Final Draft

Technical Support Document

Segments 0806, 0841, 0822, and 0805 of the Trinity River

Bacteria TMDL

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Section 1

INTRODUCTION

1.1 Background and Water Quality Standards

Protection of our state's water resources is one of the most significant environmental challenges with which Texans currently contend. Texas' water resources are being depleted or impacted daily, through actions such as overuse, urban development, agricultural activities, and wetland degradation. Conservation and protection of our water resources will be one of the most important measures undertaken by local, state and federal agencies, as well as environmental groups, during the 21st century. As our states population increases, so does the need for dependable and employable water resources. Large cities such as Houston, San Antonio, and the Dallas/Fort Worth metroplex will require the largest percentages of clean, dependable water. In 2000 the estimated population of the Texas Water Development Board's Region C, which includes the Dallas /Fort Worth metroplex, was 5.3 million. This represents almost 25 percent of the states total population. Over 90 percent of that population is found within the Dallas/Fort Worth area, and 95 percent were estimated to live in the Trinity River basin. The region's population is expected to practically double by 2050, increasing the water supply requirements of the region, as well (TRA, 2003). This increasing need emphasizes that currently reliable water sources be protected and those that display negative impacts be restored and then maintained.

Water quality standards were developed in order to ensure that designated uses for water bodies are met (TNRCC, 2000). These standards include specific criteria set forth by the Texas Commission on Environmental Quality (TCEQ) in the Texas Surface Water Quality Standards (TSWQS) (Title 30 Texas Administrative Code (TAC) Chapter 307). Section 303(d) of the Clean Water Act (CWA) and the U.S. Environmental Protection Agency (USEPA) Water Quality Planning and Management Regulations (40 Code of Federal Regulations [CFR] Part 130) require that states perform total maximum daily loads (TMDLs) for water bodies not meeting water quality standards. TMDLs establish the allowable loadings of pollutants for a water body based on the relationship between pollution sources and in-stream water quality conditions. TMDLs allow each state to implement water-quality based controls to reduce pollution from both point and nonpoint sources and to restore and maintain the quality of its water resources (USEPA, 1991).

Designated uses for water bodies in Texas include: aquatic life use, public water supply use, fish consumption use, oyster waters use, non-contact recreation use, and contact recreation use (TCEQ, 2003). For the purposes of this report, *contact recreation use* is the only use that will be addressed. *Contact recreation use* is a use that is assigned to all water bodies in Texas, except in special situations (e.g., where ship or barge traffic make contact recreation use unsafe, thus requiring the designation of *non-contact recreation use)* (TCEQ, 2003).

Contact recreation use is based upon the concentration of fecal coliform bacteria identified in a particular body of water. Fecal coliforms are gram negative, facultative anaerobic,

lactose-fermenting bacteria that are commonly found in the intestines of homeotherms (Talaro and Talaro, 1999). *E. coli*, a species of coliform bacteria, is often used as an indicator of the possible presence of fecal pathogens in water, because its concentration in water is relatively easy to measure and it is often the most abundant species of the fecal coliform bacteria (Talaro and Talaro, 1999). Applicable State of Texas water quality criteria for contact recreation use in freshwater state that the geometric mean concentration for *E. coli* should not exceed 126 organisms (org) per 100 ml and the single sample concentration should not exceed 394 (org) per 100 ml in greater than 25% of the individual samples. Until recent years, TCEQ has considered that a water body is fully supporting if 25% or less of the sample sets are in exceedance and not supporting if greater than 25% of the sample sets are in exceedance. However, TCEQ recognizes that the chance of falsely classifying a station or assessment unit as impaired (Type I Error) is relatively high for the historically utilized method. Therefore, new exceedance criteria was developed by TCEQ, the binomial method, in order to maintain a Type I error probability below 20%. (TCEQ, 2003).

1.2 Report Purpose and Organization

TCEQ's assessment of ambient bacteria data and more recent data assessed for the present study led to the conclusion that portions of Segments 0806 (West Fork Trinity River below Lake Worth), 0841 (Lower West Fork Trinity River), 0822 (Elm Fork Trinity River below Lewisville Lake), and 0805 (Upper Trinity River) do not support the contact recreation use. Consequently, TCEQ is using the Texas Institute for Applied Environmental Research (TIAER) at Tarleton State University as the lead performing entity to: (1) acquire data and information necessary to support modeling and assessment activities, (2) perform bacteria source tracking to support implementation plan activities, and (3) assist the TCEQ in preparing a TMDL.

The purpose of this report is to provide technical documentation for the bacteria TMDL of Segments 0806, 0841, 0822, and 0805. 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*); bacterial source tracking findings; development of the load duration curve approach for the allocation process; and application of the load duration curve approach for the TMDL allocation process. As the lead performing entity, TIAER organized a Project Team to assist in the bacterial source tracking studies. The Project Team included Parsons Water & Infrastructure, Inc. and James Miertschin & Associates, Inc., who both assisted with field efforts and data collection, and the Institute for Environmental Health, Inc. (IEH), who performed laboratory ribotyping of both ambient water and known source, library *E. coli* samples. Some additional background information on the study area is provided in TIAER et al. (2006), though most of the information in that report is repeated herein.

Section 2

HISTORICAL DATA REVIEW AND WATERSHED PROPERTIES

2.1 Definition of Study Area

The fact that the study segments within the Trinity River Basin are positioned where each segment has upstream classified segments complicates the definition of the study area, because of the hydrologic connectivity of an upstream segment with a downstream segment. The Trinity River Basin in the Dallas/Fort Worth area also contains numerous large reservoirs that effectively alter the hydrology and remove a very significant amount of downstream loadings of bacteria. Because of the hydrologic and bacteria loading connectivity of upstream segments with downstream segments and the disruption of this connectivity by the presence of large reservoirs, the study area used within this report will be defined by the drainage areas of Segments 0806, 0841, 0822, and 0805, for which TMDL loading allocations are to be developed, and upstream connecting stream Segments 0829, 0825, and 0819 (Figure 2-1). Specifically these segments are defined as follows in a generally west to east direction:

- Segment 0829 (Clear Fork Trinity River below Benbrook Lake), which is a major tributary to Segment 0806
- Segment 0806 (West Fork Trinity River below Lake Worth)
- Segment 0841 (Lower West Fork Trinity River)
- Segment 0825 (Denton Creek), which is a major tributary to Segment 0822
- Segment 0822 (Elm Fork Trinity River below Lewisville Lake)
- Segment 0819 (East Fork Trinity River), which along with Segments 0822 and 0841 represent the three major tributaries to Segment 0805
- Segment 0805 (Upper Trinity River)

The upstream hydrologic terminuses of the study area occur at the major reservoirs, which are labeled on Figure 2-1. These major reservoirs, which were assumed to effectively remove the majority of downstream bacteria loading, include Lake Ray Hubbard on the East Fork, White Rock Lake on White Rock Creek, Grapevine Lake on Denton Creek, Lake Lewisville on the Elm Fork, Mountain Creek Lake on Mountain Creek, Lake Arlington on Village Creek, Lake Benbrook on the Clear Fork, Marine Creek Lake on Marine Creek, and Lake Worth on the West Fork.

