has been applied extensively in the U.S. for assessing impaired water bodies and planning of conservation systems (for a few examples see: Chaplot et al., 2004; Du et al., 2003; Du et al., 2005; Osei et al., 2003; Saleh and Du, 2004; Santhi et al., 2002). SWAT simulates water movement, sediment, and nutrient and pesticide fates in watersheds with forest land, urban land, agricultural fields, point sources, tile drainage systems, ponds/reservoirs and streams. Its main components include weather, hydrology, erosion/sedimentation, plant/tree growth, nutrients, pesticides, agricultural management, stream and pond/reservoir routing (Arnold et al., 1998, Neitsch et al., 2002a; Neitsch et al., 2002b).

The latest version of SWAT (SWAT2003) available at the time of this study was used. SWAT2003 is equipped with an ArcView Geographic Information System (GIS) interface called AVSWATX (Di Luzio, 2004) for input data preparing. Use of the Soil Survey Geographic (SSURGO) Database, a spatially refined soils database, is the newest function in AVSWATX.

4.2.1 Simulation Period

Even though the period for which *E. coli* data are available for development of the bacteria load duration curves is limited to 2002–2004, a longer simulation period was deemed appropriate in order to develop proper streamflow duration curves. The simulation period needed to be long enough to include hydrologic responses to a reasonable range of weather conditions, especially precipitation. The importance of the daily pumping records from the Gulf Coast Water Authority (GCWA) will be discussed later. The availability of these pumping records for the 12-year period of 1993–2004, however, seemed to provide a sufficiently long period to include a reasonable range of flows under a sufficiently wide variety of weather conditions and patterns, e.g. high rainfall and low rainfall periods. Because SWAT includes many soil-moisture related processes, the simulation period was actually extended to begin January 1, 1991 allowing ample time (two years) for the model to overcome any biases to hydrologic predictions resulting from specification of inaccurate initial conditions in the model.

4.2.2 Data Requirements for SWAT2003

SWAT requires extensive amounts of data allowing characterization of the UOC watershed for hydrologic predictions. Many of the data requirements are obtained from readily available GIS data layers.

Topography: Twenty-three scenes of 30-m digital elevation models (DEM) for Fort Bend county were downloaded from webGIS (webGIS, 2005). Most of these scenes were projected in NAD 1927 UTM zone 15. However, seven were in either NAD 1983 or UTM zone 14. The DEM data at this website were originally transformed from the GeoCommunity website (GeoCommunity, 2005). The seven differently formatted DEM scenes were re-projected based on their metadata files obtained from the original data website.

The multiple DEMs were assembled using the ArcView Mosaic command. The tears, holes, or sinks in the merged DEM map were fixed using the Neighborhood Statistics of Analysis at a threshold value of three cells.

Based on the DEM layer, all other GIS data of the UOC watershed within the Fort Bend county, including soil and land use/land cover layers, were projected in NAD 1927 UTM zone 15.

Climate: The 1991-2004 precipitation data from five weather gauges and the temperature data from two sites within and around the watershed were used for the simulation (Figure 4-1). The five precipitation stations are Sugar Land, Clodine, Richmond, Thompsons 3 WSW and Katy in Fort Bend county. The weather data were downloaded from the National Climatic Data Center website (NCDC, 2005). The original precipitation data from January 2003 to July of 2003 at the Sugar Land weather station were missing, so the missed precipitation data were replaced with the data from an automated observing station located at Hull Airport in Sugar Land, which were downloaded from the National Weather Service website (National Weather Service, 2005).

Soils: The Fort Bend soil data map was downloaded from the Soil Survey Geographic (SSURGO) Database of the Natural Resources Conservation Service (NRCS) at NCGC (National Cartography and Geospatial Center) (2005). The SSURGO soil map used for the Oyster Creek watershed is shown in Figure 4-2. Table 4-1 shows the major soil categories of the UOC watershed. While there are significant numbers of soil types within the watershed, the most common soil types are Brazoria clay, Lake Charles clay, Katy fine sandy loam, Norwood silt loam, and Katy-Waller complex, which collectively comprise about 65% of the watershed's area.

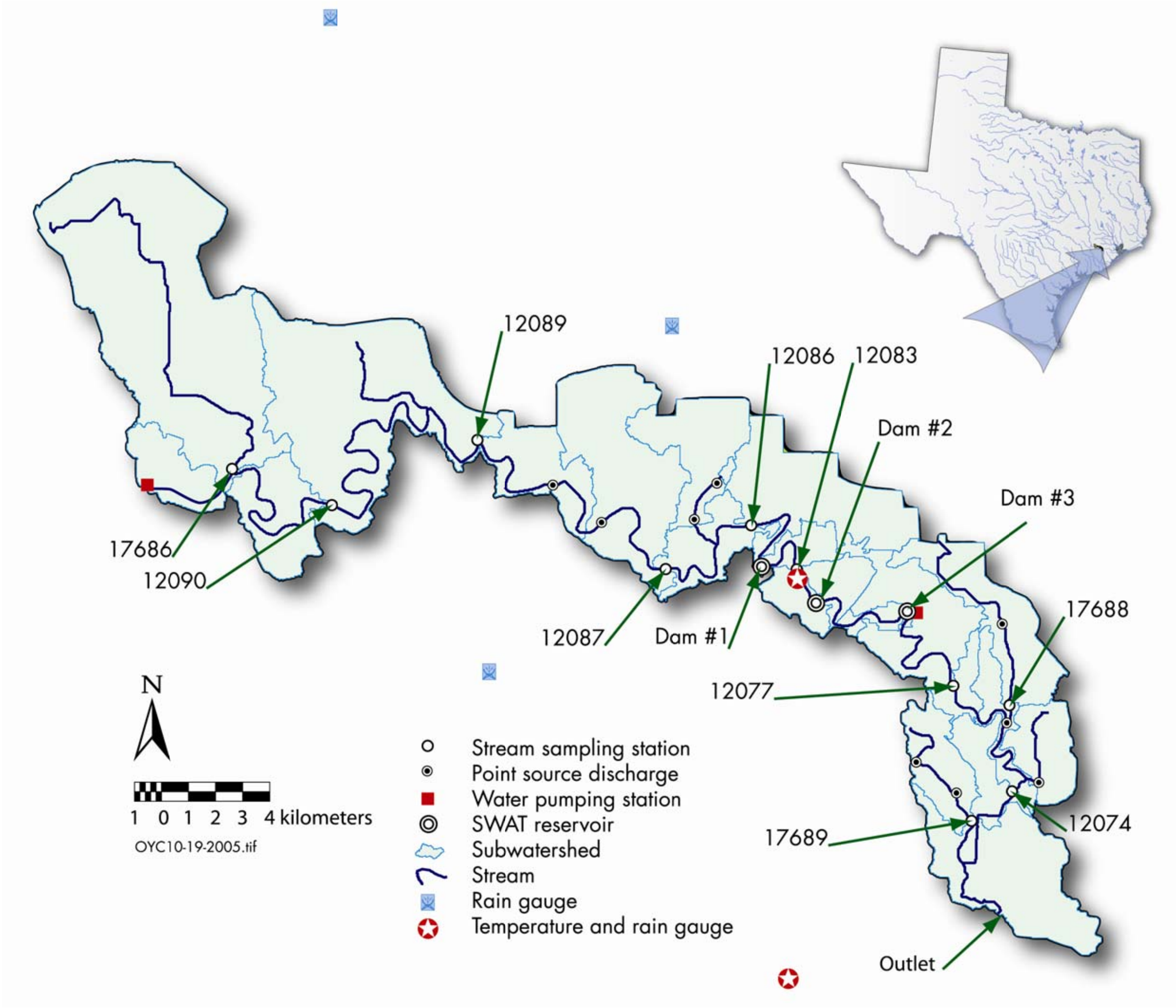

Figure 4-1 Upper Oyster Creek watershed with relevant features depicted

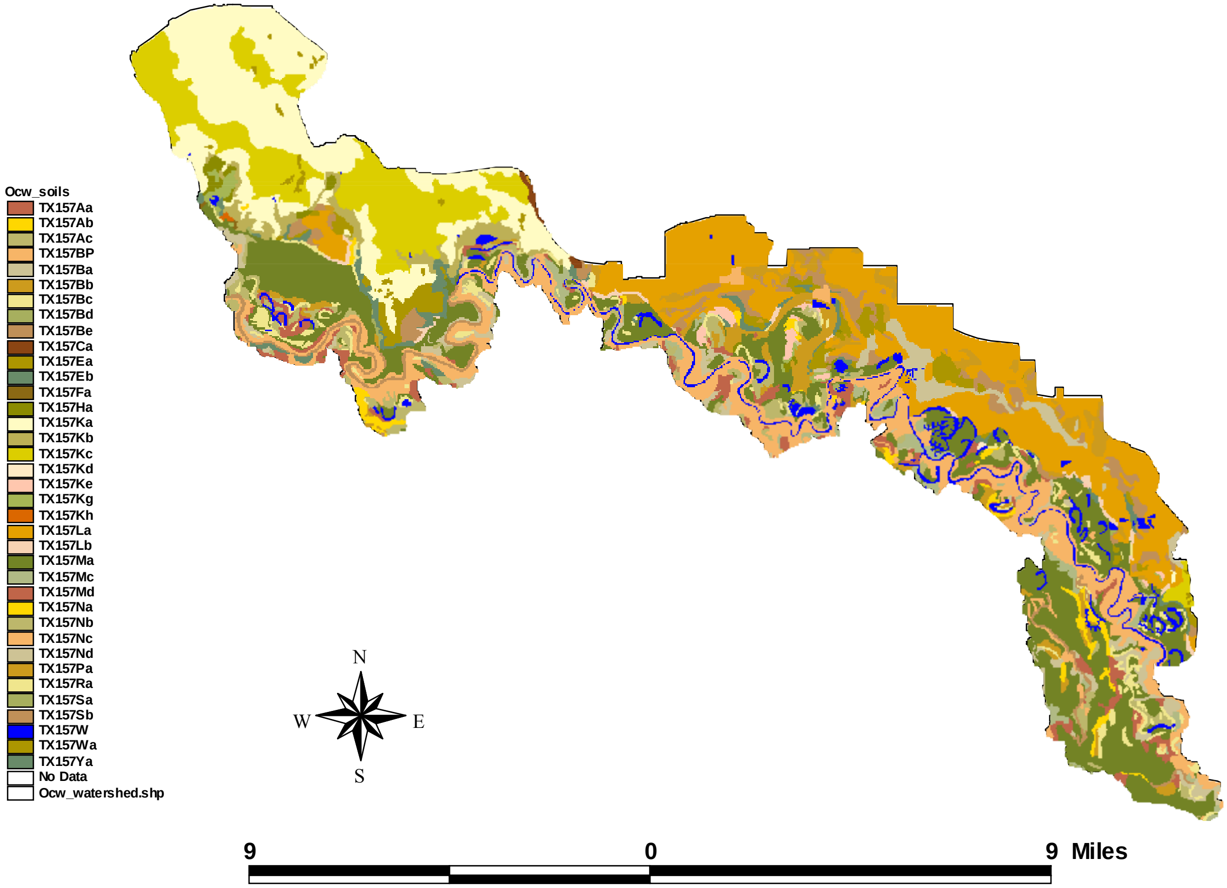

Figure 4-2 Soil types in Upper Oyster Creek watershed

Table 4-1 Soils in the Upper Oyster Creek watershed (Note: Soil identification number is used in the map of soils in Figure 4-2.)

Soil type & Soil Id. No.	Area (%)	Soil type & Soil Id. No.	Area (%)
Brazoria clay (TX157Ma)	17.8	Asa-Pledger complex (TX157Ac)	1.1
Lake Charles clay (TX157La)	16.4	Asa silty clay loam (TX157Ab)	1.1
Katy fine sandy loam (TX157Ka)	11.6	Clemville silty clay loam (TX157Md)	1.0
Norwood silt loam (TX157Nc)	10.6	Lake Charles clay (TX157Lb)	0.66
Katy-Waller complex (TX157Kc)	8.9	Waller soils (TX157Wa)	0.53
Water (TX157W)	3.2	Hockley loamy fine sand (TX157Ha)	0.45
Bernard-Edna complex (TX157Be)	3.2	Kenney loamy fine sand (TX157Ke)	0.42
Norwood silty clay loam TX157Nd)	2.5	Kenney loamy fine sand (TX157Kg)	0.37
Roebuck clay (Sumpf) (TX157Ra)	2.3	Pits, borrow (TX157BP)	0.36
Pledger clay (TX157Pa)	2.2	Clodine fine sandy loam (TX157Ca)	0.30
Edna fine sandy loam (TX157Ea)	2.2	Yahola fine sandy loam (TX157Ya)	0.23
Norwood clay (Belk) (TX157Nb)	1.7	Bernard-Edna clay loams TX157Bc)	0.19
Asa fine sandy loam (TX157Aa)	1.7	Navasota-Iuka complex (TX157Na)	0.10
Katy fine sandy loam (TX157Kb)	1.7	Bernard-Edna clay loams TX157Bd)	0.06
Bernard clay loam (TX157Bb)	1.5	Fulshear fine sandy loam TX157Fa)	0.03
Bacliff clay (TX157Ba)	1.5	Kenney-Fulshear complex (TX157Kh)	0.03
Clemville silt loam (TX157Mc)	1.5	Kaufman clay (Kaman) (TX157Kd)	0.02
Edna fine sandy loam (TX157Eb)	1.4	Sandy alluvial land (TX157Sa)	0.02
Sloping alluvial land (TX157Sb)	1.3		

<u>Land use/land cover:</u> The digital land use/land cover map of the UOC watershed is shown in Figure 4-3. The digital land use/land cover used was developed by Baylor University using satellite imagery from the period of 1996-97 (Baylor, 1997). The main land use categories in the watershed are pasture, range, forest and urban, among which pasture land cover is dominant and accounts for about 56% of total area (Section 2, Table 2-4). The urban (urban mix and residential) area occupies about 25% of land cover within the UOC watershed.

<u>Point Sources:</u> For many SWAT applications the point source features are used to allow representation of such features as municipal WWTPs. To simulate the UOC watershed, this feature was used to not only allow representation of WWTPs, but also to represent GCWA pumping into and out of the watershed.

There are two GCWA operated pumping stations in the UOC watershed. One is the Shannon Pump Station, which is located on the west side of the watershed (Figure 4-1) and pumps water from the Brazos River into the system. The other is the Second Lift Station on the east side. Water is pumped into the watershed from the Shannon Pump Station, and further downstream at the Second Lift Station water is pumped into a canal, which carries the water out of the watershed to the Texas City area where much of the water use occurs. As previously discussed, daily water pumping records for both pump stations were available for the years 1993 through 2004. The pumping records at both stations exhibit a strong seasonal component (Table 4-2) with minimum pumping occurring during winter months and maximum pumping during summer months.

The monthly self-reporting discharges from the nine municipal WWTPs operating in the watershed (Figure 4-1; Table 4-3) were obtained for the five-year period of 2000 to 2004. The average daily discharge for each month from January through December was calculated for each WWTP using the self-reporting data of 2000 to 2004 (Table 4-3). SWAT was operated to simulate the period 1991 to 2004 using as input the average daily discharge data for each month and for each WWTP. The UOC watershed is rapidly urbanizing with an urban population increase of over 80% from 1990 to 2000, and an approximately commensurate increase in WWTP discharges would have been anticipated. Therefore recent self-reporting data were used to better reflect WWTP discharges for present watershed conditions. The Fort Bend County MUD No. 41 and the Fort Bend County MUD #25 WWTPs are in the same subbasin of the delineated UOC watershed, so their discharges are combined. The City of Sugar Land and the City of Missouri City WWTPs are combined for the same reason. The delineation of the watershed into computational subbasins as required by SWAT is discussed later.