2.2 Watershed Hydrology and Climate

"Generally, streamflow in the Trinity River Basin follows the rainfall pattern of the area" (TRA, 2003). Although the Trinity River Basin has moderate rainfall and runoff on average, its hydrology is notoriously erratic, ranging from floods to drought. During normal years much of the rain and streamflow occur in late spring, followed by very hot, dry weather from mid-June through August, into September (TRA, 2003). According to the Trinity River Authority (2003),

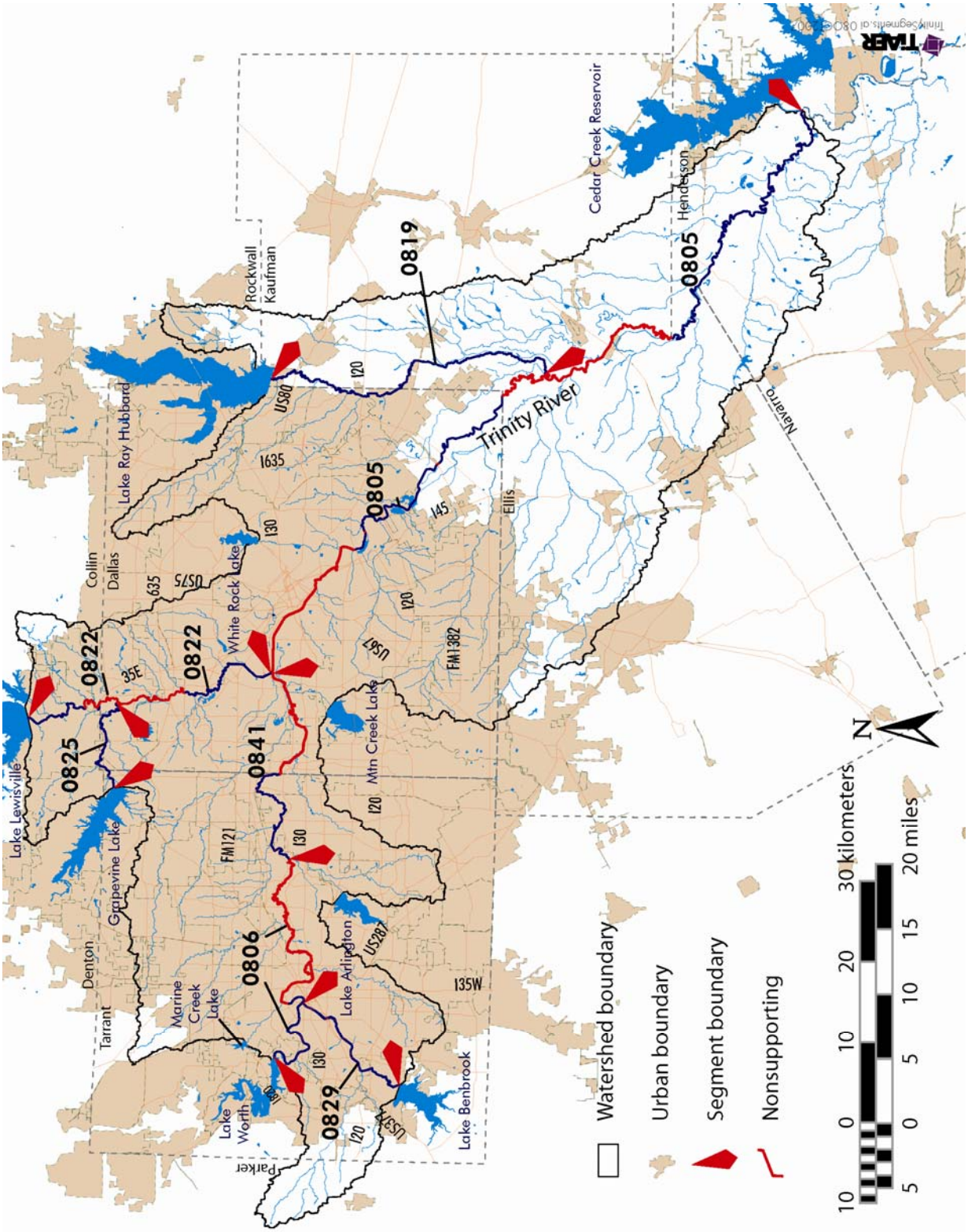

Figure 2-1. Trinity River Basin study area showing nonsupporting reaches

"the natural flow in the great majority of streams in the Trinity Basin is highly variable" and "most of the smaller streams in the basin cease to flow within a few days or weeks without rain, depending on the season and drainage area." Many of the Trinity River's tributaries, and the river itself below Dallas, have a base flow which consists mainly of effluent discharged from wastewater treatment facilities. "Extensive sampling and monitoring have proven that more than 90% of the river's flow, below Dallas, during periods of dry weather originates from the wastewater treatment plants of Fort Worth, Dallas, Garland, and the Trinity River Authority" (TRA 2003). These streams, or portions of streams, are often referred to as being "effluent dominated." With regard to the Trinity River, "the biggest effluent dominated reach is the main stem from Dallas and Fort Worth to Lake Livingston. In dry weather the flow in this reach is almost entirely made up of discharges from wastewater treatment plants (WWTPs)" (TRA, 2003). In addition, many of the smaller streams in the Dallas/Fort Worth area have a small base flow which consists of point and nonpoint discharge from various sources. The TRA (2003) states "these streams may have poor quality at base flow, as well as the leading edge of a rise. Dissolved oxygen is occasionally low and bacteria are often very high." Potential sources of nonpoint source pollution include "overflows from wastewater collection systems, septic system leakage, leachate from solid waste facilities, construction activities, and agricultural operations" (TRA, 2003).

North Central Texas has a subtropical climate characterized by hot summers and mild winters, resulting in a wide annual temperature range (National Weather Service (NWS), 2005). Average high temperatures generally reach their peak of 96°F between late July and mid August. Fair skies generally accompany the highest temperatures of summer, which are often above 100ºF; however, the low temperature rarely exceeds 80ºF at night (NWS, 2005). During winter, the average low temperature bottoms out at 33ºF in early to mid January and periods of extreme cold generally do not last long (NWS, 2005). The frost-free period generally lasts for about 248 days, with the last frost occurring in mid March and the first frost occurring in mid to late November (NWS, 2005).

Precipitation, like temperatures of the area, has a tendency to vary considerably. Yearly average precipitation ranges from 24 inches in the western areas of North Central Texas to 46 inches in the northeast areas. According to Bomar (1983), "In general, mean annual precipitation decreases about one inch for each 15 miles across Texas from east to west" (cited in Diggs et al. (1999). Diggs et al. (1999) states "severe storms and some of the largest rainfalls in the United States have occurred in this area." "All the point rainfall records for North America are held within a belt 50 miles east and west of a line from Dallas through Waco, Austin, and San Antonio"(Hayward et al., 1992, cited in Diggs et al., 1999). Rainfall in the area generally occurs at night, with most of the thunderstorms occurring during the spring. Snowfall in this area is a rare occurrence (NWS, 2005).

2.3 Review of Trinity River Routine Monitoring Data

2.3.1 Data Acquisition

Two major sources of ambient *E. coli* data existed for developing the TMDL load allocation. One source was data obtained from the routine collection of *E. coli* and other water

quality data in the project area under the TCEQ Surface Water Quality Monitoring Program by the TCEQ Field Operations Division, and under the Clean Rivers Program by the Trinity River Authority, Tarrant Regional Water District, City of Fort Worth, City of Grand Prairie, and City of Irving. These data are periodically sent to the TCEQ Regulatory Activities and Compliance System (TRACS) database (recently updated into SWQMIS or Surface Water Quality Monitoring Information System) and were provided to TIAER for the specific purposes of this project. The other major source of ambient *E. coli* data was collected by the TIAER Project Team at selected stream stations for the bacterial source tracking (BST) study and also to provide information to assist in the TMDL allocation process.

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.

2.3.2 Analysis of Bacteria Data

Recent environmental monitoring along the West Fork Trinity River (Segments 0806 and 0841), the Elm Fork Trinity River (Segment 0822), and the Upper Trinity River (Segment 0805) has shown that *E. coli* bacteria have reached unacceptably high concentrations, exceeding the specified criteria for contact recreation use in portions of those segments (Figure 2-1). Descriptions of those segments, beginning at the uppermost portion of the watershed, and their impaired reaches are listed as follows:

Segment 0806 (West Fork Trinity River below Lake Worth), a 33 mile freshwater stream, runs from Lake Worth in Tarrant County to a point immediately upstream of the confluence with Village Creek, also in Tarrant County. *E. coli* impairments have been reported for the lower 22 miles (assessment unit # 1) of the segment (Texas 303(d) lists: 2002, 2004, 2006 draft).

Segment 0841 (Lower West Fork Trinity River), a 27 mile freshwater stream, begins immediately upstream of the confluence of Village Creek (where Segment 0806 ends) in Tarrant County and runs to a point immediately upstream of the confluence with the Elm Fork of the Trinity in Dallas County. *E. coli* impairments have been reported for the lower 14 miles (assessment unit # 1) of the segment (Texas 303(d) lists: 2002, 2004, 2006 draft).

Segment 0822 (Elm Fork Trinity River Below Lewisville Lake), a 30 mile freshwater stream, begins immediately below the Lake Lewisville Dam in Denton County and runs to a point immediately upstream of the confluence with the West Fork Trinity River in Dallas County. *E. coli* impairments have been reported for assessment unit # 2, which is a reach located 4.5 miles upstream to 7.5 miles downstream of the Dallas Water Utilities intake (Texas 303(d) list: 2006 draft).

Segment 0805 (Upper Trinity River), a 100 mile freshwater stream, begins immediately upstream of the confluence with the Elm Fork (where Segments 0841 and 0822 end) in Dallas County and runs to a point immediately upstream of the confluence with Cedar Creek

Reservoir's discharge canal, along the Henderson/ Navarro County line. *E. coli* impairments have been reported for:

- the upper 8 miles of the segment (assessment unit # 4),
- the 11-mile reach near South Loop 12 (assessment unit # 3), and
- the 25-mile reach near SH 34 (assessment unit # 2; Texas 303(d) list: 2002, 2004, 2006 draft).

Available *E. coli* data from September 2000 to September 2005 were reviewed for Segments 0806, 0841, and 0805. Available *E. coli* data from December 2001 to February 2006 were reviewed for Segment 0822. These routine monitoring data were used to assess the water quality according to TCEQ (2003) procedures. TCEQ (2003) states that the most recent five years of data should be used in order to properly assess the status of the stream. The data indicated that 17 monitoring stations had routine monitoring *E. coli* data during these five-year time periods. According to the assessment of the data, nine of the stations failed to meet the contact recreation use (Figure 2-2; Table 2-1)—stations 17863, 11080, 16120, 17669, 11081, 17162, 10937, 10934, and 10925. Stations 17863 and 16120 are located in Segment 0806; stations 11080, 17669, and 11081 are located in Segment 0841; station 17162 is located in Segment 0822, and stations 10937, 10934, and 10925 are located in Segment 0805. The geometric mean prevented all of these stations from meeting their contact recreation use. In addition, stations 16120, 11081, 10937, 10934, and 10925 also failed to meet the percent single sample exceedance criteria based on the binomial method.

2.4 Potential Sources of Fecal Indicator Bacteria

2.4.1 Land Use

The land use/land cover data were obtained from the 1992 Multi-Resolution Land Characteristic land use data by the U.S. Geological Survey (USGS, 1992) and are provided for Segments 0806, 0841, 0822, and 0805 for which the TMDL load allocations were developed. The watershed area encompassing Segments 0806, 0841, 0822, and 0805 of the Trinity River Basin covers slightly less than 1,082,000 acres.

The land use/ land cover is represented by the following categories:

- **Improved Pasture**- Improved pasture is represented by land that has been converted into livestock grazing or hay production by replacing native forage with improved varieties or non-native species of grasses and/or forbs in order to increase forage production for livestock.

- **Residential**- Residential is property that has homes and/or some other housing development present on it.

- **Forest**- Forest is land that contains a relatively high density of trees.

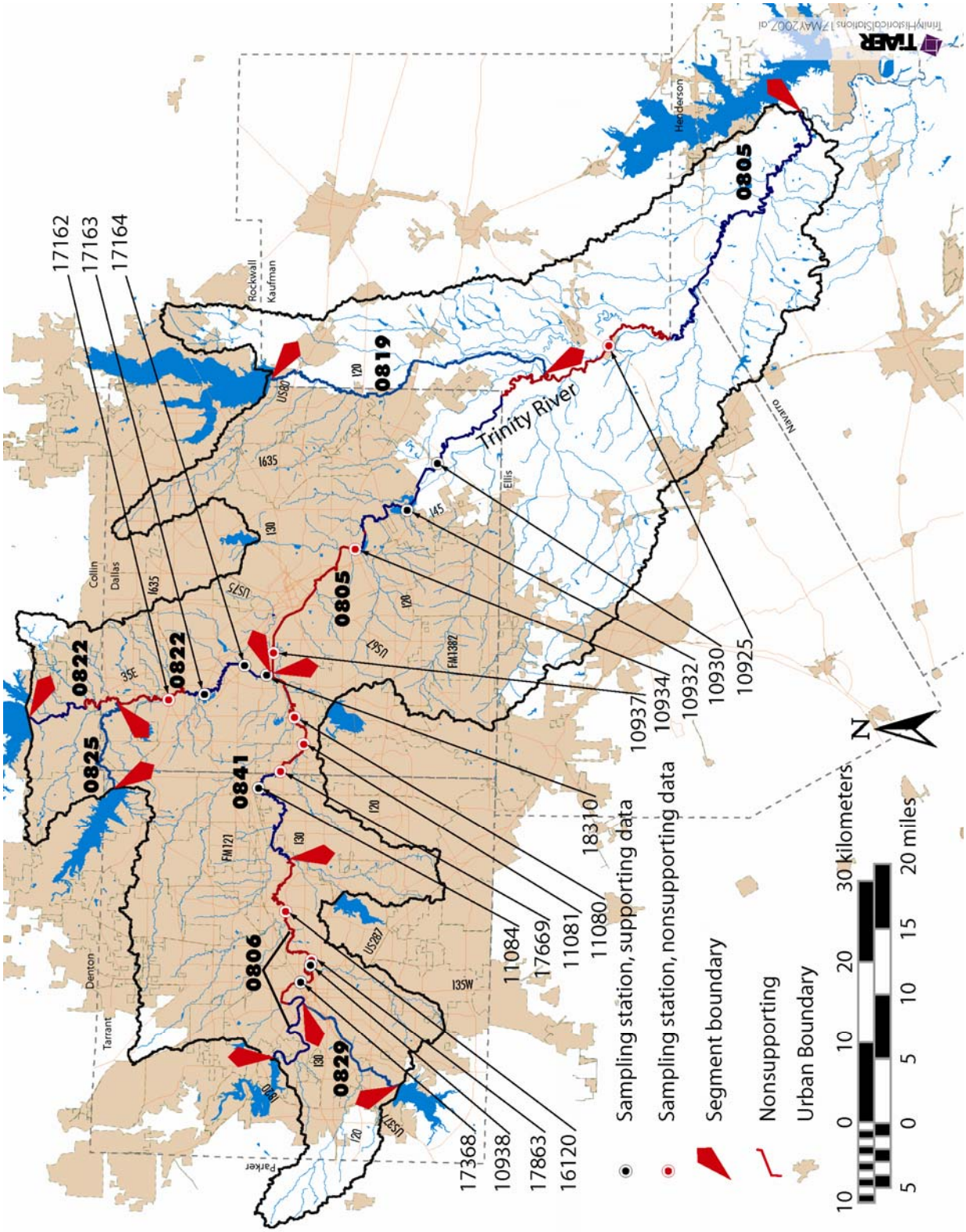

Figure 2-2. Trinity River Basin study area showing stations with *E. coli* data used to assess contact recreation use.