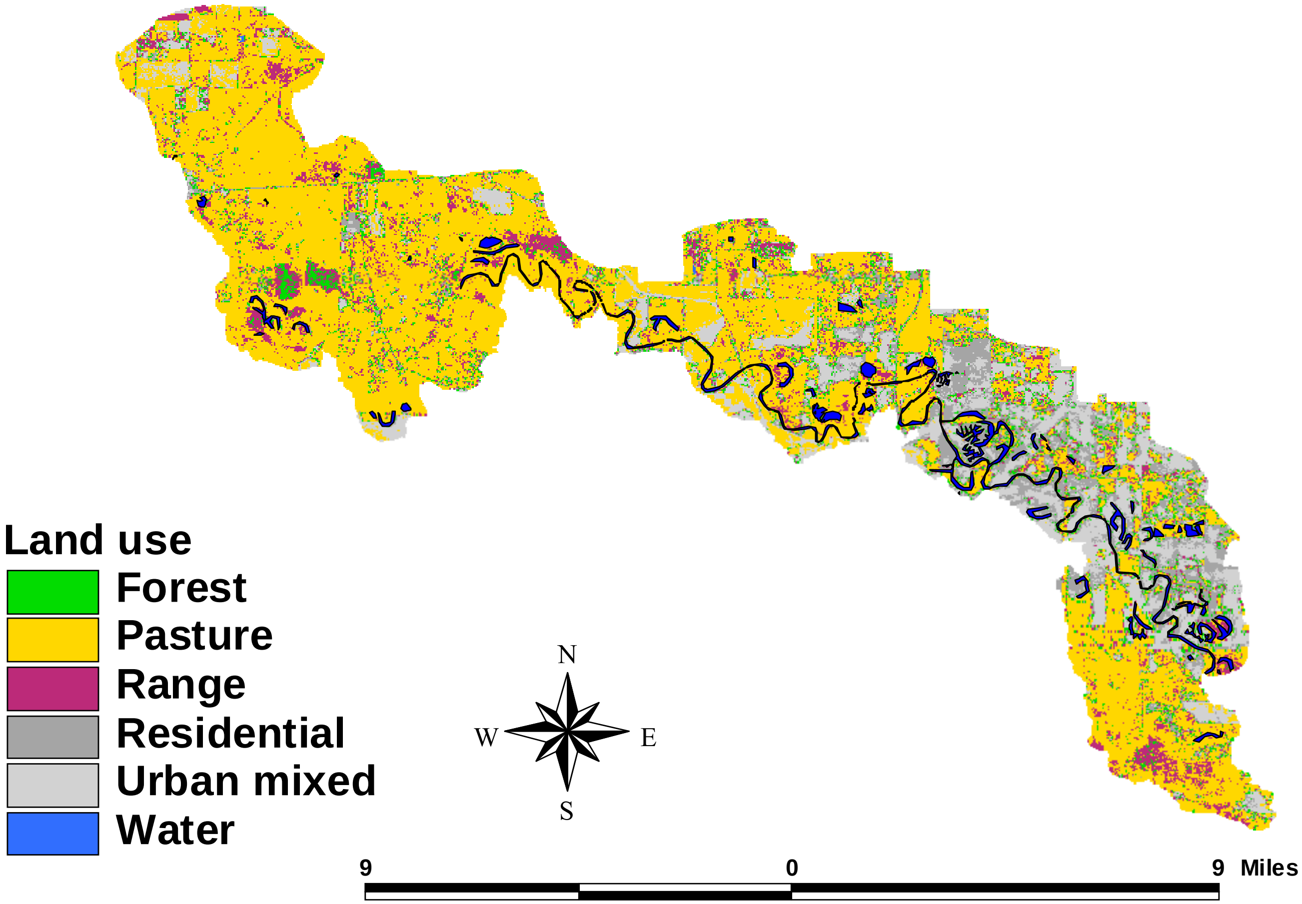

Figure 4-3 Land use/land cover for Upper Oyster Creek watershed (Source: Baylor, 1997)

Table 4-2 Gulf Coast Water Authority monthly average pumping records (1993-2004) at Shannon Pump and Second Lift stations

Month	Shannon Pump Station (m^3/d)	Second Lift Station(m^3/d)
January	40,700	75,004
February	36,557	49,733
March	72,424	91,762
April	148,549	152266
May	214,586	206,490
June	272,563	252,489
July	391,082	326,538
August	318,629	295,000
September	242,333	246,656
October	152,796	170,633
November	132,863	156,664
December	92,533	124,929

Table 4-3 Monthly average municipal WWTP discharges for 2000–2004 (For WWTP location identification see Figure 3-2)

Location ID	18210	18209	18214+18297	18208	18207+18206	18205	18204
---------------------------- m^3 / day ------------------------------							
January	12,391	6,706	2,620	1,106	19,935	946	251
February	12,916	6,294	2,523	1,030	19,976	931	251
March	12,774	6,594	2,579	1,062	19,783	984	262
April	12,386	6,224	2,580	1,113	19,567	1,030	287
May	12,257	6,370	2,668	1,133	22,343	918	205
June	14,260	5,688	1,983	1,147	20,786	995	246
July	13,543	6,911	2,099	1,129	20,641	1,045	257
August	13,333	7,261	1,798	1,157	21,225	1,054	269
September	13,847	7,094	1,790	1,160	21,840	973	274
October	14,164	6,758	2,010	1,133	21,418	965	177
November	13,864	6,753	2,154	1,135	21,808	825	176
December	11,799	6,663	2,065	1,083	19,821	1,037	190

4.2.3 Creation of Input Data Using AVSWATX

The AVSWATX interface program was used to create input data for SWAT2003. The 30-m DEM, soil, and land use/land cover digital data, along with precipitation and temperature data, point sources, and reservoir configurations data were prepared from AVSWATX providing the necessary input data and files to operate SWAT2003.

Watershed delineation: The UOC watershed has relatively flat landscape and three small dams located on Oyster Creek (Figure 4-1). The flat topography made it difficult to proceed with a completely auto-delineation process, as available in AVSWATX, to divide the watershed into the computational subbasins used by SWAT. To facilitate demarcation of the watershed's boundary, information and maps were provided by the Fort Bend County Drainage District that reflect modifications to the natural drainage patterns and UOC watershed boundaries as a result of drainage improvements (Jalowy, 2005). A GIS mask was used to prevent the boundaries of the watershed from extending out of the referenced drainage area or into the Brazos River area due to the low-relief landscape. The watershed was re-delineated by superimposing the fixed stream onto the DEM and using the mask. The boundaries on the northeast part of the delineated watershed were modified based on the digitized drawing of the drainage area, which was spatially registered into ArcView using Smartimage.

The locations of monitoring stations from water sampling surveys for the bacteria and dissolved oxygen TMDLs were primarily used to determine the number of subbasins, resulting in twenty-four subbasins for the watershed (Figure 4-4). The three dams were treated as three reservoirs (Figure 4-1). The multiple hydrologic response units (HRUs) feature was selected at a threshold level of 1% for land use and 10% for soil. As a result, a total of 332 HRUs were created. HRUs are unique land use and soil combinations (e.g., pasture on a Brazoria clay soil type) in which each subbasin was further subdivided to enhance representation of hydrologic responses from the various landscapes in the watershed. SWAT predictions are typically provided as daily results at the outlet of each subbasin.

Import weather data: The data from the five daily precipitation and two daily temperature stations were imported as input to SWAT. Statistical weather data from the station at Thompsons 3 WSW were used to generate solar radiation, wind speed, and relative humidity data, and some other missing weather data needed to operate SWAT. The weather generator routine within SWAT was used to automatically generate these additional data based on a statistical evaluation of available data for the Thompsons 3 WSW station.

Creation of other input data: All the other input data required by SWAT2003 were generated using default model values. These input data include the watershed configuration file, soil characteristics, subbasin general input, HRU general input, main channel characteristics (assumes trapezoidal channel cross section), groundwater coefficients, water use input, agricultural field management input, and stream water quality. Small ponds were determined from areas of the SSURGO soils database indicated to be water, and associated pond characteristics (depth, volume, etc.) were generated by default functions within the model.

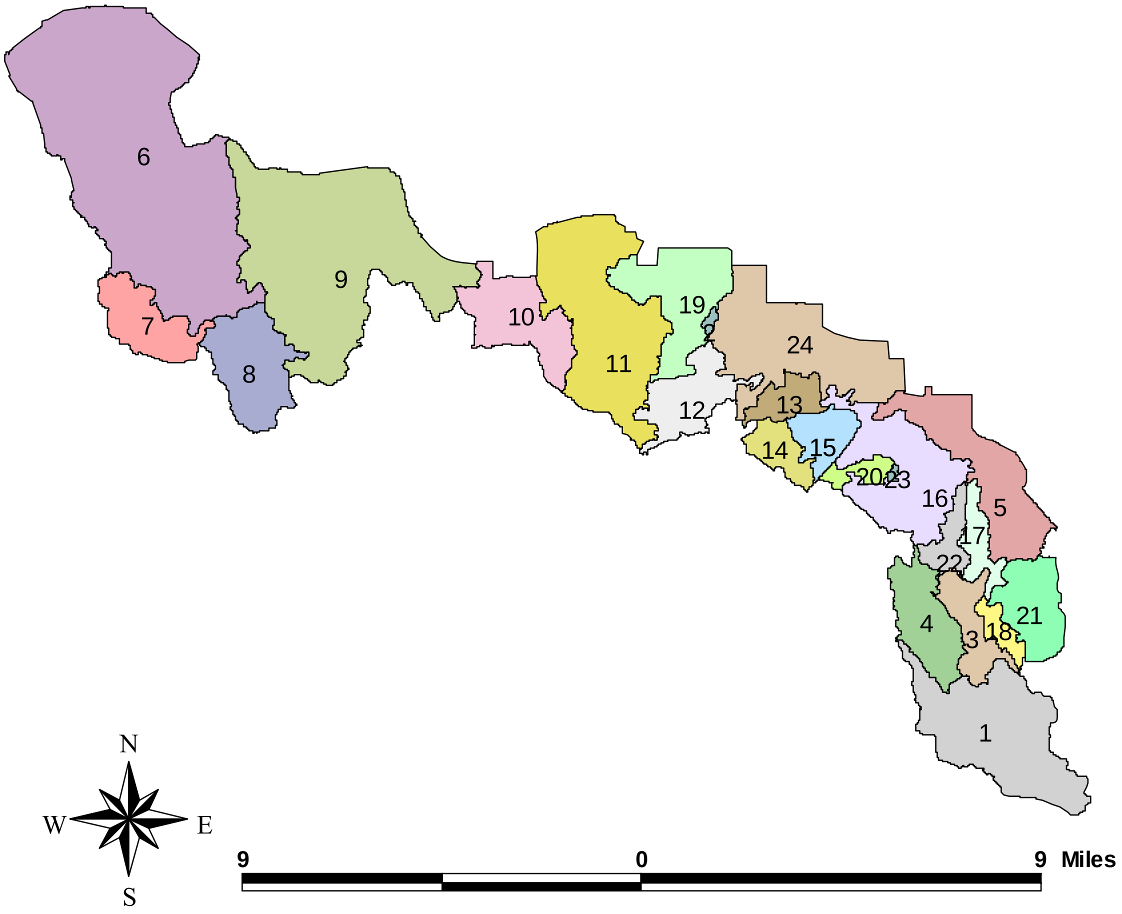

Figure 4-4 Subbasin delineation for Upper Oyster Creek watershed

4.3 Calibration of SWAT2003 for Streamflow

4.3.1 Model Calibration Methodology

The calibration of SWAT2003 to measured streamflow was conducted for data obtained during the period 2002 through 2004. During this period several stations were monitored for bacteria, dissolved oxygen, and other parameters in support of the bacteria and dissolved oxygen TMDLs for Segment 1245. During the monitoring surveys a streamflow measurement at times accompanied the other data collection activities. The measured flows at the stations represent conditions during the time of monitoring, usually a period of 30 minutes or less. In contrast, SWAT2003 predicts a daily average streamflow. The difference in time scales represented by measured and predicted flows does not present difficulties during base flow conditions when temporal variability of flow is minimal. During rainfall-runoff conditions, however, the two different time-scales present a major, though unavoidable, issue. The single physical measurement during rainfall-runoff conditions is unlikely to represent daily average streamflow and may either be too high or too low based on the portion of the hydrograph captured by the measurement. Consequentially the comparison of measured and predicted streamflows suffers from this unavoidable difference in time scales resulting in difficulties in calibrating the model. Nonetheless, these streamflow data represent the best available information for calibration of SWAT2003.

The methodology for calibration consisted of adjusting various input parameters within an acceptable range for each parameter and comparing SWAT2003 streamflow predictions with the adjusted parameters against the measured streamflow. The objective is to maximize model predictions against several accepted measures of model performance. The statistical measures used in the calibration process are discussed in the following.

The Nash-Sutcliffe model efficiency (*E*) (Nash and Sutcliffe, 1970) and mean relative error (MRE) were used to compare the pattern and magnitude of the model output values to those of measured values. *E* value was calculated as follows:

$$E = 1 - \frac{\sum_{i=1}^{n}(X_{mi} - X_{pi})^2}{\sum_{i=1}^{n}(X_{mi} - \overline{X}_m)^2}$$

where E is the efficiency (goodness of fit) of the model that indicates how well the plot of predicted versus measured values fits the 1:1 line, $\overline{X}_m$ is the average measured values, X_{mi} is the i_{th} measured value, and X_{pi} is the predicted i_{th} value. A value of $E = 1.0$ indicates that the pattern of model prediction perfectly matches the measured data. Application of E requires a sufficient number of data points. Otherwise, the measure is overly sensitive to pairs of measured and predicted data that significantly differ. Hence, this measure of model performance was only used for the combined data set for all streamflow data.

The MRE is calculated as follows:

$$\text{MRE} = \frac{\sum_{i=1}^{n}(X_{mi} - X_{pi})}{\sum_{i=1}^{n}(X_{mi})}$$

A value of MRE = 0 indicates the predicted average amount of flow equals the measured value.

Either a parametric (paired t test) or a non-parametric (sign test) statistic was considered to evaluate the difference between the means of measured versus predicted flows depending upon normality of the distribution of the streamflow. A 95% level of confidence was applied to all of the results of the paired t tests or sign tests of the eight monitoring sites and the pooled data. The null hypothesis (H_o) was constructed for both tests so that acceptance of H_o (i.e., a P-value > 0.05) indicates no statistical difference between the means of the measured and predicted streamflows. A normality test of the distribution of flow data was preformed using the Shapiro-Wilk test. If the distributions were normal, the paired t test was applied, otherwise the sign test was applied. The results of statistical computations were obtained by running the UNIVARIATE procedure in SAS (SAS, 1999)

In addition, graphics and R^2 (the coefficient of determination) were also employed to evaluate reliability of model streamflow predictions.

4.3.2 Streamflow Data for Calibrating SWAT2003

SWAT2003 streamflow predictions were compared to streamflow measurements made at eight stations monitored during surveys conducted in support of both the bacteria and dissolved oxygen TMDLs for Segment 1245. The eight stations represent locations both of interest in determining adequacy of model predictions and where streamflow was routinely measured during 2002 through 2004. The eight stations are as follows:

- Station 12090, Jones Creek at FM 723
- Station 12087, Upper Oyster Creek at FM 1464,
- Station 12086, Upper Oyster Creek at Highway 6 near Hull Airport,
- Station 12077, Upper Oyster Creek at Cartwright Road,
- Station 12074, Flat Bank Creek at Highway 6,
- Station 17686, Flewellen Creek at Briscoe Road,
- Station 17688, Stafford Run at El Dorado Blvd., and
- Station 17689, Steep Bank Creek at Thompsons Ferry Road

(Figure 4-1 shows the eight stations and other stations discussed in this section).

4.3.3 Model Calibration Process

SWAT2003 was calibrated to measured data at the eight monitoring stations in the UOC watershed by a process involving adjustment of key input parameters and evaluation of these adjustments on the statistical measures described above. The adjustment process was continued until acceptable streamflow predictions were obtained.

The two main adjustable parameters used for the calibration of streamflow in SWAT (Neitsch et al., 2002b) are *esco* (a soil evaporation compensation coefficient) and *cn*2 (condition II runoff curve number). The main groundwater parameters describing water movement, such as *gwqmn* (threshold depth of water in the shallow aquifer required for return flow to occur), *gw_revap* (the coefficient of groundwater moving to an adjacent unsaturated zone), and *alpha_bf* (baseflow alpha factor) were adjusted when predicted base flow or total water balance deviated from measured values. The other calibrated parameter used in this study was s*urlag* (surface runoff lag time), which influences flow peak calibration. The ranges of adjusted parameters suggested for use in SWAT2003 and the calibrated values of the adjusted parameters used for flow calibration for UOC watershed are listed in Table 4-4.

Table 4-4 Calibrated values of adjusted SWAT2003 input parameters

Parameter	Description	Range	Calibrated Value
esco	Soil evaporation compensation factor	0.2 to 1.0	0.92
*cn*2	Initial SCS runoff curve number for moisture condition II	30 to 100	49 to 92
gwqmn	Threshold depth of water in the shallow aquifer required for return flow to occur (mm)	--	50
gw_revap	Coefficient of groundwater moving to an adjacent unsaturated zone	0.02 to 0.2	0.05 to 0.2
alpha_bf	Baseflow alpha factor (days)	0.0 to 1.0	0.148 to 0.748
surlag	Surface runoff lag coefficient	1 to 12	4

4.3.4 Model Calibration for Tributary Flows

The flows at the three tributary stations (17686, 17688 and 17689) were periodically monitored during the years 2002 to 2004 as part of various surveys performed for the bacteria and dissolved oxygen TMDLs. The accuracy of SWAT streamflow predictions for these three stations is provided as follows.

The station 17686 is located in the western portion of the system near the downstream end of Flewellen Creek. Figure 4-5 illustrates that most predicted flows were close to measured flows. The average flows of measured and predicted were 0.46 and 0.42 cms, respectively, with no significant difference in means based on the paired t test with a P-value = 0.632 (Table 4-5).

The station 17688 is located near the downstream end of another major tributary to the Oyster Creek system, Stafford Run. The streamflow data for this station was non-normally distributed, which required the sign test to compare means. The statistical results (Table 4-5) show that the average predicted flow was significantly different from the measured flow. The model underestimated flow with a MRE of -46%. Figure 4-6 shows that most of the flow predictions were well matched to the measurements except the under predictions on October 9, 2002 and July 16, 2003.

The station 17689 was located on Steep Bank Creek in the southeast portion of the watershed. Although the paired t test (Table 4-5) indicated that the model predicted mean streamflow varied from the measured one, the MRE value of 23% indicated that the over prediction of streamflow was relatively small. Most of the predicted and measured flows were relatively similar (Figure 4-7).

4.3.5 Model Calibration to Main Stem Stations

Station 12090 is the most upstream monitoring site with several streamflow measurements and is located on Jones Creek (Figure 4-1). The statistical results (Table 4-5) indicate that the model performed well in predicting the flow at this station. The predicted and measured flows were almost the same with an extremely small MRE of -2%. Figure 4-8 illustrates that the predicted points were relatively close to their corresponding measured ones under conditions of both high and low flows.

Station 12087 is located on Oyster Creek in the middle of the UOC watershed and upstream of the three dams (Figure 4-1). Figure 4-9 illustrates that the model over-predicted most streamflows with a 50% MRE on average (Table 4-5). Especially on May 21, 2003, March 24, 2004 and July 1, 2004, the prediction errors were relatively large, which impacted the average prediction level. The reason for the consistent over-prediction of high flows could be improper representation of the relatively complex hydrologic controls in the vicinity of station 12089 (Figure 4-1) as well as the previously mentioned unavoidable errors introduced when comparing daily model predictions to streamflow measured on a much smaller time scale. At station 12089 five culverts with control gates regulate downstream flow. Whenever water levels behind the culverts are sufficiently high, excess water that can not pass through the culverts is diverted down Jones Creek southward and out of the watershed. This hydrologic control is manually regulated to avoid downstream flooding and could only be approximated by SWAT2003.

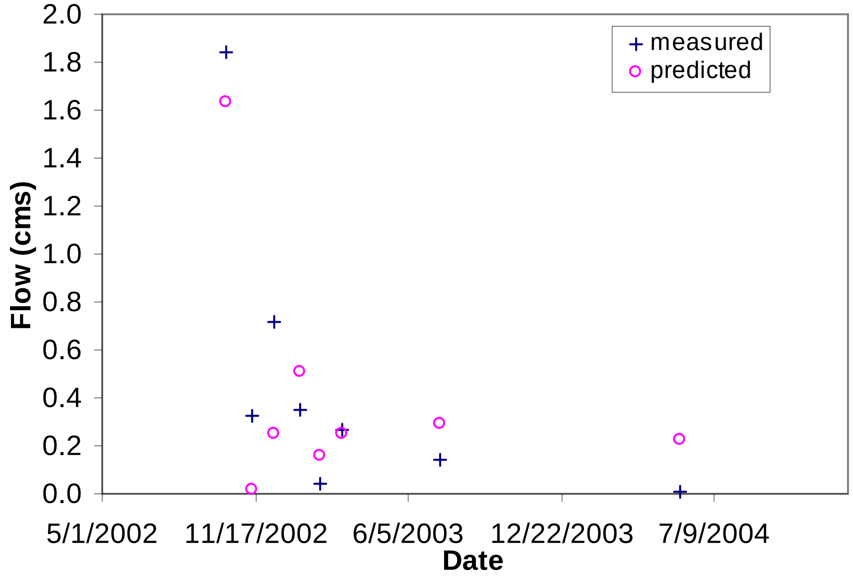

Figure 4-5 **Measured versus predicted flows at Station 17686, Flewellen Creek**

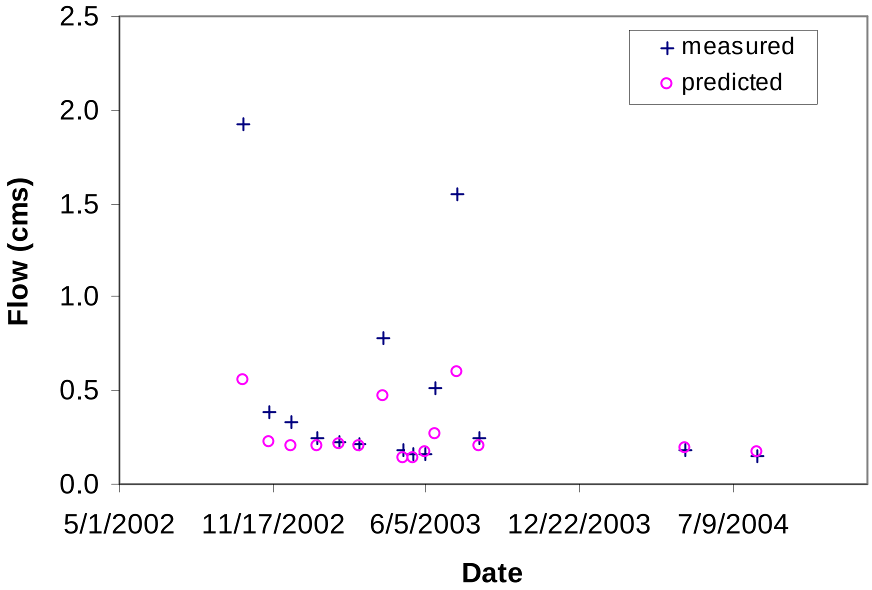

Figure 4-6 **Measured versus predicted flows at Station 17688, Stafford Run**

Table 4-5 Statistical measures of measured versus predicted flows at the eight calibration stations

Station	Measured or Predicted	Mean	SD[a]	MRE[b]	paired t test (P-value) [c]	Sign test (P-value) [c]	Normality (Shapiro-Wilk P-value)
17686	**Measured flow (cms)**	0.46	0.26	—	—	—	—
	Predicted flow (cms)	0.42	0.12	-0.10	0.62	—	Yes (0.2292)
17688	**Measured flow (cms)**	0.48	0.39	—	—	—	—
	Predicted flow (cms)	0.26	0.14	-0.46	—	0.035	No (<0.0001)
17689	**Measured flow (cms)**	0.24	0.12	—	—	—	—
	Predicted flow (cms)	0.30	0.07	0.23	0.020	—	Yes (0.0624)
12090	**Measured flow (cms)**	3.43	1.42	—	—	—	—
	Predicted flow (cms)	3.37	1.42	-0.02	0.804	—	Yes (0.744)
12087	**Measured flow (cms)**	2.69	0.69	—	—	—	—
	Predicted flow (cms)	4.03	1.17	0.50	0.006	—	Yes (0.132)
12086	**Measured flow (cms)**	3.07	1.11	—	—	—	—
	Predicted flow (cms)	3.90	1.23	0.27	0.058	—	Yes (0.671)
12077	**Measured flow (cms)**	0.63	0.50	—	—	—	—
	Predicted flow (cms)	0.62	0.69	-0.01	0.982	—	Yes (0.181)
12074	**Measured flow (cms)**	1.36	1.32	—	—	—	—
	Predicted flow (cms)	1.36	0.95	0.00	—	0.286	No

[a] Standard Deviation
[b] Mean Relative Error
[c] Null hypothesis constructed so that its acceptance at a 95 % level of confidence (i.e., P > 0.05) indicates that measured and predicted means are statistically the same.

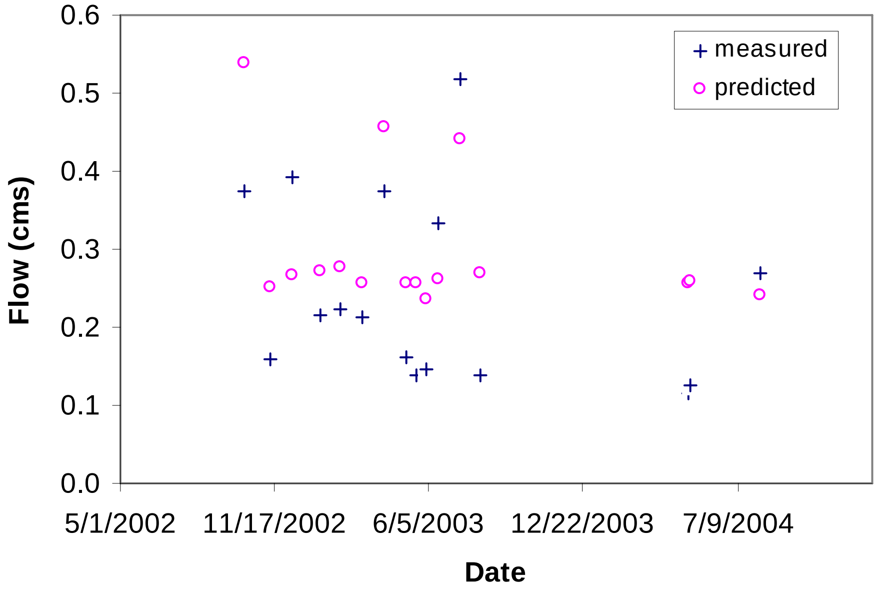

Figure 4-7 **Measured versus predicted flows at Station 17689, Steep Bank Creek**

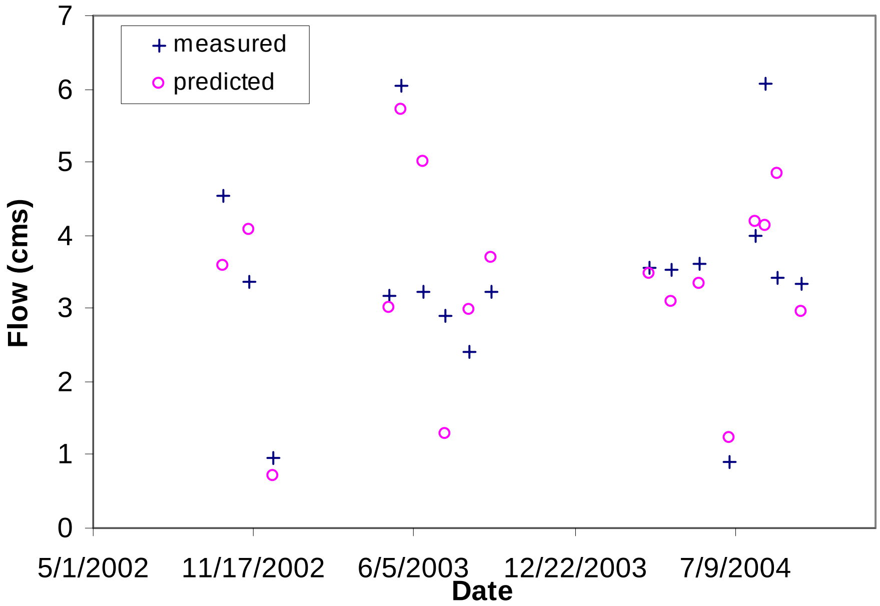

Figure 4-8 **Measured versus predicted flows at Station 12090, Jones Creek**

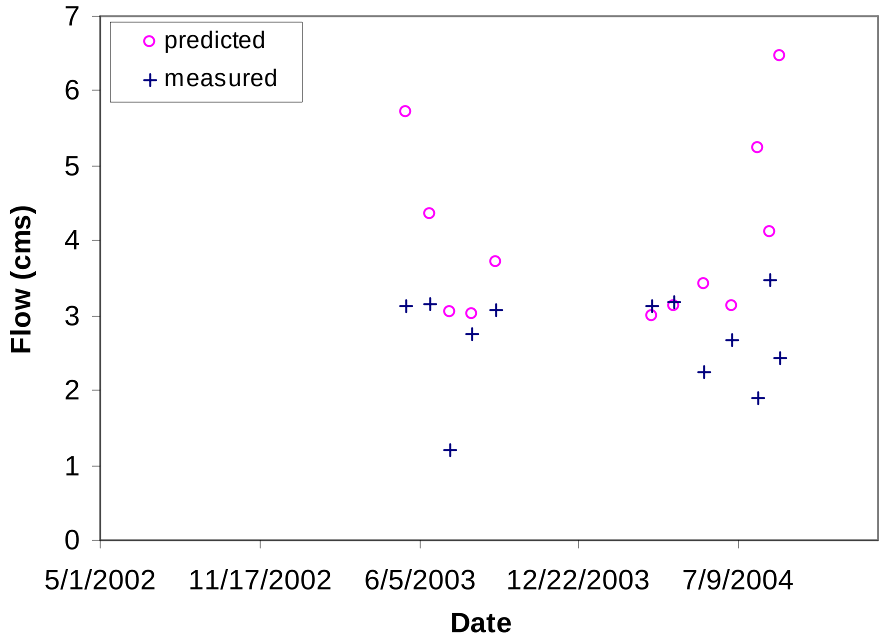

Figure 4-9 **Measured versus predicted flows at Station 12087, Oyster Creek at FM 1464**

Station 12086 is located on Oyster Creek downstream of station 12087 and upstream of Dam #1. Average predicted flow (3.07 cms) at this station was not significantly different from the average measured flow (3.90 cms) (Table 4-5), although the MRE was 27% which indicated that the model slightly over-predicted the average flow. As indicated on Figure 4-10, on August 3, 2004 and August 31, 2004, predicted streamflows were much higher than the measured flows. The same over-prediction was observed on those same two days at previously discussed station 12087.

Below Dam #3 is located station 12077 (Figure 4-1). The Second Lift is located in the pool of Dam #3, and the pumping at this location removes large amounts of water from Oyster Creek resulting in much lower streamflows at station 12077 than at more upstream stations. Another hydrologic complexity that reduces high flows at station 12077 is flood control operations at Dam #2 in tandem with control gates on the west end of Brooks Lake. When streamflows result in water levels at Dam #2 that portend potential downstream flooding, the control gates on Brooks Lake open releasing water out of the system. The complexities of this flood control operation were approximated in the SWAT2003 representation of Segment 1245. The paired t test indicated that the average flow (0.62 cms) predicted by the model was similar to the measured one (0.63 cms) at the site 12077, and the MRE was only -1% (Table 4-5). Comparison of predicted and measured streamflows for station 12077 is provided in Figure 4-11.

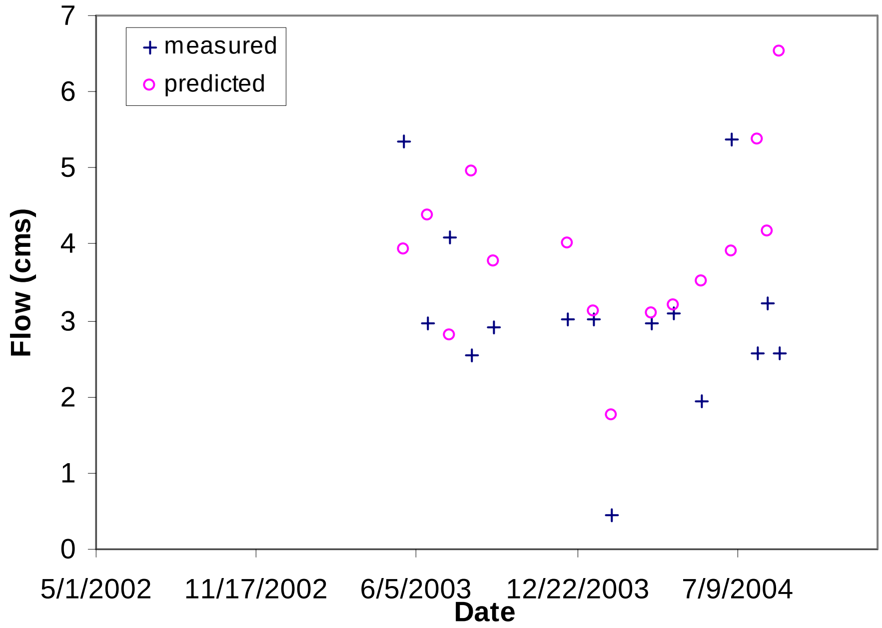

Figure 4-10 **Measured versus predicted flows at Station 12086, Oyster Creek at Highway 6**

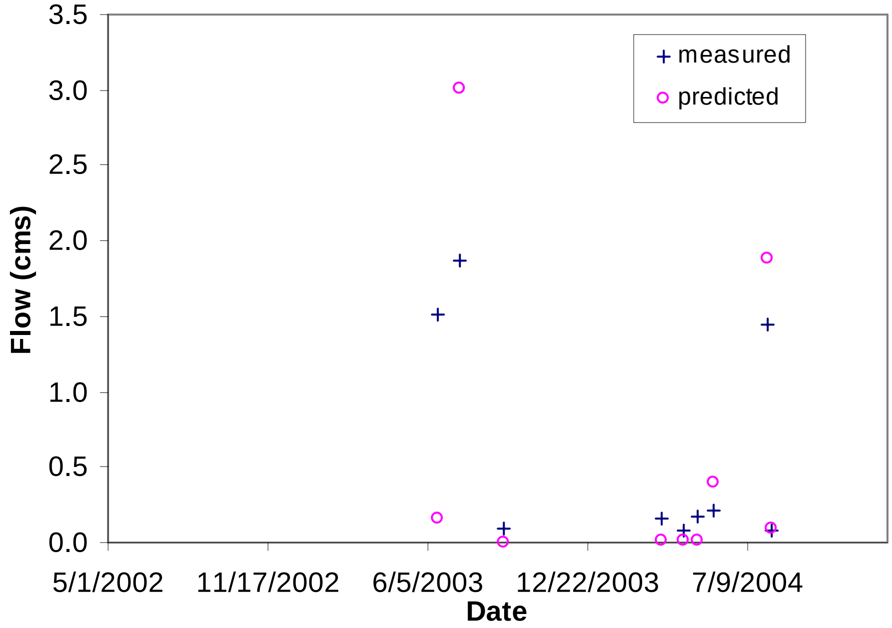

Figure 4-11 **Measured versus predicted flows at Station 12077, Oyster Creek at Cartwright Road**

The station 12074 is located in the eastern portion of watershed on Flat Bank Creek, which is the downstream continuation of Oyster Creek. Similar to the flow simulation at station 12077, the average predicted flow on this site was statistically the same as the measured data (sign test, P-value = 0.286), and its MRE equaled 0% (Table 4-5). Comparison of predicted and measured streamflows for station 12074 is provided in Figure 4-12.

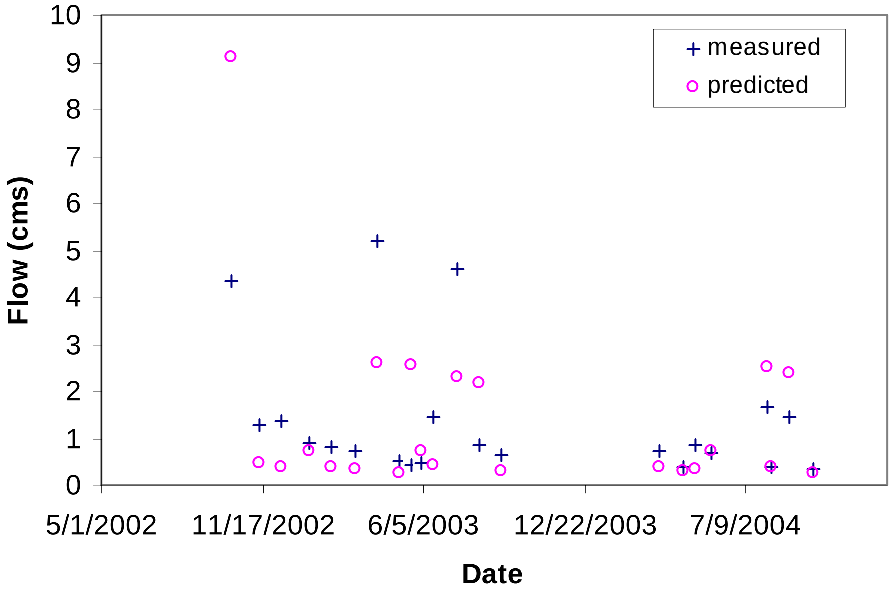

Figure 4-12 Measured versus predicted flows at Station 12074, Flat Bank Creek

4.3.6 Overall Model Performance in Simulating Flow

The 2002-2004 streamflow data at all eight stations were combined to evaluate overall performance of model simulation of flow. Since the distribution of the flow data was non-normal (Shapiro-Wilk P-value<0.0001), the sign test was used to evaluate difference of means. Based on the sign test (P-value = 0.64), the average predicted flow of 1.85 cms was not significantly different from the measured flow of 1.64 cms (Table 4-6). In addition, the E value, R^2, slope, and interception were 0.52, 0.66, 1.00, and 0.22 respectively, indicating the pattern of the predicted streamflows was relatively similar to that of the measured streamflows (Table 4-6; Figure 4-13).