Table 2-1. Summary of routine monitoring *E. coli* data for August 2000 through September 2005, including support and nonsupport designations. Shaded stations indicate nonsupport of contact recreation use due to single sample exceedances and/or geometric mean exceedance.

Segment	Station ID	No. of Samples Aug. 2000-Sept. 2005	Min. Measured *E. coli* Conc.	Max. Measured *E. coli* Conc.	Single Sample Exceedences	Single Sample Percent Exceedances	Geometric Mean	Location
0806								
	17368	70	1	3640	12	17%	47	4th St./ Tarrant Co.
	10938	78	1	4840	17	22%	59	Beach St./ Tarrant Co.
	17863	31	2	24200	8	26%	131	Gateway Park/ Tarrant Co.
	16120	62	1	98040	23	37%	169	Handley-Ederville/ Tarrant Co.
0841								
	11084	16	18	452	1	6%	55	SH 360/ Tarrant Co.
	17669	38	17	4838	9	24%	159	Roy Orr/ Dallas Co.
	11081	38	2	19900	16	42%	278	Belt Line Rd./ Dallas Co.
	11080	33	13	3470	8	24%	170	South MacArthur Blvd./ Dallas Co.
0822*								
	17162	34	10	3460	10	29%	141	Valley View Lane/ Dallas Co.
	17163	33	15	1630	7	21%	97	State Spur 348/ Dallas Co.
	17164	17	1	3970	4	24%	77	Proctor St./ Dallas Co.
	18310	39	2	11900	8	22%	102	E. Irving Blvd./ Dallas Co.
0805								
	10937	46	12	24200	18	39%	238	Mockingbird Ln./ Dallas Co.
	10934	45	21	39700	19	42%	383	South Loop 12/ Dallas Co.
	10932	13	11	980	2	15%	85	Dowdy Ferry Rd./ Dallas Co.
	10930	35	3	1540	6	17%	64	Belt Line Rd. near Wilmer/ Dallas
	10925	54	2	4840	17	31%	139	SH 34/ Ellis-Kaufman Co. Line
Fully Supporting Contact Recreation								
Not Supporting Contact Recreation								

*Routine monitoring *E. coli* data date range for Segment 0822 were for the five year period of December 2001 to February 2006

- **Cropland**- Cropland is land which has been cultivated and put into some sort of crop production. Crops may include small grains, row crops, orchards, vineyards, etc.

- **Commercial/ Industrial**- Commercial/ Industrial land is property that is occupied by commercial businesses, industrial complexes, and/ or transportational areas, such as highways, parking lots, or rail systems.

- **Open Water/Wetlands**- Open Water/ Wetlands are areas that are occupied by rivers, streams, ponds, lakes, or reservoirs. These areas also include land that is inundated for periods long enough to develop wetland characteristics.

- **Native Pasture**- Native Pasture is land that is occupied by native grasses and/or forbs.

- **Turf**- Turf is land that is occupied by grasses suitable for parks, soccer fields, football fields, or other recreational complexes.

- **Shrubland**- Shrubland is land occupied by a high density of shrubbery.

- **Other**- Land categorized as "Other" includes bare rock, sand, or clay areas; quarries, stripmines, gravel pits, or other "transitional" areas.

Segment 0806

The Upper West Fork Trinity River (Segment 0806) has a total drainage area of 121,628 acres. Overall, Segment 0806 has dominant land uses consisting of 39% residential, 28% improved pasture, 13% commercial/ industrial property, and 5% native pasture (Figure 2-3; Table 2-2).

Segment 0841

The Lower West Fork Trinity River (Segment 0841) has a total drainage area of 164,740 acres. Its dominant land use categories consist of residential areas (38%), improved pasture (23%), forest (12%), and commercial/ industrial (11%) (Figure 2-3; Table 2-2).

Segment 0822

Elm Fork Trinity River (Segment 0822) has a total drainage area of 126,664 acres. Its dominant land use categories consist of residential (30%), improved pasture (25%), commercial/ industrial (15%), and forest (9%) (Figure 2-3, Table 2-2).

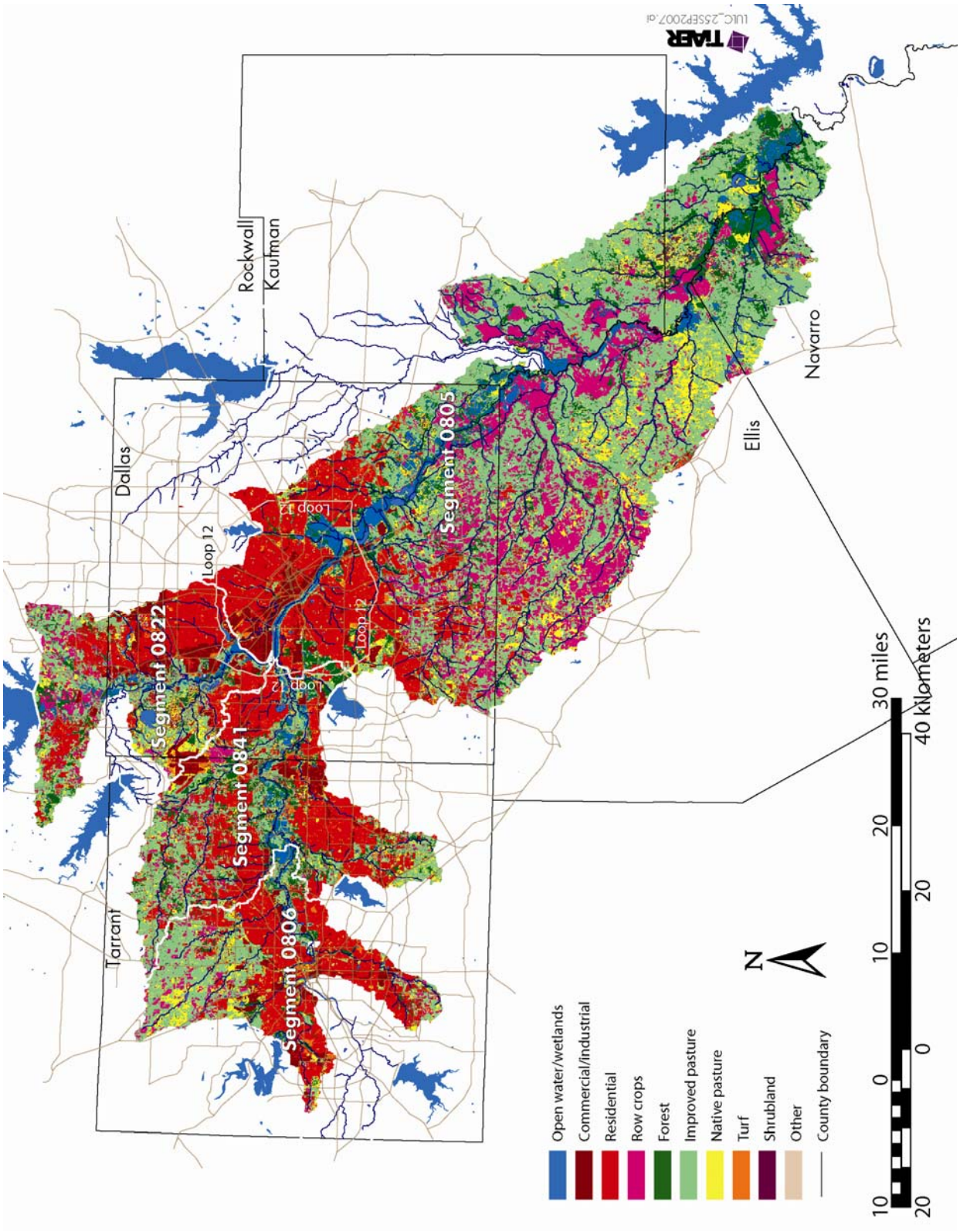

Figure 2-3 Land use/land cover data for the Trinity River Basin study area
Source: USGS (1992)