4.3.7 Spatial Analysis of Flow Simulations

The eight monitored stations are distributed across the whole watershed. For the five main stem stations, one is close to the watershed's headwaters on Jones Creek (12090), one on Steep Bank Creek toward the watershed outlet (12074), one in the middle of the watershed (12087), one before Dam #1 (12086), and one below Dam #3 (12077). The three tributary stations are located on three of the four main tributaries of the UOC watershed.

Table 4-6 Statistical measures of measured versus predicted flows for aggregated data of all eight calibration stations

	Mean	SD[a]	MRE	sign test	Normality (Shapiro_Wilk P-value)	E	R^2 (slope/interception)
Measured flow (cms)	1.64	1.57	—	—	—	—	—
Predicted flow (cms)	1.86	1.94	0.13	0.640	No (<0.0001)	0.52	0.65 (1.00/0.22)

[a] Standard Deviation

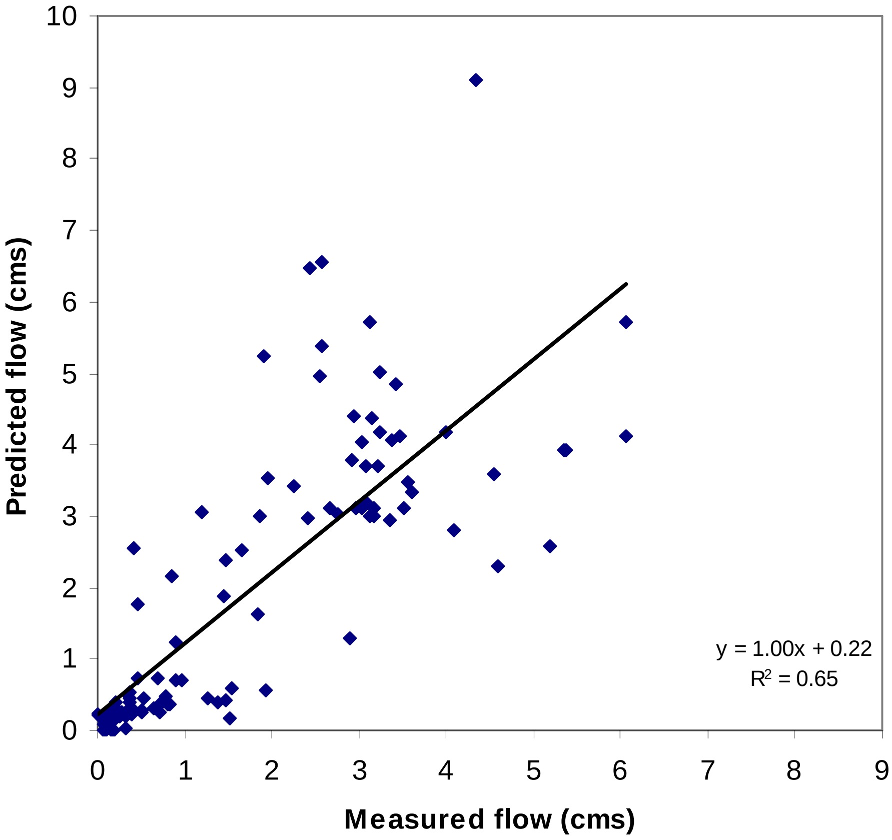

Figure 4-13 Measured versus predicted streamflows for the eight calibration stations

The reasonableness of model streamflow predictions was investigated in terms of the spatial locations of these stations within UOC watershed. Means of the pairs of predicted and measured flows for each of the eight stations are provided in Figure 4-14. The spatial pattern of the predicted flows matched that of the measured flows, including the substantial decrease in mean flows below Dam #3 (i.e., stations 12077 and 12074). Streamflow sharply declined to 0.62 cms at station 12077 and then increased to 1.31 cms at station 12074, because of inflows from Stafford Run and two WWTPs. Average streamflows at the three tributary stations reasonably matched the average of measured values.

4.3.8 Conclusions on SWAT2003 Calibration

In conclusion, the SWAT2003 hydrologic model of UOC watershed was successfully calibrated against available streamflow data collected in support of the TMDLs for Segment 1245. Complexities of manmade hydrologic controls in the system, which could only be approximated by the model, and the differences in the time scales of the streamflow predictions of SWAT and the measured streamflows presented challenges to the calibration process. Nonetheless, model and measured results were in fair agreement for most stations and in very good agreement at some stations.

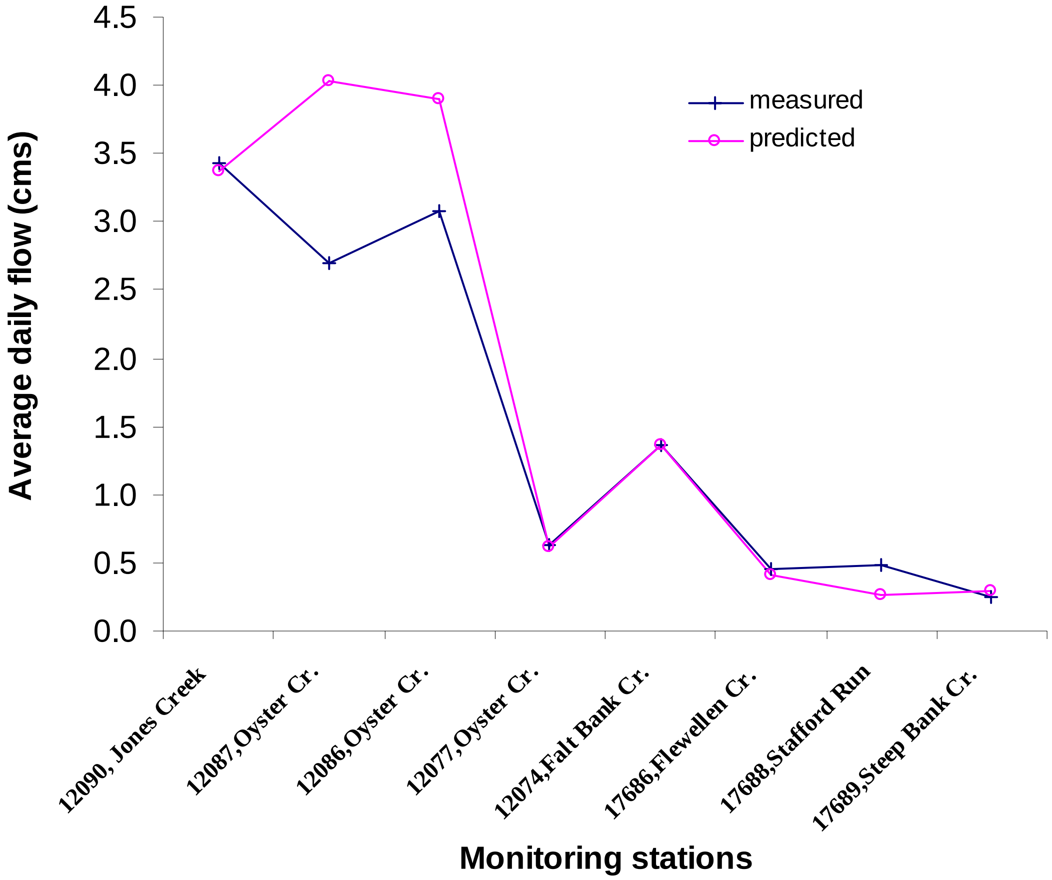

Figure 4-14 **Average measured versus predicted flows at eight stations in Segment 1245**

In the bacteria load duration curve method, the importance of the daily streamflow data is that the streamflows reflect relative, and not necessarily absolute, conditions. Hence it is more important that the model predicted streamflows reflect increases when GCWA authority pumping is higher and during periods of hydrologic response to rainfall-runoff events than the model accurately predict the "true" streamflow. The calibration process resulted in a hydrologic model that is properly responsive to hydrologic forcings (e.g., rainfall, WWTP discharges, and GCWA pumping rates) and capable of providing acceptably reliable simulated daily streamflow data at desired locations for use in the load duration curve method.

4.4 Bacteria Load Duration Curve Method

The 1993-2004 daily streamflow data from the calibrated SWAT2003 model of Segment 1245 with historical *E. coli* data could now be used to develop the bacteria load duration curve tool for desired locations in the UOC watershed. Six stations were selected for development of load duration curves based on availability of sufficient *E. coli* data and the ambient water sampling of these stations during the bacterial source tracking study. As further developed in Section 5: Bacteria Load Allocation Process, these six stations are used to characterize conditions in the two allocation reaches specified for the TMDL. Most of these stations were the same locations used in streamflow calibration of SWAT2003. These common stations include 12074, 17688, 12086, 12087, and 12090. The sixth station is 12083, Oyster Creek at Highway 6 (Figure 4-1). This station could not be used in the model calibration process, because the station is located in the pooled area behind Dam # 2. Water velocities at station 12083 were typically too low for accurate determination of streamflow, because of the large stream cross-sectional area relative to actual flow, i.e., the velocities were often at or below the threshold of the instrumentation.

The following steps were undertaken to develop the desired bacteria load duration curves:

Step One: The 1993-2004 model predicted daily streamflow data for each of the six desired stations (12074, 17688, 12083, 12086, 12087, and 12090) were obtained as model output. The daily data were used to develop a flow duration curve for each station. The flow duration curve is generated by 1) ranking the daily flow data from highest to lowest, 2) calculating the percent of days each flow was exceeded (rank ÷ number of data points), and 3) plotting each flow value (y-axis) against its exceedance value (x-axis).

Step Two: In the next step, the flow duration curve is combined with the pertinent numeric water quality criteria established to protect the contact recreation use. The pertinent criteria are a geometric mean concentration of *E. coli* not to exceed 126 cfu/100 ml and a single sample *E. coli* concentration not to exceed 394 cfu/100 ml. A load duration curve is developed by multiplying each streamflow value (daily average in cubic meters per second—m^3/s) from Step One by the *E. coli* criterion (either 126 or 394 cfu/100 ml) and by the conversion factor to give colonies per day (8.64×10^8). Separate load duration curves were developed for both criteria at each station.

Step Three: For each station, each historical *E. coli* measurement is associated with the predicted streamflow on the day of measurement. The historical *E. coli* measurements are combined with the appropriate predicted streamflow to give a loading as performed for the criterion in Step Two. The associated streamflow for each bacteria loading is compared to the flow duration curve data to determine its value for "percent days flow exceeded," which becomes the "percent of days load exceeded" value for purposes of plotting the *E. coli* loading. Each load is then plotted on the load duration curve at its percent exceedance. This process is repeated for each *E. coli* measurement at each station. Points above a curve represent exceedances of that bacteria criterion and its associated allowable loadings. *E. coli* data from both the October 2002 through August 2003 assessment effort and the March–2004 bacterial source tracking study were combined to provide as much data as possible for use with the method. The model predicted streamflows and associated *E. coli* concentrations at each of the six stations are provided in Appendix H.[4]

The flow duration curve and the *E. coli* load duration curve with both the geometric and single sample exceedance lines shown are provided in Figures 4-15 – 4-20 for stations 12074, 17688, 12083, 12086, 12087, and 12090, respectively. The flow duration and corresponding load duration curves for stations 12083, 12086, 12087, and 12090 (Figures 4-17 – 4-20) reflect a shape highly influenced by the GCWA pumping at the Shannon Pump and Second Lift stations, which results in the relatively constant flows between 1 and 8 m^3/s that occur about 70% of the time. Stations 12074 and 17688 (Figures 4-15 & 4-16), which are outside the influence of the pumping, had flow duration curves with shapes typical of stream systems were flow is not as heavily dominated by large amounts of nearly constant flow. The flow duration curves for both stations do, however, show the influence of continuous municipal WWTP discharges, which are reflected in flows below about 0.2 m^3/s. The *E. coli* load duration curves with superimposed historical data show at every station, except 12083, a high occurrence of historical *E. coli* loadings exceeding the geometric mean standard.

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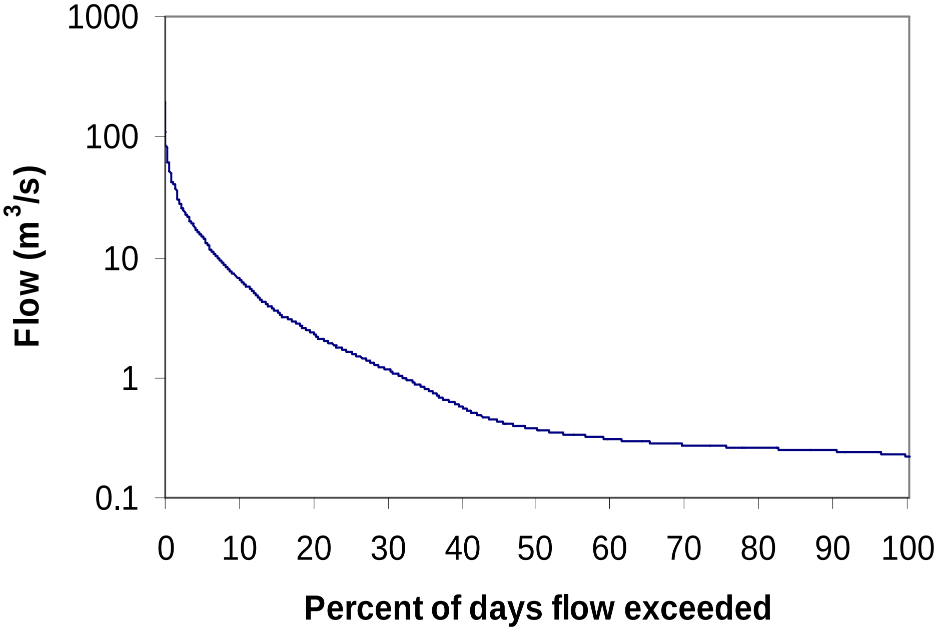
[4] The median concentration was used for *E. coli* data collected during the ambient water sampling under the bacterial source tracking study conducted from March through November 2004. In the source tracking study, five water samples, rather than one sample, were collected at each station during each survey to provide the statistical sampling specified in the monitoring design. The median of the five *E. coli* concentrations comprising each station's sampling event was used in the load duration curve method. The median concentration was selected as the measure of central tendency, since the median of five concentrations is actually represented by one of the measured values, i.e., the third value when ranked in either ascending or descending order. Hence the median concentration is an actual measured data point rather than a derived concentration from an averaging process.



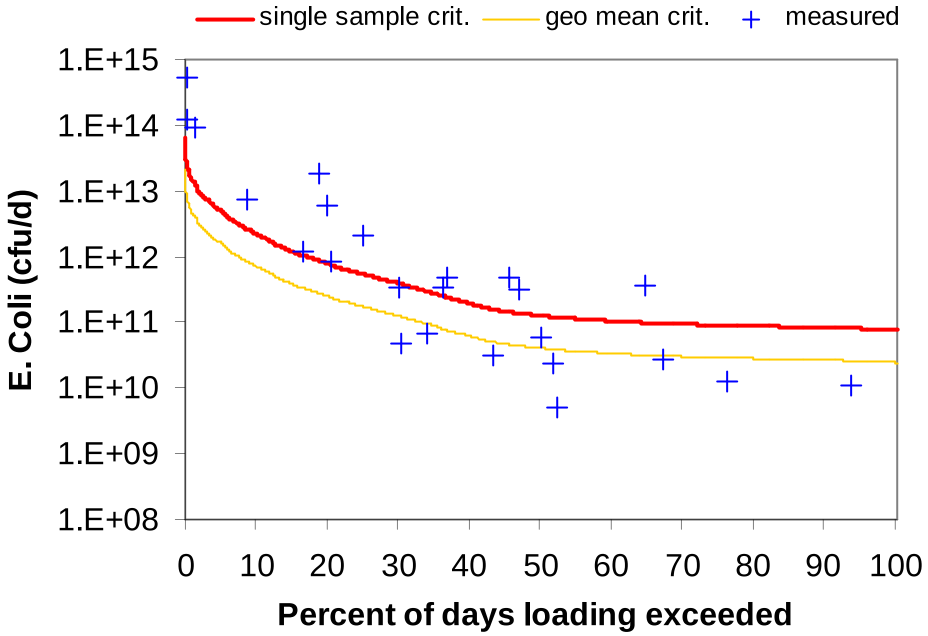
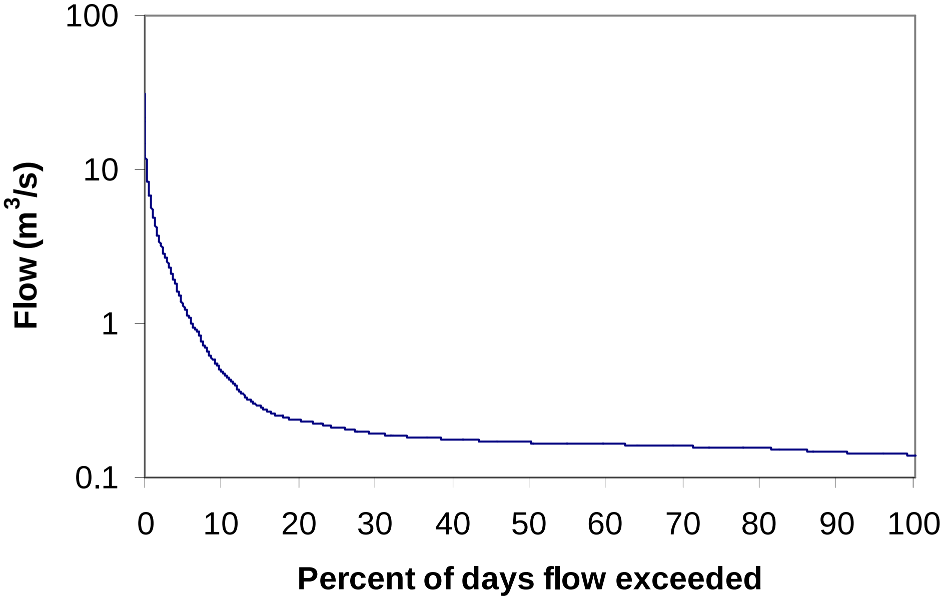


Figure 4-15 **Flow duration and bacteria load duration curves, Station 12074**



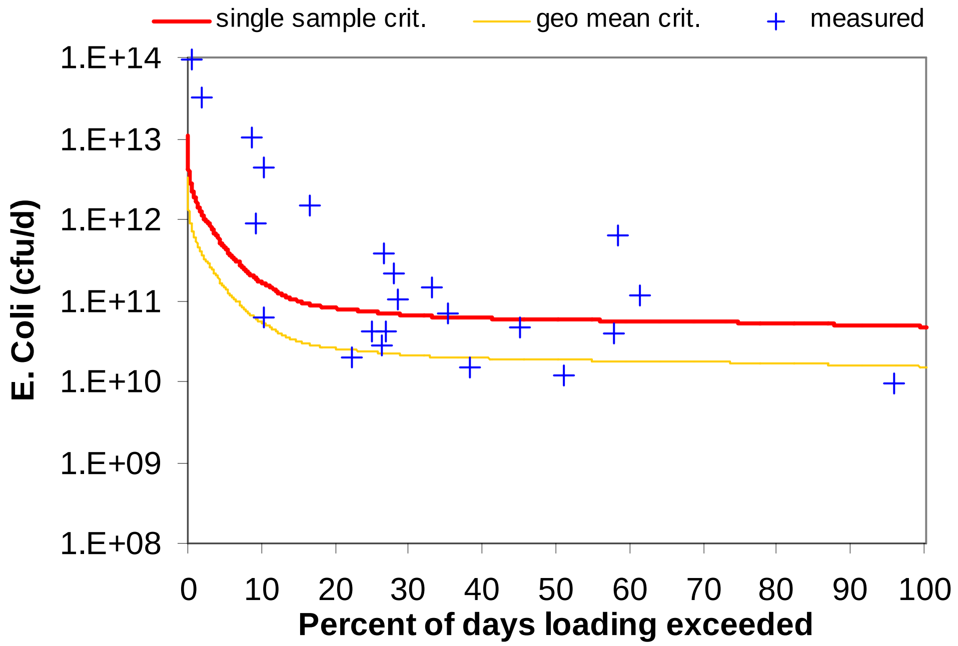


Figure 4-16 Flow duration and bacteria load duration curves, Station 17688

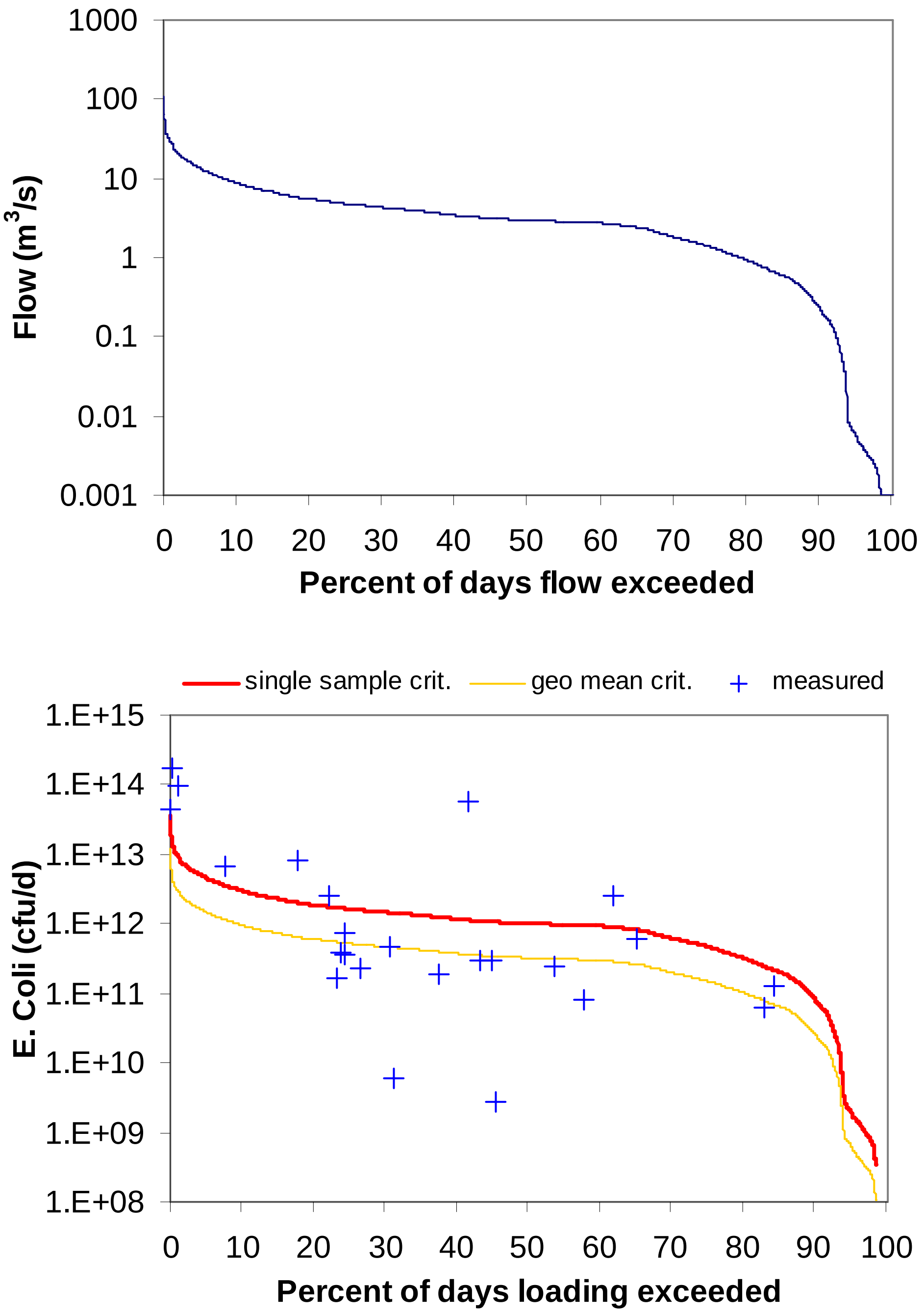


Figure 4-17 Flow duration and bacteria load duration curves, Station 12083

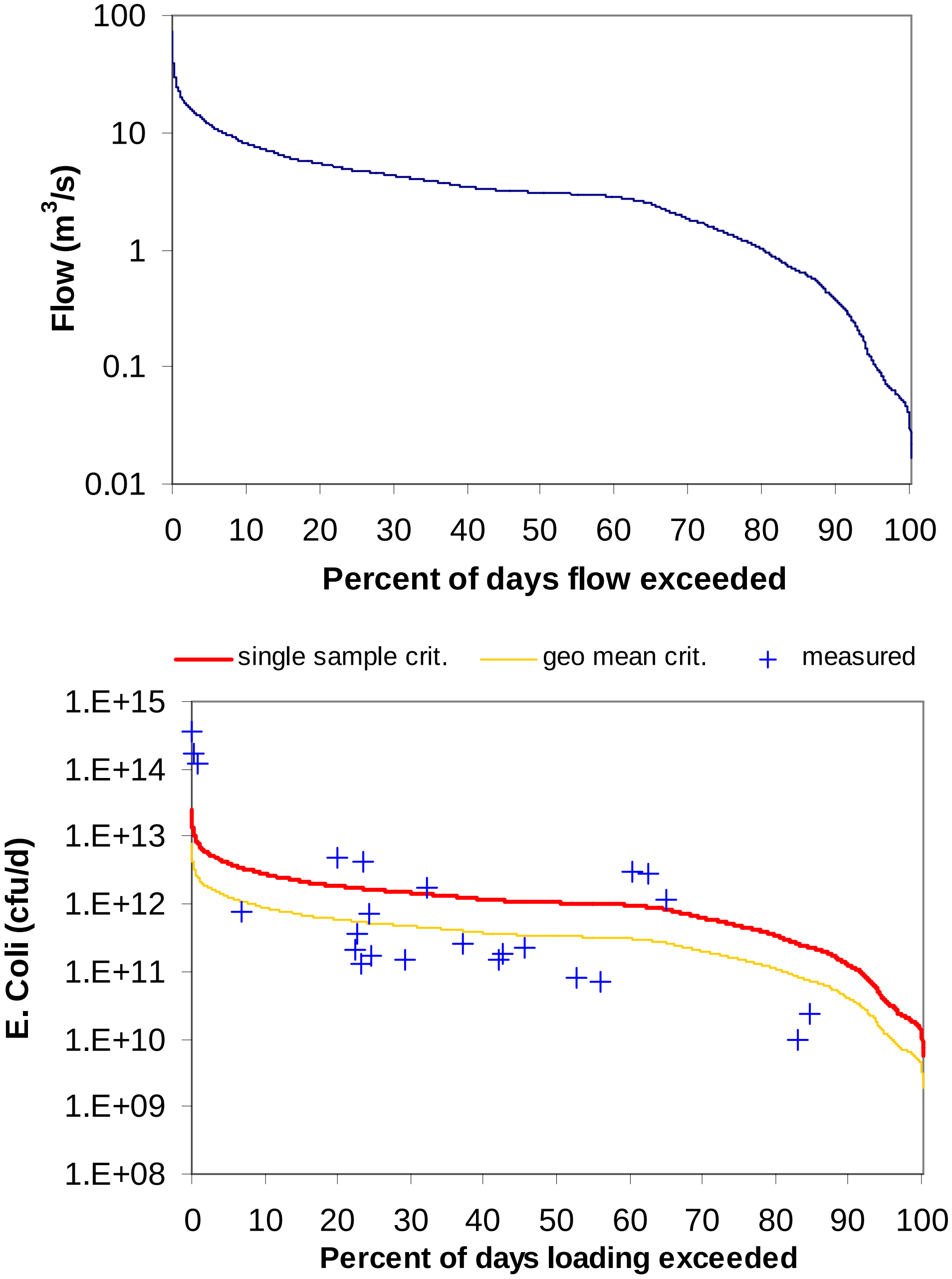
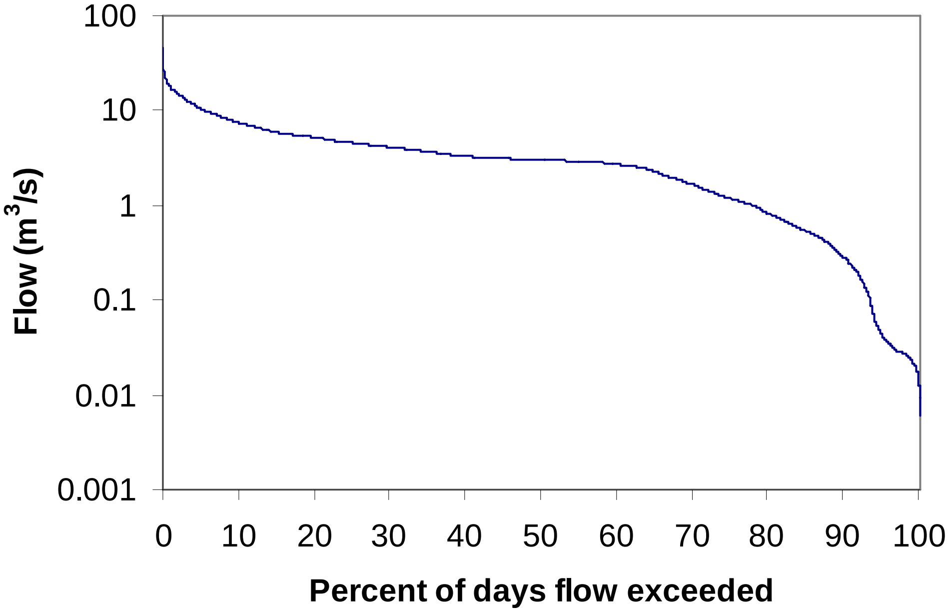


Figure 4-18 Flow duration and bacteria load duration curves, Station 12086



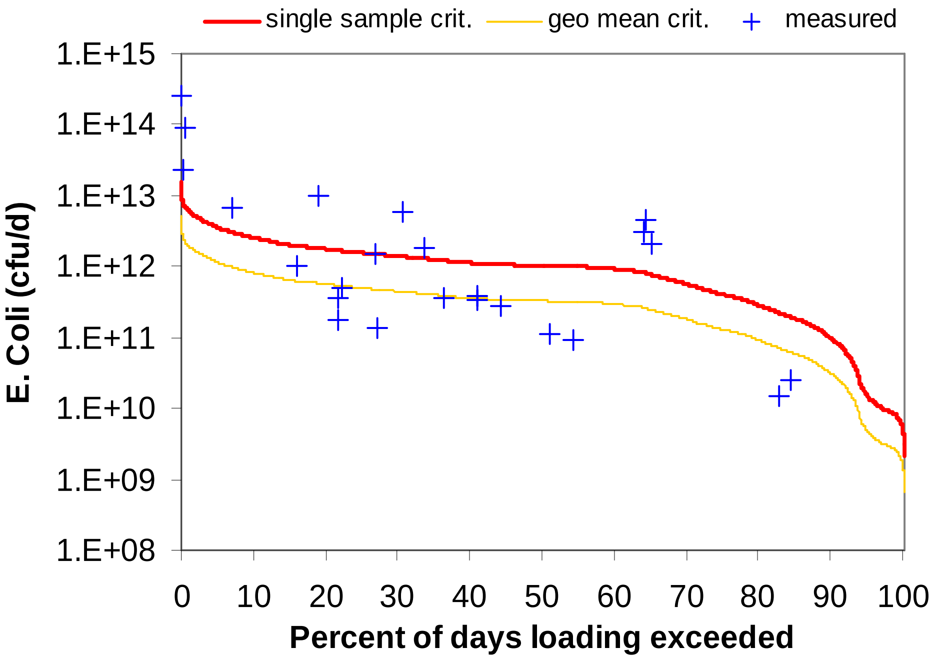
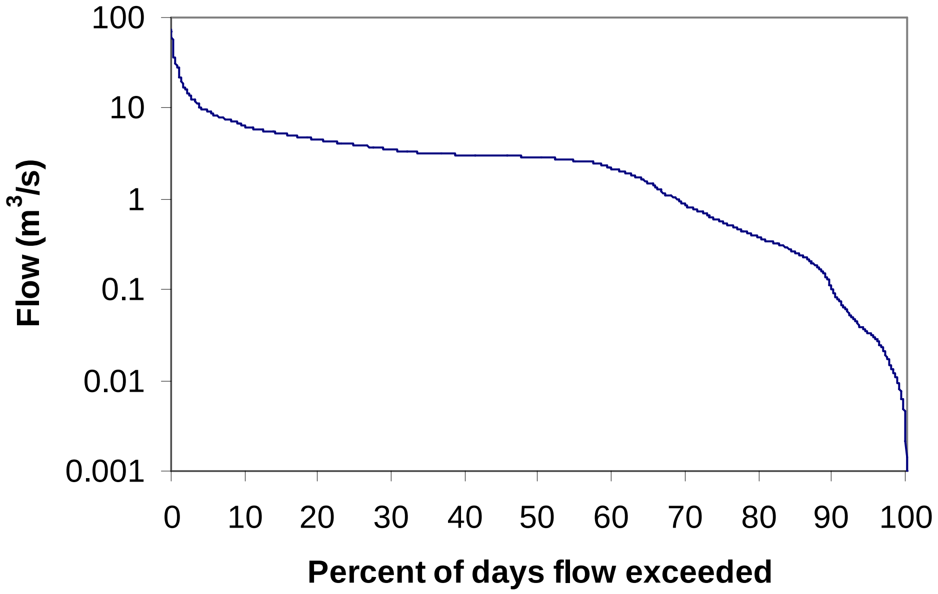


Figure 4-19 **Flow duration and bacteria load duration curves, Station 12087**



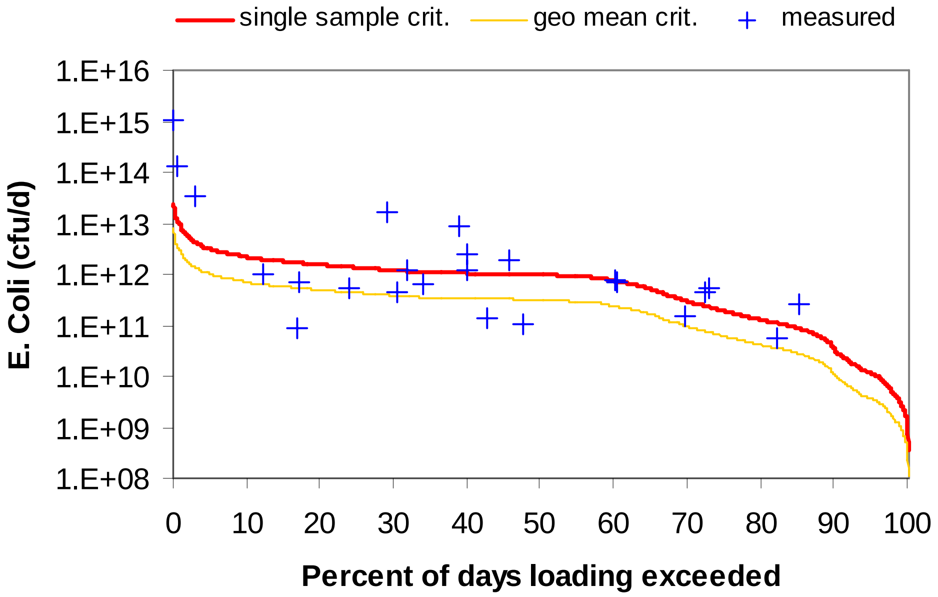


Figure 4-20 Flow duration and bacteria load duration curves, Station 12090

SECTION 5

BACTERIA LOAD ALLOCATION ANALYSIS

Within this report section is presented the development of the bacteria load allocation. The allocation tool used for the Upper Oyster Creek (segment 1245) bacteria TMDL was the load duration curve method previously described in Section 4: Bacteria Allocation Tool Development. Endpoint identification, margin of safety, load reduction analysis, and load allocations are described herein.