Table 2-2. Land use/land cover summary and drainage areas for Segments 0806, 0841, 0822, and 0805 of the Trinity River Basin study area.

Description	0806 Total	0841 Total	0822 Total	0805 Total
Residential (acres)	47,941	62,965	38,216	93,104
Residential (%)	39	38	30	14
Improved Pasture (acres)	34,115	38,605	31,928	281,753
Improved Pasture (%)	28	23	25	42
Native Pasture (acres)	6018	4968	5775	32,740
Native pasture (%)	5	3	5	5
Commercial/ Industrial (acres)	15,587	18,599	19,523	26,212
Commercial/ Industrial (%)	13	11	15	4
Forest (acres)	5458	20,431	11,438	97,703
Forest (%)	4	12	9	15
Cropland (acres)	4678	4442	7193	77,407
Cropland (%)	4	3	6	12
Turf (acres)	2989	4555	2903	6733
Turf (%)	2	3	2	1
Open Water/ Wetlands (acres)	4545	9524	8852	48,630
Open Water/ Wetlands (%)	4	6	7	7
Shrubland (acres)	220	537	763	4140
Shrubland (%)	0	0	1	1
Other (acres)	78	115	74	441
Other (%)	0	0	0	0
Total Acres	121,628	164,740	126,664	668,863
Total Percent (%)	100	100	100	100

Segment 0805

Upper Trinity River (Segment 0805) has a total drainage area of 668,863 acres, substantially larger than the previous three segments. It too has a diverse land use distribution, led by improved pasture land at 42%, forest at 15%, residential property 14% and cropland with 12% (Figure 2-3; Table 2-2). This diversity of land use/land cover can be attributed to the upstream to downstream transition from dominance of urban land uses to rural uses (Figure 2-3; Table 2-3).

2.4.2 Permitted Discharges

Under the Texas Pollution Discharge Elimination System (TPDES), 15 facilities within the study area hold permits to discharge treated domestic wastewater (Table 2-4, Figure 2-4). Seven wastewater treatment facilities (WWTFs) are located within Segment 0841, one facility is located within Segment 0822, and seven facilities are located within Segment 0805. Currently there is no authorized domestic wastewater discharger located within Segment 0806.

Table 2-3. Land use/land cover differences within the Upper Trinity River (Segment 0805) above (Upper) and below (Lower) South Loop 12 in Dallas.

Description	Upper	Lower
Improved Pasture (acres)	3061	278,692
Improved Pasture (%)	4	47
Residential (acres)	42,247	50,857
Residential (%)	57	9
Forest (acres)	3288	94,415
Forest (%)	4	16
Cropland (acres)	104	77,303
Cropland (%)	0	13
Commercial/ Industrial (acres)	15,048	11,164
Commercial/ Industrial (%)	20	2
Open Water/ Wetlands (acres)	6792	41,838
Open Water/ Wetlands (%)	9	7
Native Pasture (acres)	599	32,141
Native pasture (%)	1	5
Turf (acres)	3148	3585
Turf (%)	4	1
Shrubland (acres)	65	4075
Shrubland (%)	0	1
Other (acres)	5	436
Other (%)	0	0
Total Acres	74,357	594,506
Total Percent (%)	100	100

Table 2-4. Permitted domestic wastewater operations in Lower West Fork, Elm Fork and Upper Trinity River watersheds.

TPDES Permit No.	Facility	Segment	Final Permitted Discharge (MGD)	Actual (MGD)[a]
WQ0010303-001	TRA Central Regional	0841	162	106.9
WQ0010494-013	City of Fort Worth Village Creek	0841	166	110.8
WQ0011032-001	Alta Vista Mobile Home Park	0841	0.008	0.0042
WQ0012807-001	Golden Triangle Estates	0841	0.09	0.0290
WQ0012982-001	Regency Conversions	0841	0.005	0.0027
WQ0013036-001	Pine Tree MHP Landowners Association	0841	0.042	0.0300
WQ0013831-001	Pine Tree Estates No. 2 Landowners Association	0841	0.042	0.0251
WQ0010662-001	City of Lewisville WWTF	0822	18	8.186
WQ0010060-001	City of Dallas Central	0805	150	141.8
WQ0010060-006	City of Dallas Southside	0805	110	66.63
WQ0010984-001	TRA Ten Mile Creek	0805	24	15.17
WQ0014628-001[b]	D Bar B MHP	0805	0.024	0.0043[c]
WQ0013415-001	TRA Red Oak Creek	0805	6	2.368
WQ0013620-001	City of Palmer	0805	0.226	0.2372[d]
WQ0014471-001	Scurry-Rosser	0805	0.04	0.0009[e]

[a] Average measured discharge from Jan. 2001 through Jan. 2006
[b] Formerly operating under Permit 11166-001 and operating under Permit 14628-001 since Jan. 26, 2007
[c] Due to incomplete dataset average measured discharge from Jan. 2001 to Dec 2002
[d] Self-reported actual average discharge is greater than final permitted discharge
[e] Facility not online prior to Jan. 2005 so actual average discharge is average measured discharge from Jan. 2005 to Jan. 2006

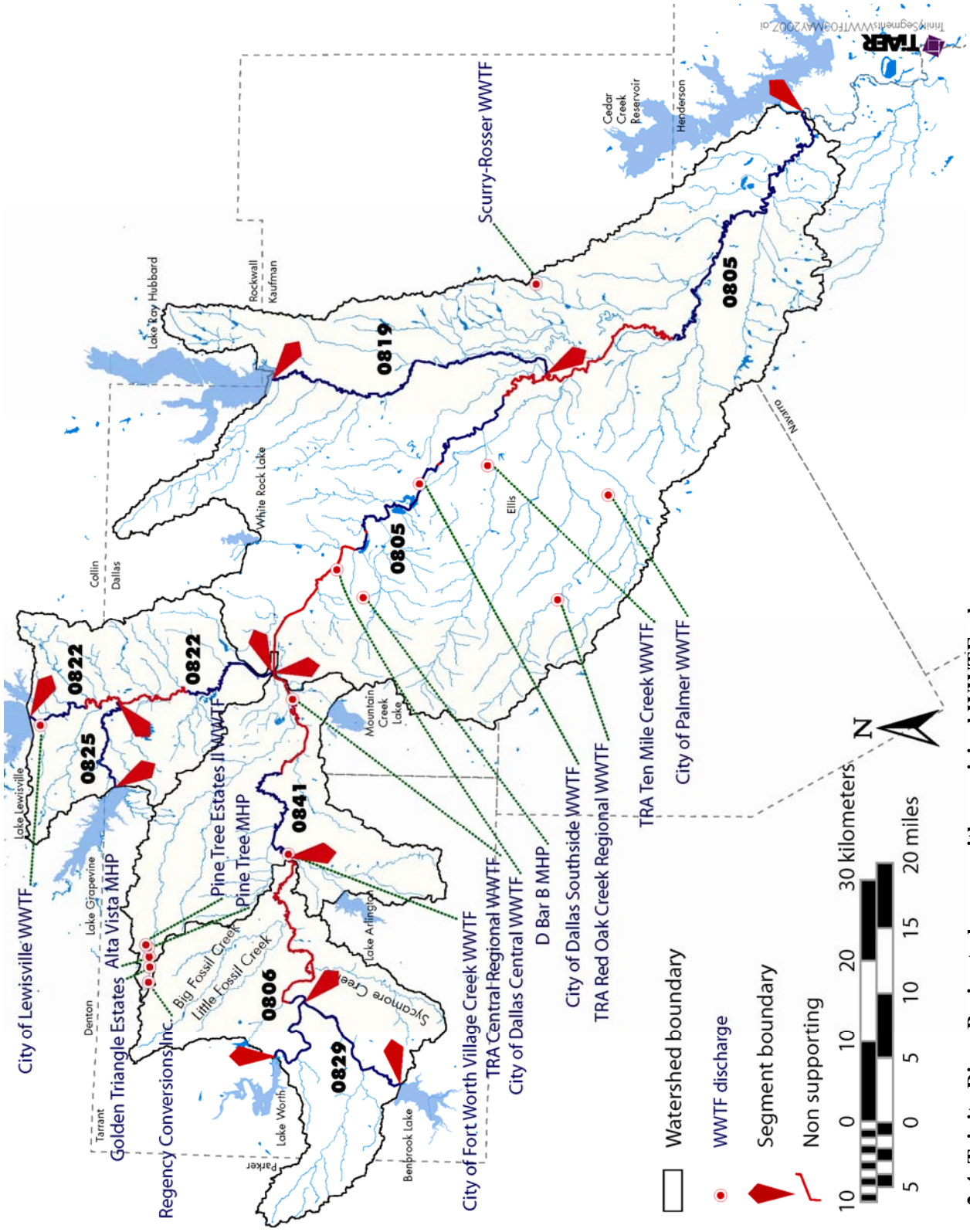

Figure 2-4 Trinity River Basin study area with municipal WWTFs shown

The National Pollutant Discharge Elimination System Municipal Separate Storm Sewer System (MS4) Phase I and II rules require municipalities and certain other entities in urban areas to obtain permits for their stormwater systems. Both the Phase I and II permits include any conveyance such as ditches, curbs, gutters, and storm sewers that do not connect to a wastewater collection system or treatment facility. Phase I permits are individual permits for large and medium sized communities, whereas Phase II permits are for small communities and are regulated by a general permit. The purpose of a MS4 permit is 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 best management practices (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

The geographic region covered by Phase I and II MS4 permits is that portion of the study area included in the Urbanized Area defined in the 2000 Census for the greater Dallas/Ft. Worth area (US Census Bureau, 2007). The Urbanized Area for Segments 0806, 0841, 0822, and 0805 comprises 47 % of the total drainage area, 83 % of Segment 0806, 95% of Segment 0841, 73% of Segment 0822, and 27% of Segment 0805 (Figure 2-5).

Permitted industrial wastewater dischargers are also located within the Trinity River study area; however, these industrial dischargers were not considered as potential contributors to bacterial impairment since wastewater generated from these facilities were typically either non-contact cooling water from electric generation plants or wastewater generated from other industrial processes that should not have been in contact with either human or animal fecal matter.

2.4.3 Estimated Human, Pet and Livestock Populations in Watershed Counties.

The estimated population data for humans, pets and various livestock species present in counties that are drained by the West Fork and Upper Trinity River watersheds were obtained from the U.S. Census Bureau, the American Veterinary Medical Association, the USDA National Agricultural Statistics Service, and the Texas Agriculture Statistics Service (Table 2-5).

2.4.4 Sewered and Non-Sewered Areas

The method of sewage disposal for housing units in the Trinity River Basin study area 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). An estimate of the total number of on-site sewage facilities that were located within the study area for each county was performed by taking a simple area ratio of the area covered by the study area for each county to the total county area multiplied by the total number of on-site sewage facilities located within each county

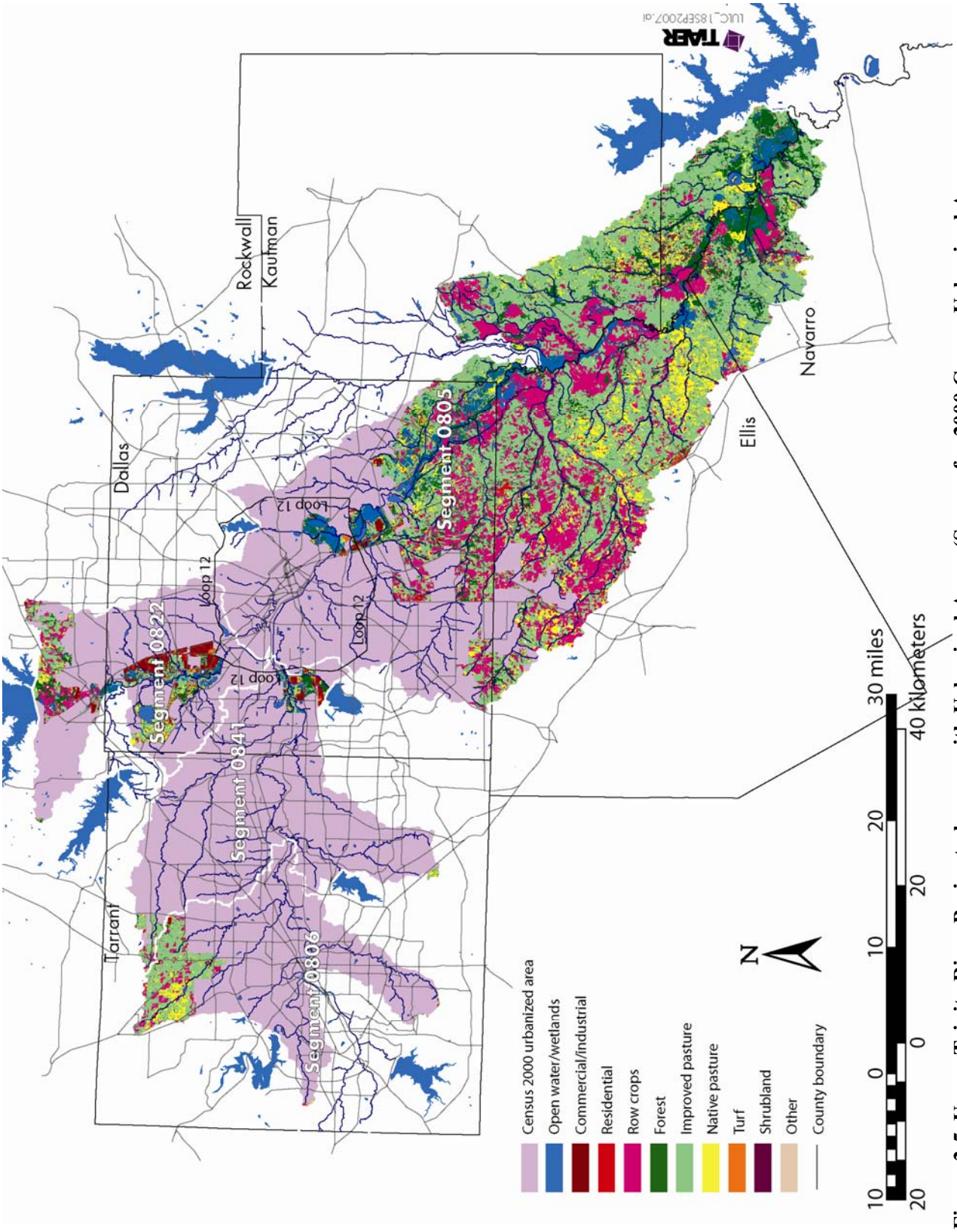

Figure 2-5 Upper Trinity River Basin study area with Urbanized Areas (Source for 2000 Census Urbanized Area: http://www.census.gov/geo/www/cob/metadata.html)

Table 2-5. Estimated population data for humans, pets and various livestock and wildlife species present in counties that are drained by the West Fork and Upper Trinity River watersheds.