The load duration curve method provided a flow-based approach to determine necessary reductions in bacteria loadings to segment 1245. As developed previously in this report, the duration curve method uses frequency distributions to assess a bacteria criterion over the historical range of flows, providing a means to determine the necessary load reduction to achieve support of the contact recreation use.

5.1 Endpoint Identification

Upper Oyster Creek has a designated use for contact recreation, which is protected by numeric criteria for the indicator bacteria of fecal coliform and *E. coli*. The preferred indicator bacteria provided in the presently effective water quality standards is *E. coli*, though the standards did allow a transition period wherein fecal coliform bacteria could be used until sufficient *E. coli* data were available (TNRCC, 2000). Indicator bacteria are not generally pathogenic and are indicative of potential viral, bacterial, and protozoan contamination originating from the feces of warm-blooded animals. *E. coli* criteria to protect freshwater contact recreation consist of single sample and geometric mean concentrations of 394 cfu/100 ml and 126 cfu/100 ml (TNRCC, 2000). Further, for a water body to be considered as supporting contact recreation use the single sample criterion of 394 cfu/100 ml should not be exceeded more than 25 percent of the time. The binomial method is used to determine the minimum number of samples in the monitored population that indicate the single sample criterion is being exceeded more than 25 percent of the time and also does not result in greater than a 20 percent probability of improperly assessing the water body as not supporting when it is actually supporting (TCEQ, 2003).

For purposes of this bacteria TMDL, the single sample criterion for *E. coli* was used as the endpoint concentration not to be exceeded; specifically a not to be exceeded concentration of 394 cfu/100 ml. The single sample criterion provided an endpoint to which each monitored *E. coli* concentration may be compared, though not without recognition of the confounding implications that support is indicated as long as 25 percent or less of the data exceed the criterion. The geometric mean criterion can only meaningfully provide an endpoint to appropriately averaged groupings of monitored data—thus negating its applicability as a comparative endpoint measure for individual data values. The single sample criterion, therefore, was considered the more readily applicable endpoint for this TMDL. Though the TMDL endpoint was based on the single sample criterion, it was recognized that the geometric mean criterion must also be met for segment 1245 to support its contact recreation use, and that reductions to meet the single sample criterion will commensurately bring reductions to the geometric mean. As shown later in this section, if the percent reduction in *E. coli* concentrations determined as necessary to provide support for the single sample criterion is applied to historical data, the geometric mean criterion will also be met.

5.2 Assessment Results from Historical *E. coli* Data

As previously presented in this report, the fecal coliform and *E. coli* data collected from October 2002 through August 2003 confirmed that much of Upper Oyster Creek does not support the contact recreation use (see section 2.2.3—Analysis of Bacteria Data). Bacteria data from each station were used to characterize water quality in the portions of Upper Oyster Creek adjacent to each station. Based on the historical *E. coli* data, portions of segment 1245 were indicated to support the contact recreation use, though these portions represented a relatively small length of the entire system (Figure 5-1). Specifically, the portion of Oyster Creek below Dam #3 and above Oyster Creek's confluence with Stafford Run was indicated to support the contact recreation use based on station 12077 data. The remainder of Upper Oyster Creek below Dam #3 was indicated in the assessment survey to be in nonsupport of the contact recreation use. In Upper Oyster Creek above Dam # 3, the lower portion of that reach, as represented by stations 12079 and 17373, was indicated to support the contact recreation use. The likely reason for support in this portion of Oyster Creek was the low water velocities and reduced turbulence due to the widening of the creek behind the dams, which provides favorable conditions for settling of *E. coli* from the water column. Also the short stretch in Jones Creek above the confluence with Flewellen Creek to the Shannon Pump Station supported the contact recreation use as characterized by data from station 17685. The support finding in the uppermost portion of segment 1245 indicated that the water being pumped from the Brazos River typically contains *E. coli* concentrations that support the contact recreation use.

5.3 Definition of Allocation Reaches

For purposes of performing load reduction analysis, Upper Oyster Creek was separated into two distinct reaches. As previously presented in this report (Section 2.1—Watershed Hydrology and Climate), the portion of Upper Oyster Creek above Dam #3 serves as conveyance for water pumped by the GCWA from the Brazos River (see Figure 1-2). Much of the creek below Dam #3 has characteristics of a typical southeast Texas urban/suburban creek including modifications to reduce flooding potential and enhancements to speed water conveyance. Above Dam #3, the Upper Oyster Creek channel system is maintained by the GCWA for conveyance of water and annually carries approximately 50,000 acre-feet of Brazos River water.

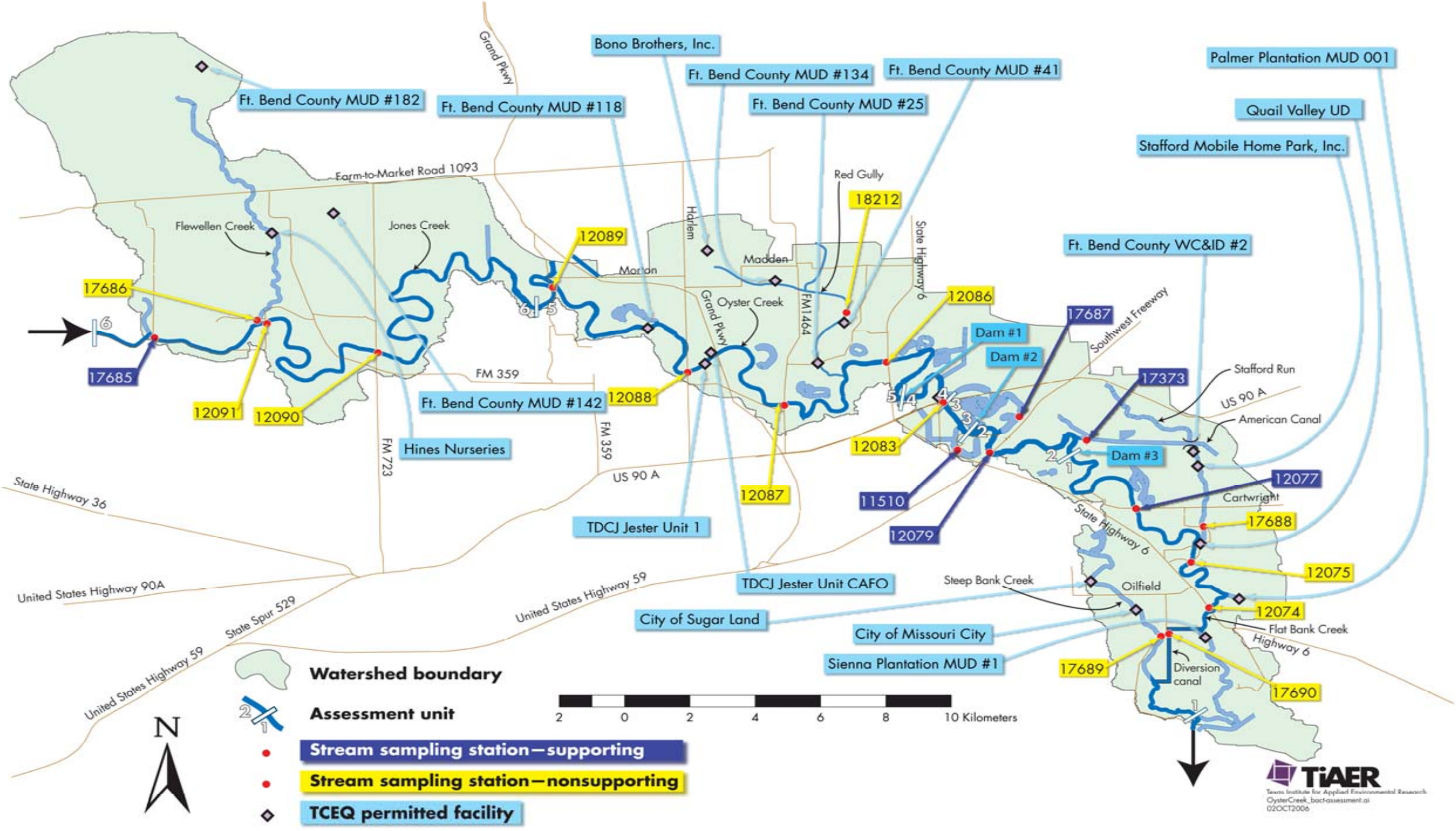


Figure 5-1 Upper Oyster Creek showing bacteria assessment stations (Also showing indications of support and nonsupport of contact recreation use by station)

Based on these hydrological distinctions Upper Oyster Creek was divided into two allocation reaches for this bacteria load reduction analysis.

- <u>Allocation Reach 1:</u> Segment 1245 from its downstream confluence with the Brazos River up to Dam #3.
- <u>Allocation Reach 2:</u> Segment 1245 from Dam #3 to the GCWA Shannon Pump Station.

While portions of both allocation reaches contain monitoring stations where data indicate support of contact recreation (see Table 2-2), the majority of the length of Segment 1245 experiences elevated *E. coli* levels. Therefore, to achieve desired bacteria load reductions throughout the entire watershed, the two allocation reaches comprise the entire length of the segment.

5.4. Load Reduction Analysis

A single percent load reduction was determined for each allocation reach using the loadings represented by the exponential regression line and single sample criterion information at the six stations for which load duration curves were developed. The following steps were used to determine the percent reduction by allocation reach:

1. Obtain the load duration curves by station for each reach. For allocation reach 1, stations 12074 and 17688 were used. For allocation reach 2, stations 12083, 12086, 12087, and 12090 were used.
2. For each station develop an exponential regression line through <u>relevant</u> *E. coli* data points used to characterize the existing, nonsupport loading of bacteria (Figures 5-2 through 5-7 for the stations 12074, 17688, 12083, 12086, 12087, and 12090 respectively). Relevant data for determining the regression line were considered as those data at concentrations exceeding the single sample criterion and also occurring at a flow exceeded on greater than 0.27 percent or days (or on average occurring at a flow exceeded more than one day per year). By happenstance, the November 2 and 23, 2004 bacteria sampling events occurred during periods of high rainfall and at several stations produced data points that had a very small exceedance percentage (<0.27 percent) and became “leverage” points in the exponential regression, which increased the downward (left to right) slope of the regression at these stations. Removal of these data points provided a regression line that more closely fit through more of the relevant data points, thus better reflecting the existing loading that exceeded the single sample criterion.
3. For each station determine the required percent removal at five-percent intervals along the x-axis (i.e., five-percent intervals of days loading exceeded). The extreme high flow interval was defined at one (1) percent, which represented a reasonably extreme event occurring three or four days a year on average. Thus the first interval was defined as one percent, the next as five percent, and then included all five-percent intervals thereafter as restricted to either the nearest five-percent interval near the last measured *E. coli* data point exceeding the criterion or to the last five-percent interval having an associated positive load reduction (i.e., where the regression line lies above the criterion line). The immediately preceding restriction to determining the percent

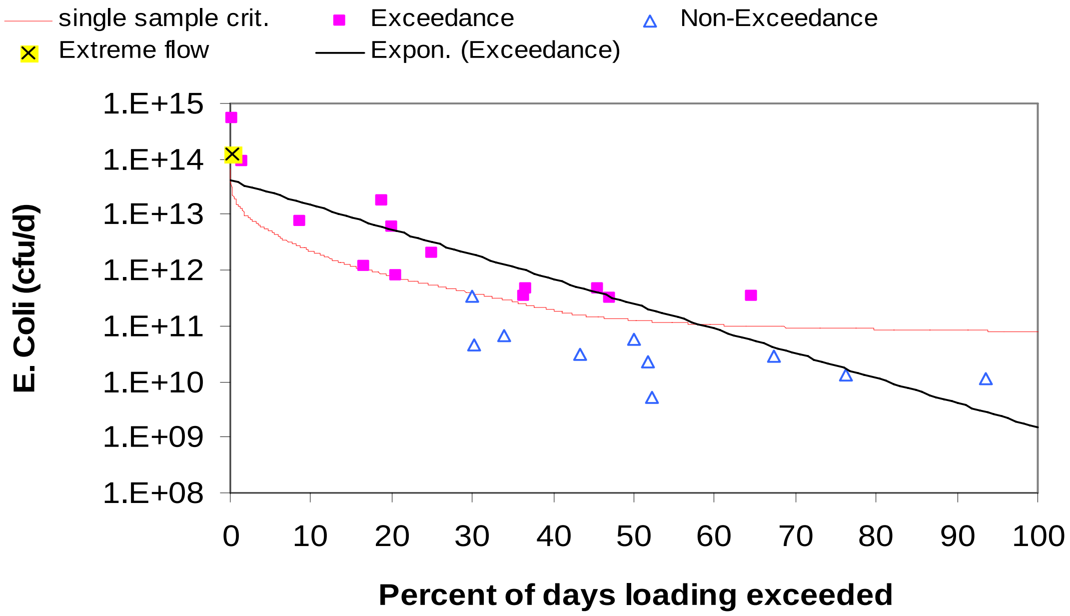


Figure 5-2 **Load duration curve single sample criterion and exponential regression line for sampled population exceeding criterion, Station 12074 in allocation reach 1**

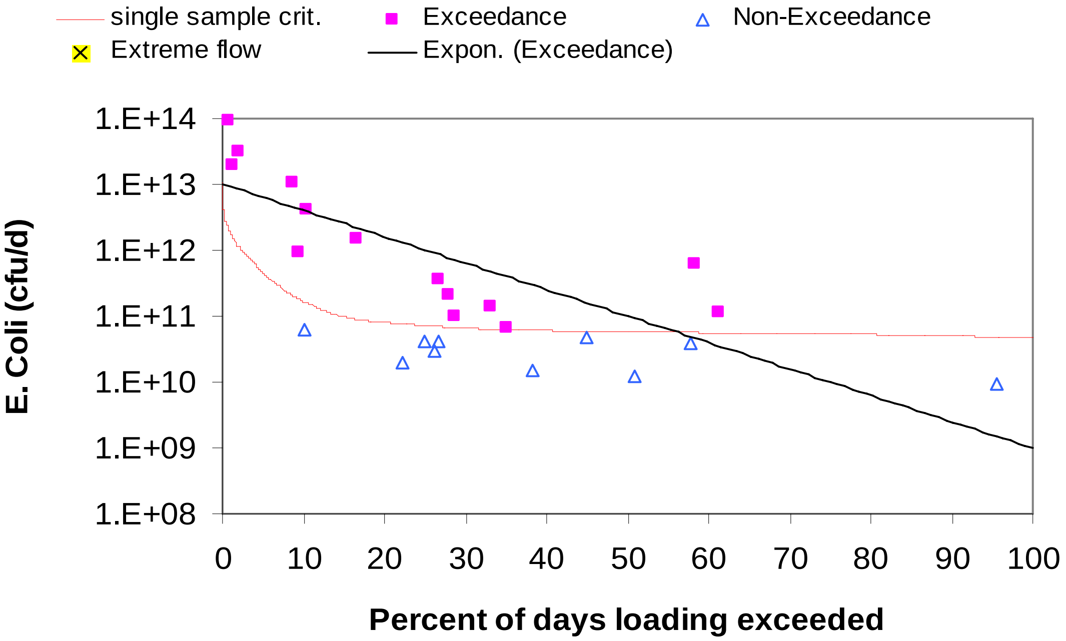


Figure 5-3 **Load duration curve single sample criterion and exponential regression line for sampled population exceeding criterion, Station 17688 in allocation reach 1**

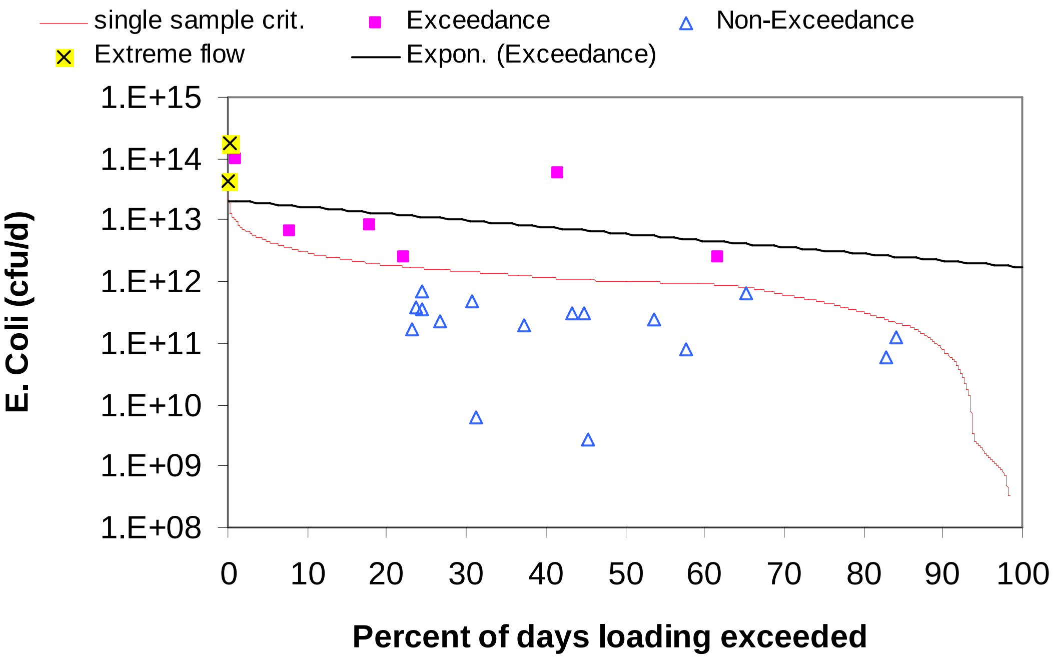


Figure 5-4 **Load duration curve single sample criterion and exponential regression line for sampled population exceeding criterion, Station 12083 in allocation reach 2**

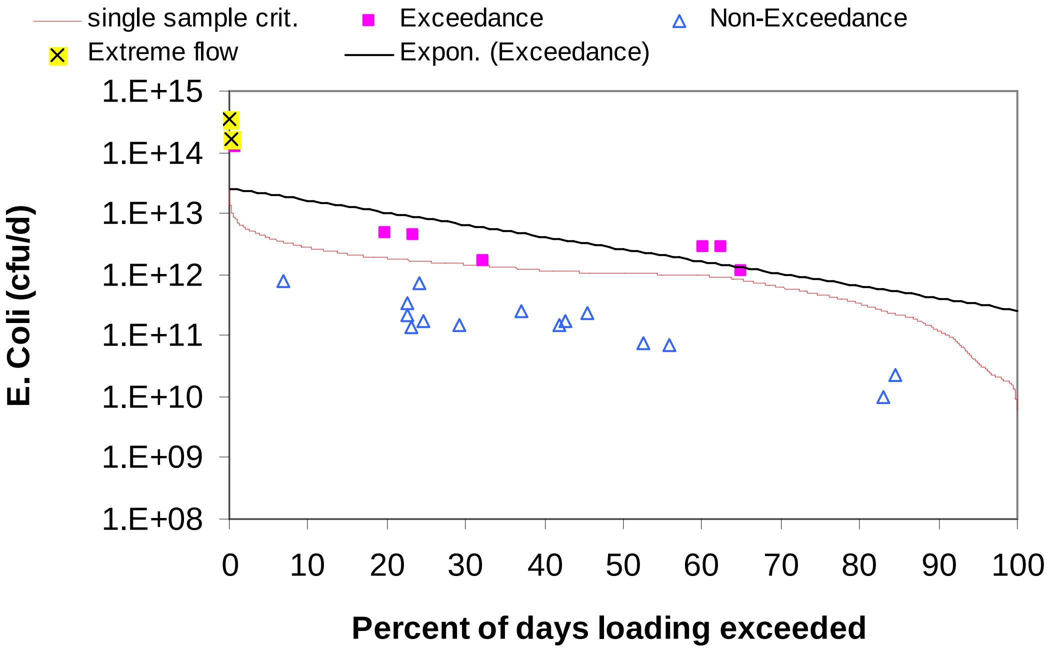


Figure 5-5 **Load duration curve single sample criterion and exponential regression line for sampled population exceeding criterion, Station 12086 in allocation reach 2**

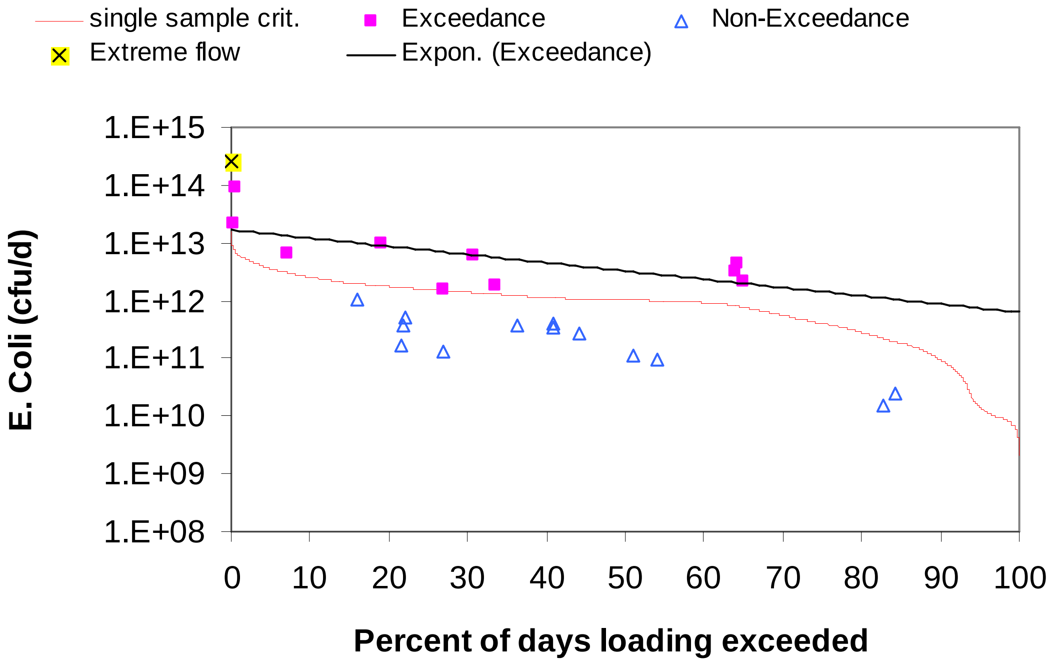


Figure 5-6 **Load duration curve single sample criterion and exponential regression line for sampled population exceeding criterion, Station 12087 in allocation reach 2**

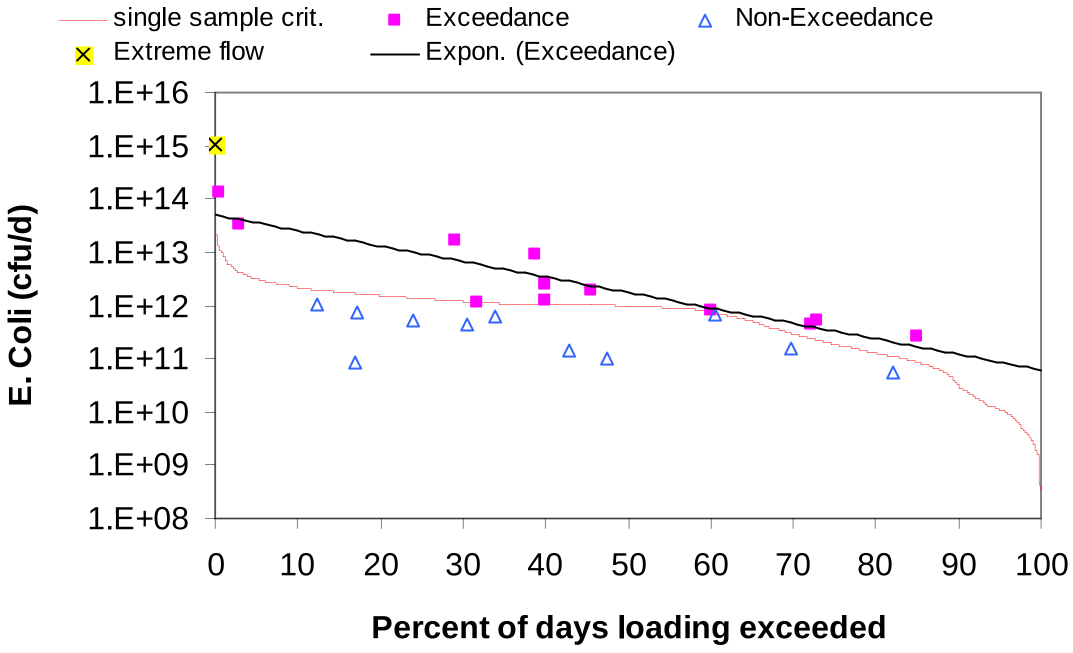


Figure 5-7 **Load duration curve single sample criterion and exponential regression line for sampled population exceeding criterion, Station 12090 in allocation reach 2**

reduction was necessitated by the paucity of *E. coli* data with associated low daily streamflows providing loadings exceeded greater than 70 percent of days. Collectively these refinements allowed determination of percent reduction for load duration curve stations in both allocation reaches for the range of streamflow conditions under which bacteria exceedances occurred (Table 5-1).

4. The required load reduction to meet the single sample criterion was calculated as the arithmetic average of the percent reductions at the defined intervals from step 3 (Table 5-1).
5. As the final step the required load reduction for both allocation reaches was calculated as the average of the percent reductions from step 4 for the stations associated with each reach. Averaging the percent load reductions for stations 12074 and 17688 in allocation reach 1 gave a value of 73 percent, and likewise averaging the four stations in allocation reach 2 (stations 12083, 12086, 12087, and 12090) also gave a value of 73 percent.

Therefore the calculated *E. coli* load reductions as a percent to meet the single sample grab criterion are as follows:

- **Allocation reach 1, calculated load reduction to meet single sample *E. coli* criterion is 73 percent.**
- **Allocation reach 2, calculated load reduction to meet single sample *E. coli* criterion is 73 percent.**

5.5 Geometric Mean Criterion Analysis

Though the primary endpoint for this bacteria TMDL is the single sample criterion, the geometric mean criterion was considered a secondary criterion that also should be met in order for segment 1245 to fully support its contact recreation use. The average percent reduction to the existing *E. coli* loading of 73 percent will beneficially reduce the existing geometric mean. Applying this reduction to the combined dataset from all stations with historical *E. coli* data not supporting contact recreation results in the geometric mean criterion being met in both allocation reaches (Table 5-2). The calculated value for allocation reach 1 is right at the geometric mean criterion concentration of 126 cfu/100 ml. Hence, the required load reduction to achieve the single sample criterion also achieved the geometric mean criterion.

5.6 Implicit Margin of Safety

The bacteria load reduction was based on the duration curve of the single sample criterion and the exponential regression line through sampled data exceeding that criterion for each station (stations 12074, 17688, 12083, 12086, 12087, and 12090 in Figures 5-2 through 5-7 respectively). The exponential regression line provided a reasonable representation of existing bacteria loadings for those monitored periods when contact recreation was not supported.

Table 5-1 Percent reduction to meet single sample criterion for exponential regression line of sampled data exceeding criterion (Highlighted table entries are those used in the computation of average percent reduction.)

% Exceed.	12074 (Allocation Reach 1)	17688 (Allocation Reach 1)	12083 (Allocation Reach 2)	12086 (Allocation Reach 2)	12087 (Allocation Reach 2)	12090 (Allocation Reach 2)
1	60	80	50	73	69	80
5	79	93	74	83	79	91
10	85	96	81	85	82	92
15	86	96	83	86	84	90
20	85	95	85	85	83	88
25	82	93	85	83	82	86
30	79	90	85	81	81	82
35	75	84	84	78	80	78
40	71	76	84	76	79	70
45	63	63	84	71	77	59
50	47	42	82	65	73	44
55	20	9	81	58	70	29
60	0	0	79	50	67	19
65	0	0	79	45	67	21
70	0	0	82	49	72	38
75	0	0	85	51	76	43
80	0	0	88	56	80	47
85	0	0	92	63	85	49
90	0	0	96	74	91	74
95	0	0	100	91	98	87
99	0	0	100	95	99	96
Average	69	76	80	73	77	61

Table 5-2 Geometric mean of historical *E. coli* data for all stations in allocation reaches and geometric mean with load reduction of 73 percent uniformly applied

Allocation Reach	Count	Geometric Mean of Historical data (cfu/100ml)	Geometric Mean with Percent Reduction Applied (cfu/100 ml)
1	83	467	126
2	123	282	76

Using only data exceeding the single sample criterion to develop the exponential regression line provided an implicit margin of safety, since *E. coli* concentrations meeting the criterion (i.e., the data with values ≤394 cfu/100 ml) were measured with relatively high frequency at each of the six stations and not included in the analysis. Further, this approach has the additional implicit margin of safety that the State's water quality assessment methodology specifies 25 percent or less of the data can exceed the single sample criterion and still support the contact recreation use (TCEQ, 2003), and these allowable exceedances were not factored into the load reduction analysis.

5.7 Existing Loads

For each allocation reach the existing daily *E. coli* load was estimated using data from the most downstream station for which the load reduction analysis was performed — Station 12074 for allocation reach 1 and station 12083 for allocation reach 2. By selecting the most downstream station, the greatest amount of each allocation reach was included based on data availability. The exponential regression line through *E. coli* data points exceeding the single sample criterion formed the basis for estimating existing loadings. The existing *E. coli* loadings were estimated by averaging the daily loadings from the exponential regression line at the same percent exceedances used in the calculations of percent reduction (Table 5-3). This method of estimating the existing loading is both excepted when using load duration curves and provides an implicit margin of safety as discussed previously (see the "Margin of Safety" section. Based on this approach the following average daily existing *E. coli* loadings were estimated:

- **Allocation reach 1, existing daily average *E. coli* loading = 4,570 billion cfu per day**
- **Allocation reach 2, existing daily average *E. coli* loading = 7,492 billion cfu per day**

5.8 TMDL Allocation

The TMDL represents the maximum amount of pollutant (in this case *E. coli*) that the stream can receive without exceeding the water quality standard. For purposes of bacteria load allocation, the TMDL allocation is defined by the following simple equation:

Table 5-3 Estimates of existing daily load and maximum allowable daily load by allocation reach (Data based on Figures 5-2 and 5-4)

Reach	**Allocation Reach 1 (station 12074)**		**Allocation Reach 2 (station 12083)**	
% Exceed.	**Existing daily load (billion cfu/d)**	**Maximum allowable daily load (billion cfu/d)**	**Existing daily load (billion cfu/d)**	**Maximum allowable daily load (billion cfu/d)**
1	36,100	14,400	19,500	9,810
5	24,000	5,100	17,600	4,610
10	14,400	2,210	15,600	3,000
15	8,610	1,210	13,700	2,310
20	5,160	791	12,100	1,860
25	3,090	549	10,700	1,630
30	1,850	394	9,450	1,460
35	1,110	279	8,340	1,320
40	666	194	7,360	1,170
45	399	147	6,490	1,060
50	239	127	5,730	1,010
55	143	114	5,060	970
60	86	105	4,460	930
65	52	99	3,940	819
70	31	94	3,480	615
75	19	91	3,070	467
80	11	88	2,710	321
85	7	86	2,390	202
90	4	84	2,110	79
95	2	81	1,860	2
99	2	77	1,680	0
Average	4,570	1,253	7,492	1,602
Additional Loading[1]	—	200	—	80
Total	—	1,453	—	1,682

[1] Additional loading is the increase in allowable *E. coli* loading from the discharge condition of WWTPs used to develop the single sample criterion load duration curve to the allowable loading for the final permitted discharge from WWTPs.

$$\text{TMDL} = \Sigma\,\text{WLA} + \Sigma\,\text{LA} + \text{MOS}$$

where,

WLA is waste load allocation for point (TPDES-regulated) source reductions,
LA is the load allocation for nonpoint source reductions, and
MOS is the margin of safety, which is implicit for this allocation (see Section 5-6).

The TMDL load allocation for segment 1245 was performed to provide the flexibility necessary to accommodate the pending Small Municipal Separate Storm Sewer Systems (Phase II MS4) general permit, which will provide authorization for certain storm water discharges. The geographic region for segment 1245 to be covered by the Phase II MS4 general permit is that portion of the watershed contained within the Urbanized Area defined in the 2000 Census for the greater Houston area. Approval of the general permit and subsequent permittee applications are anticipated to occur within the year 2007. The TMDL load allocation is presented for two conditions:

1. without the Phase II MS4 general permit, and
2. with the Phase II MS4 general permit.

5.8.1 TMDL Allocation for Allocation Reach 1

The allowable loading of *E. coli* that allocation reach 1 can receive on an average daily basis was determined using the single sample criterion load duration curve for station 12074 (Figure 5-2) and the same percent exceedance intervals used to estimate the existing loading. The average maximum allowable daily loading determined from the load duration curve was increased to reflect the additional loading originating from the difference between allowable loading that would occur for WWTPs operating at their permitted daily discharge and the WWTP loading allowed under recent (or existing) conditions. The reason for including this additional load follows. The daily streamflow record used in developing the single sample criterion load duration curve was based on recent discharge information from permitted discharge facilities, and this information was used as input in the SWAT model (see Section 4, especially Table 4-3). However, it is desired that the TMDL allocation be based on the permitted discharge for each facility, not the recent discharges. Inclusion of permitted levels of discharge means the additional allowable loading associated with the difference between permitted discharges and recent discharges needs to be included in the allowable loading. In allocation reach 1, the combined permitted discharge of all facilities is 24.602 MGD (as shown in more detail immediately below) and the recent combined discharge used in SWAT averaged 11.204 MGD, resulting in a difference between recent and actual allowed discharge of 13.398 MGD. Because this allowed increase in discharge and the associated allowed loading are continuous (i.e., would apply equally to all days of each year regardless of streamflow), the difference between the two discharge rates multiplied by the single sample criterion is the additional allowable loading as reflected in Table 5-3. The computed additional allowable loading for the 13.398 MGD at the single sample criterion concentration of 394 cfu/100 ml is 200 billion cfu per day. The estimated maximum allowable daily average loading is 1,453 billion cfu per day with the additional loading included (Table 5-3).

Seven municipal-type wastewater treatment plants operate within allocation reach 1. Several of these facilities operate under a phased permit, which allows progressively higher daily average permitted discharges through facility expansions in response to anticipated growth. The final and largest discharge for each facility was used in the load allocation process. The seven facilities and their final permitted daily average discharges follows:

1.	City of Missouri City	3.0 MGD
2.	City of Sugar Land	10.0 MGD
3.	Fort Bend Co. WTCID # 3	6.0 MGD
4.	Palmer Plantation MUD # 1	0.60 MGD
5.	Quail Valley UD	4.0 MGD
6.	Sienna Plantation MUD # 1	0.902 MGD
7.	Stafford Mobile Home Park	0.10 MGD

The combined permitted discharge from these facilities is 24.602 MGD. The maximum allowable *E. coli* concentration for each of these facilities is the single sample criterion (394 cfu/100 ml). The combined discharge and single sample criterion were multiplied together providing the WLA for continuous discharges of 367 billion cfu per day. It is anticipated that these treatment facilities will typically operate well below the allowable single sample criterion based on the limited bacteria data available for effluents from permitted facilities in the Upper Oyster Creek watershed.