Category	Source	County									
		Collin	Dallas	Denton	Ellis	Henderson	Kaufman	Navarro	Parker	Rockwall	Tarrant
Avian	Pigeons °	199	N/A	74	280	25	97	178	348	60	N/A
Avian	Poultry (Ducks, Geese, Other) °	2001	1658	4361	5068	1581	2780	1513	2597	487	2444
Human	(Households)*	181,970	807,621	158,903	37,020	28,804	24,367	16,491	31,131	14,530	533,864
Human	Humans*	627,938	2,218,899	530,597	128,710	79,184	85,377	48,243	100,336	58,260	1,588,088
Humans	On-site sewage facilities⌂	59	8,586	1,187	4,753	1,363	2,852	508	508	428	11,538
Livestock	Bison °	N/A	N/A	73	408	57	N/A	6	35	N/A	73
Livestock	Cattle (All) ‡	42,000	9,000	51,000	53,000	76,000	87,000	82,000	69,000	7,000	19,000
Livestock	Goats ‡	6,000	1,100	3,000	3,200	1,300	2,100	2,700	6,900	N/A	1,000
Livestock	Hogs/ Pigs °	374	728	165	333	501	613	750	781	57	944
Livestock	Horses/ Ponies°	4,779	2,032	9,517	3,443	3,476	5,155	2,419	9,379	1,068	3,676
Livestock	Mules/ Burros/ Donkeys °	274	70	333	359	268	447	253	635	31	110
Livestock	Poultry (Chickens &Turkeys) °	2393	970	347	6522	1324	6801	3442	6451	978	2932
Livestock	Sheep ‡	N/A	N/A	1,000	1,000	N/A	N/A	N/A	N/A	N/A	N/A
Mammalian Wildlife	Deer (Domestic) °	29	12	N/A	160	303	N/A	210	114	N/A	435
Mammalian Wildlife	Rabbits °	220	1,895	64	145	85	677	735	372	7	200
Pet	Cats †*	120,100	533,030	104,876	24,433	19,011	16,082	10,884	20,546	9,590	352,350
Pet	Dogs †*	105,543	468,420	92,164	21,472	16,706	14,133	9,565	18,056	8,427	309,641

° = based on 2002 USDA Census of Agriculture-County Data; National Agriculture Statistics Service

‡ = based on 2005 Texas Agricultural Statistics Service

† = based on 2001 statistics from *2002 U.S. Pet Ownership and Demographic Sourcebook*, American Veterinary Medical Association

*** = based on U.S. Census Bureau's Online State and County Quickfacts; accessed 5/11/2006.**

⌂ = based on 1990 U.S. Census Bureau's Online American Fact Finder; accessed 6/13/2007; county statistics prorated by area to the Upper Trinity River basin study area.

(Table 2-5). It should be noted that the resulting estimate of the total number of on-site sewage facilities may be inaccurate due to both increased urbanization in the study area since 1990 and the assumption that on-site sewage facilities are distributed uniformly throughout each county. The areas included in centralized wastewater collection and treatment systems are shown in Figure 2-6. According to the North Central Council of Governments, who supplied this information, small portions of the areas included in the centralized collection and treatment areas are still likely serviced by on-site sewage facilities.

TIAER performed an informal inquiry into the general conditions of on-site sewage facilities within five of the counties whose boundaries are within the study area, which were the counties of Dallas, Tarrant, Ellis, Kaufman, and Navarro. The purpose of this inquiry was to obtain only general information regarding on-site sewage facilities within each county and possibly determine if any areas of concern exist.

Dallas County indicated that there were no major issues within the county with failing on-sites sewage facilities and that when complaints were filed on a system, the system was generally brought quickly back into compliance. Tarrant County indicated that complaints regarding on-site sewage facilities occur throughout the county and mostly occur during periods of prolonged or heavy rainfall. While specific numbers of complaints were not available at the time of the inquiry, Tarrant County did indicate that often times the complaints are in regard to aerobic on-site sewage facilities. Ellis County indicated that a large amount of on-site sewage facilities do occur within the county; however, the area of Ellis County that is within the study area is sparsely populated. At the time of the inquiry no major problems were indicated regarding the operation of on-site sewage facilities within the portion of the study area located in Ellis County. Similar to Tarrant County, Kaufman County also indicated that aerobic systems tended to receive the most complaints. Within Kaufman County the city of Forney was indicated as an area of concern due to the relatively high number of complaints received regarding on-site sewage facilities within and around the city limits. Navarro County indicated that there were some problems with inadequate on-site sewage facility plans being developed for new housing units. In addition to the new housing units, Navarro County indicated that there have been a number of complaints regarding housing units that lack any form of sewage treatment. Similar to Ellis County the portion of Navarro County within the study area was characterized as being sparsely populated. It is anticipated that a more formal inquiry will be performed under implementation plan activities.