For the conditions without the Phase II MS4 general permit, the LA was computed by subtracting the WLA from the TMDL allowable loading, which provided the total LA of 1,086 billion cfu per day. The LA was separated into the Urbanized Area that is anticipated to become included under the Phase II MS4 general permit and the "Other" category, which consists of all other non-regulated, nonpoint sources (Figure 5-8). The drainage area of allocation reach 1 includes 7,522 hectare (ha) of which 4,843 ha are within the Urbanized Area. The LA specifically for the Urbanized Area was computed as the total computed LA multiplied by the area ratio of the Urbanized Area to the total drainage area within allocation reach 1 (4,843 / 7522 = 0.6438). In a similar manner, the "Other " category was computed using the ratio of its area to the total drainage area ((7,522-4,843) / 7,522 = 0.3562). Multiplying the total LA by the appropriate area ratios provides the LA Urbanized Area load of 699 billion cfu per day and the LA "Other" load of 387 billion cfu per day.

The TMDL load allocation for allocation reach 1 without the Phase II MS4 general permit (i.e., with no sources in the WLA non-continuous category) is provided in Table 5-4. By addition, the total WLA is 367 billion cfu per day and the total LA is 1,086 billion cfu per day.

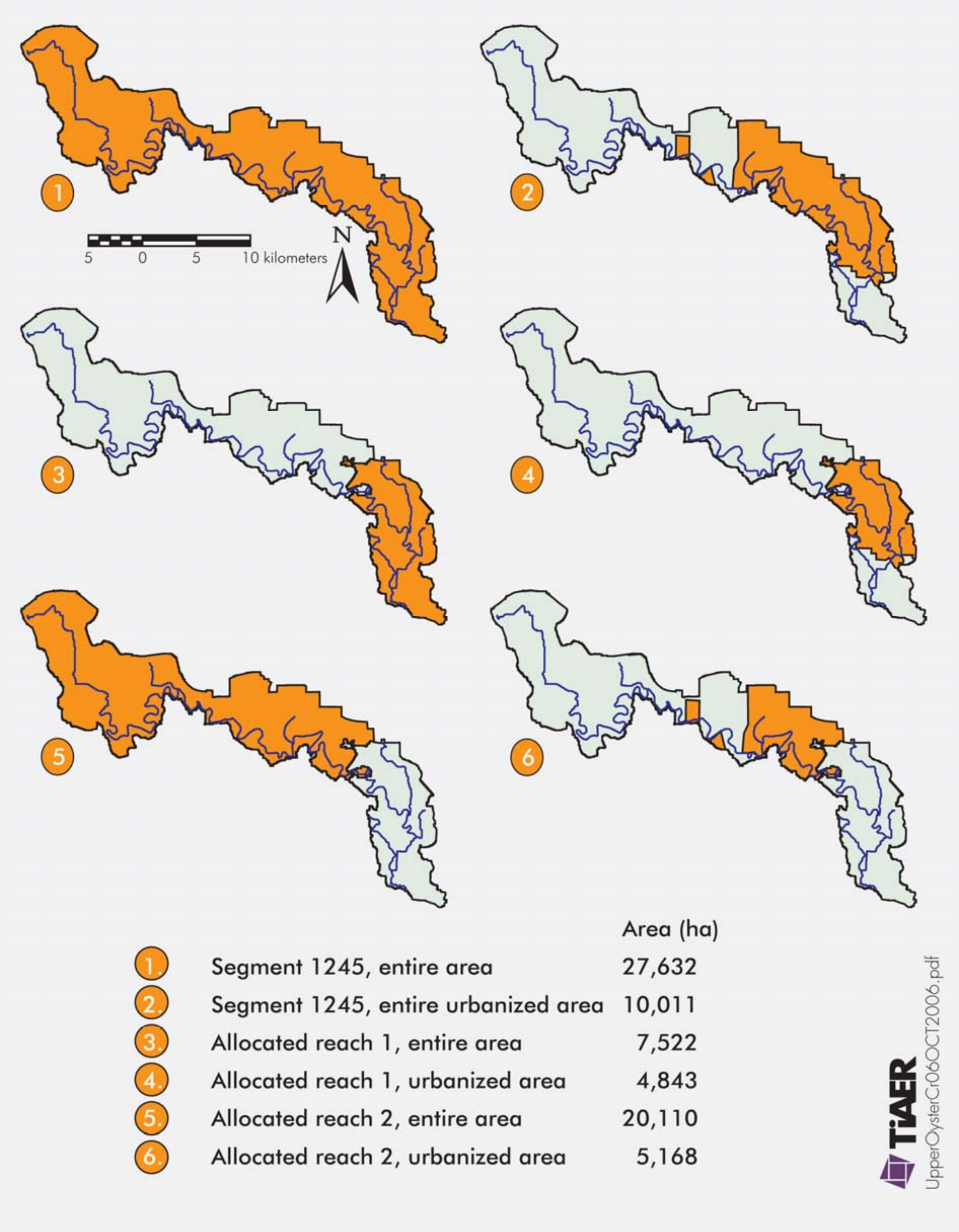


Figure 5-8 **Upper Oyster Creek watershed with Urbanized Areas and area of allocation reaches (Source for 2000 Census Urbanized Area:** http://www.census.gov/geo/www/cob/metadata.html)

Table 5-4 TMDL load allocation summary for allocation reaches 1 <u>without</u> Phase II MS4 general permit

Alloc. Reach	TMDL	WLA Continuous	WLA Non-continuous	LA Urbanized Area	LA Other	MOS
(all units in billion cfu per day)						
1	1,453	367	N/A	699	387	Implicit

N/A – not applicable, no sources in WLA Non-continuous under this condition

For conditions with the Phase II MS4 general permit, the LA Urbanized Area load becomes the WLA Non-continuous load as provided in Table 5-5. By addition, the total WLA is 1,066 billion cfu per day and the total LA is 387 billion cfu per day.

Table 5-5 TMDL load allocation summary for allocation reaches 1 <u>with</u> Phase II MS4 general permit

Alloc. Reach	TMDL	WLA Continuous	WLA Non-continuous	LA Urbanized Area	LA Other	MOS
(all units in billion cfu per day)						
1	1,453	367	699	N/A	387	Implicit

N/A – not applicable, no sources in LA Urbanized Area under this condition

5.8.2 TMDL Allocation for Allocation Reach 2

The allowable loading of *E. coli* that allocation reach 2 of Upper Oyster Creek can receive on an average daily basis was determined using the single sample criterion load duration curve for station 12083 (Figure 5-4) and the same percent exceedance intervals used to estimate the existing loading. As was required for allocation reach 1, an additional allowable loading from permitted WWTPs was added to the average allowable loading. That additional loading resulted from the increase of the combined final permitted WWTP daily discharge (6.2785 MGD) over recent discharges (0.9292 MGD) used in the SWAT model for load duration curve development. The computed additional allowable loading for the 5.3493 MGD (6.2785 – 0.9292) at the single sample criterion concentration of 394 cfu/100 ml is 80 billion cfu per day. The estimated maximum allowable daily average loading is 1,682 billion cfu per day, including the additional loading from WWTPs operating at permitted daily discharges (Table 2-3).

Eight municipal-type wastewater treatment plants operate or are in the process of being permitted to operate within allocation reach 2. Several of these facilities operate under a phased permit, which allows progressively higher daily average permitted discharges through facility expansions in response to anticipated growth. The final and largest discharge for each facility was used in the load allocation process. The eight facilities and their final permitted daily average discharges follows:

1. Fort Bend Co. MUD # 25	1.6 MGD
2. Fort Bend Co. MUD # 41	0.86 MGD
3. Fort Bend Co. MUD # 118	1.2 MGD
4. Fort Bend Co. MUD # 134	0.30 MGD
5. Fort Bend Co. MUD # 142	1.2 MGD
6. Fort Bend Co. MUD # 192	0.80 MGD
7. Hines Nurseries	0.0035 MGD
8. TDCJ Jester Unit # 1	0.315 MGD

The combined permitted discharge from these facilities is 6.2785 MGD. The allowable *E. coli* concentration for each of these facilities is the single sample criterion (394 cfu/100 ml). The WLA from regulated continuous discharges was calculated as the discharge of these facilities multiplied by the single sample criterion, which provides a load of 94 billion cfu per day.

For the conditions without the Phase II MS4 general permit, the remaining components in the computation of the TMDL allocation include the Non-continuous WLA and the Urbanized Area and “Other” components of the LA. Because of the nature of sources in allocation reach 2 and the complicating factor of the GCWA pumping of Brazos River water into the reach from the Shannon Pump Station, these remaining allocation were computed in a progressive manner that immediately follows.

The GCWA pumping of Brazos River water was considered a portion of the “Other” component of the LA. The bacteria contribution of the pumped water through allocation reach 2 is difficult to estimate due to the extremely dynamic response of *E. coli* to die-off, settling, and other processes. The following process was used to estimate the allowable loading for this source as part of the “Other” component. The allowable load from the GCWA Shannon Pump Station pumping was determined using the average daily pumping rate at the Shannon Pump Station (2.05 m^3/s) and the geometric mean *E. coli* concentration (75 cfu/100 ml) measured during the October 2002 through August 2003 bacteria assessment monitoring at station 17685 (Jones Creek at Bois D’Arc Lane; Figure 2-1 and Table 2-2). Use of the geometric mean concentration rather than the single sample criterion to compute the allowable loading reflects the fact that *E. coli* concentrations are typically lower than the criterion for water pumped from the Brazos River. The computed loading of 133 billion cfu per day was included in the Other category of the LA.

As in allocation reach 1, portions of the drainage area of allocation reach 2 are within the Urbanized Area of the 2000 Census, which is to be included within the Phase II MS4 general permits (Figures 5-8). The drainage area of allocation reach 2 includes 20,110 ha of which 5,168 ha are within the Urbanized Area. Two other complexities to the allocation exist in the watershed of allocation reach 2. First, Hines Nurseries has a stormwater permit in addition to its discharge permit, which is already included under the Continuous WLA component. Second, Bono Brothers and TDCJ Jester Unit CAFO each have permits that do not provide for discharge, but do allow use of agricultural lands for the beneficial land application of organic wastes. These three permitted facilities were included within the Non-continuous WLA category based on their combined operational areas of approximately 451 ha. A similar area ratio procedure as used for allocation reach 1 was used in this reach to separate the LA into the two components of Urbanized Area and "Other" and to determine the Non-continuous WLA. The loading to be allocated in this manner was the total allowable loading minus both the Continuous WLA and the GCWA pumping load, which is 1,455 billion cfu per day (1682 – 94 – 133). The additional loading from the GCWA pumping was added to the "Other" component of LA after completing the area ratio computations.

The following area ratios were used in the computation of the remaining TMDL loadings:

- WLA Non-continuous: 451 / 20,110 = 0.0224
- LA Urbanized Area: 5,168 / 20,110 = 0.2570
- LA Other (20,100 – 5,168 - 451) / 20,110 = 0.7206

Multiplying 1,455 billion cfu per day by the appropriate area ratio and adding the previously computed allowable GCWA load to the LA "Other" category provides a WLA Non-continuous load of 33 billion cfu per day, a LA Urbanized Area load of 374 billion cfu per day, and a LA "Other" load of 1,181 billion cfu per day.

The TMDL load allocation for allocation reach 2 without the Phase II MS4 general permit (i.e., with no sources in the WLA non-continuous category) is provided in Table 5-6. By simple addition, the combined or total WLA is 127 billion cfu per day and the total LA is 1,555 billion cfu per day.

Table 5-6 TMDL load allocation summary for allocation reaches 2 <u>without</u> Phase II MS4 general permit

Alloc. Reach	TMDL	WLA Continuous	WLA Non-continuous	LA Urbanized Area	LA Other	MOS
(all units in billion cfu per day)						
1	1,682	94	33	374	1,181	Implicit

For conditions with the Phase II MS4 general permit, the LA Urbanized Area load becomes part of the WLA Non-continuous load. The revised area ratios under conditions with the general permit are as follows:

- WLA Non-continuous: (451 + 5,168) / 20,110 = 0.2794
- LA Urbanized Area: Not Applicable
- LA Other (20,100 – 5,168 - 451) / 20,110 = 0.7206

Multiplying 1,455 billion cfu per day by the appropriate area ratio and adding the previously computed allowable GCWA load to the LA "Other" category provides a WLA Non-continuous load of 407 billion cfu per day and a LA "Other" load of 1,181 billion cfu per day.

The TMDL load allocation for allocation reach 2 with the Phase II MS4 general permit is provided in Table 5-7. By simple addition, the combined or total WLA is 501 billion cfu per day and the total LA is 1,181 billion cfu per day.

Table 5-7 TMDL load allocation summary for allocation reaches 2 with Phase II MS4 general permit

Alloc. Reach	TMDL	WLA Continuous	WLA Non-continuous	LA Urbanized Area	LA Other	MOS
(all units in billion cfu per day)						
1	1,682	94	407	N/A	1,181	Implicit

N/A – not applicable, no sources in LA Urbanized Area under this condition

5.9 Future Growth and Other Considerations

Because of the rapid urbanization of much of the Upper Oyster Creek watershed, additional increases in permitted discharges for treating municipal-type wastes are anticipated. Regarding this bacteria TMDL, any new permitted discharges and any additional increases in permitted daily flow for existing facilities will be held to the same *E. coli* limits as considered in this allocation process. The *E. coli* limits on these discharges also meet the ambient stream criteria for segment 1245. Hence, the effluent of any additional permitted discharges will not result in nonsupport of the contact recreation use. As a worst case, additional discharges result in a neutral impact on segment 1245 by increasing streamflow and adding *E. coli* at concentrations meeting protective criteria. However, it is anticipated that these discharges will generally be at concentrations less than the protective criteria.

The rapid urbanization in Upper Oyster Creek will change land uses in addition to increasing permitted discharges. Under future conditions, urban lands in the watershed will increase and agricultural and rural lands will decrease. Relative contributions to bacteria loadings by different sources would also be anticipated to change, though it is not possible to reasonably estimate whether loadings to Upper Oyster Creek will increase or decrease. Bacteria control practices will need to be adjusted in response to future increases in urban land use.

Further, it is recognized that the existing loading includes *E. coli* contributions from mammal and avian sources that are difficult or infeasible to control. These sources include mammalian wildlife, feral pigs, and most avian species, including water fowl.

5.10 TMDL Allocation Summary

The load duration curve method was used to develop the load allocation for Upper Oyster Creek (segment 1245). Because of distinct hydrologic differences, segment 1245 was separated into two allocation reaches:

- Allocation Reach 1: Segment 1245 from its downstream confluence with the Brazos River up to Dam #3.
- Allocation Reach 2: Segment 1245 from Dam #3 to the GCWA Shannon Pump Station.

An implicit margin of safety was used in calculating the TMDL based on the use of the exponential regression line through measured *E. coli* data exceeding the single sample criterion of 394 cfu/100 ml. The calculated percent reduction required to meet the allowable loading for the single sample criterion also met the geometric mean criterion in both allocation reaches.

The TMDL allocations for both reaches and with/without Phase II MS4 general permit conditions are summarized in Table 5-8. It should be noted that the two required percent load reductions provided in Table 5-8 are somewhat different from the values that would be calculated from computations based on the existing and allowable loadings in the table. The reason for the differences is twofold. First, the required percent reduction for each allocation reach was based on the average for two or more locations within each reach, thus giving an average percent reduction that will provide for support of the contract recreation use along the entire length of the reach rather than at just one location. Second, each required percent reduction reported in the table was computed as the average of the individual percent reductions calculated at 5 percent increments (see Table 5-1), which gives a different value from that calculated using average values of existing and allowable loading.

Table 5-8 TMDL allocation summary for allocation reaches 1 and 2 of Upper Oyster Creek

Single Sample Criterion	*E. coli* concentrations shall not exceed 394 cfu/100 ml in more than 25 percent of samples	
Condition	**Without Phase II MS4 General Permit**	**With Phase II MS4 General Permit**
Allocation Reach 1		
Existing Loading	4,571 billion cfu/day	4,571 billion cfu/day
Allowable Loading	1,453 billion cfu/day	1,453 billion cfu/day
Waste Load Allocation (Continuous)	367 billion cfu/day	367 billion cfu/day
Waste Load Allocation (Non-continuous)	N/A	699 billion cfu/day
Waste Load Allocation (Total)	367 billion cfu/day	1,066 billion cfu/day
Load Allocation (Urbanized Area)	699 billion cfu/day	N/A
Load Allocation (Other)	387 billion cfu/day	387 billion cfu/day
Load Allocation (Total)	1,086 billion cfu/day	387 billion cfu/day
Margin of Safety	Implicit	Implicit
Required Percent Reduction	73 %	73 %
Allocation Reach 2		
Existing Loading	7,492 billion cfu/day	7,492 billion cfu/day
Allowable Loading	1,682 billion cfu/day	1,682 billion cfu/day
Waste Load Allocation (Continuous)	94 billion cfu/day	94 billion cfu/day

Single Sample Criterion	*E. coli* concentrations shall not exceed 394 cfu/100 ml in more than 25 percent of samples	
Condition	**Without Phase II MS4 General Permit**	**With Phase II MS4 General Permit**
Waste Load Allocation (Non-continuous)	33 billion cfu/day	407 billion cfu/day
Waste Load Allocation (Total)	127 billion cfu/day	501 billion cfu/day
Load Allocation (Urbanized Area)	374 billion cfu/day	N/A
Load Allocation (Other)	1,181 billion cfu/day	1,181 billion cfu/day
Load Allocation (Total)	1,555 billion cfu/day	1,181 billion cfu/day
Margin of Safety	Implicit	Implicit
Required Percent Reduction	73 %	73 %

N/A – not applicable, no sources

SECTION 6

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