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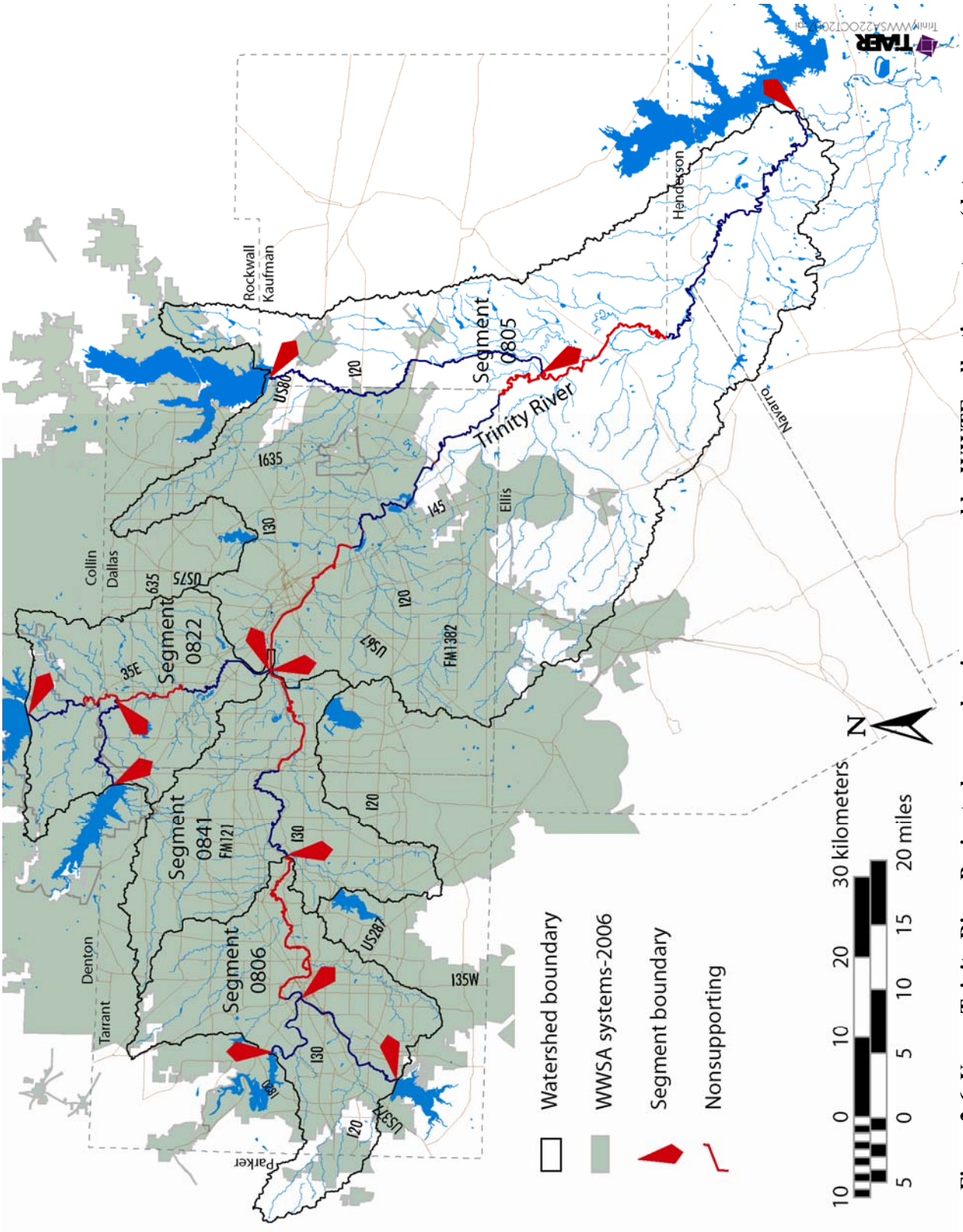

Figure 2-6 Upper Trinity River Basin study area showing area covered by WWTF collection systems (data source: North Central Council of Governments; WWSA = centralized wastewater treatment and sewered collection areas).

Section 3

BACTERIAL SOURCE TRACKING

3.1 Objectives and Methods

3.1.1 Fundamentals of Bacterial Source Tracking and Ribotyping[1]

E. coli is a common inhabitant of animal and human intestines, and a few strains, notably strain O157:H7, are pathogenic (Talaro and Talaro, 1999). Recent studies have shown that *E. coli* isolates from humans and various other host animals (e.g., cattle, chickens, and pigs) may differ both genetically and phenotypically. These differences allow the use of genetic and biochemical tests in order to identify the original host animal, a process often referred to as bacterial source tracking (BST).

BST is based upon two principles. The first principle is that the bacterial population genetic structure is clonal. This principle is a well-established element of microbial genetics. Bacteria reproduce by binary fission or dividing in half. The two daughter cells that are 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 to form one or several new clonal groups. BST makes use of the clonal population structure of bacteria to classify organisms based on their genetic fingerprints into groups of clonal descent.

The second principle behind the 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 host's 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. Many transient strains have also been found to be non-specific with regard to the host species. Hartl and Dykhuizen (1984) illustrate 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 by using this subtyping method (ribosomal RNA typing using two restriction enzyme reactions) more than 96% 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% of the *E. coli* strains are transient and not attributable to one specific source.

[1] This report subsection was provided by Parson Water & Infrastructure, Inc.

Historically, the key methodological problem in tracing sources of microbial contamination in the environment was the lack of a universal single-reagent typing scheme for bacteria. This problem has been overcome by the work of several investigators in the fields of population genetics, molecular systematics, and molecular epidemiology. In 1986 Grimont and Grimont showed that DNA probes corresponding to specific regions of the ribosomal ribonucleic acid (rRNA) operon could be used to differentiate bacteria. Stull et al. (1988) and LiPuma et al. (1988) used the rRNA operon to study the molecular epidemiology of several species of bacteria. In order to trace the indicator bacterium, *E. coli*, from the 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 for interstrain differentiation. Since the *E. coli* chromosome contains seven copies of the rRNA operon, an rDNA probe can be used as a definitive taxonomic tool (Grimont and Grimont, 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.

Molecular tools appear to hold the greatest promise for BST, providing the most conclusive characterization and the highest level of discrimination for isolates. Of the molecular tools available, ribosomal ribonucleic acid genetic fingerprinting (Ribotyping) and pulsed-field gel electrophoresis (PFGE) are emerging as versatile and feasible BST techniques. However, reference "libraries" of bacterial genetic fingerprints and antibiotic resistance profiles are needed to correctly identify the source of bacteria isolated from environmental water samples. PFGE, while excellent at resolving different source species, requires a very large and expensive library due to the high variation in PFGE profiles. A phenotypic characterization method, antibiotic resistance analysis, also has the potential to identify the human or animal origin of isolates. However, there is substantial uncertainty over the efficacy of antibiotic resistance analysis at distinguishing bacterial sources. Ribotyping is a common bacterial source tracking method because it balances high source specificity with moderate requirements for library size.

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 cepia* 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 ribosomal RNA typing to identify the *Aeromonas spp.* 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 moncytogenes* 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 (GEMs) in the environment.

3.1.2 Station Selection

At the time of the BST study, portions of Segments 0806, 0841, and 0805 were identified as being in nonsupport of the contact recreation use due to bacteria, and, therefore, these segments were the focus of the study. The nonsupport status of a portion of Segment 0822 was not identified until development of the draft 2006 Texas 303(d) list, which occurred after completion of the BST study. Therefore, no stations for BST water sampling stations were identified for this Segment 0822. Station selection for BST water sampling started with the objective to identify the sources contributing to violations in water quality criteria for bacteria in the Segments 0806, 0841, and 0805 of the Upper Trinity River basin study area. A number of factors were taken into consideration prior to selecting monitoring stations. A particularly important factor was that the confidence in source estimates depended on the number of isolates matched from ambient samples to known fecal samples. To get reasonably accurate estimates, past project experience indicated a need for a minimum of 70 – 120 isolates per station, with more being better. This study was designed for sampling at 10 main-stem stations with collection of 110 isolates per station in order to provide a reasonable database of isolates.

Another important factor was that the stations needed to be properly assigned to their corresponding segments in order to adequately characterize various reaches and to isolate, whenever possible, major contributing areas. Routine monitoring data from most of the main-stem stations indicated high bacteria concentrations that exceeded criteria. For some stations, however, the selection was based on location within an impaired reach, allowing better characterization of the upstream and downstream portions of the reach regardless of the presence of routine monitoring data or a history of bacteria impairment.

After consideration of the various factors involved, the 10 stations were chosen for monitoring. Segment 0806 had three main-stem stations (18459, 10938, and 16120), Segment 0841 also had three main-stem stations (17669, 11081, and 11089), and Segment 0805 had four main stem stations (10937, 10934, 10925, and 10924) **(**Figure 3-1**)**.

3.1.2.1 Monitoring Station Descriptions

A brief description of each station, monitoring activities, and the purpose for station selection are provided below:

Segment 0806 – West Fork Trinity River below Lake Worth

Station 18459 was located on the West Fork Trinity at W. Northside Dr. in north Fort Worth near the Stockyards. This station was selected because it was the upper most accessible site on the impaired portion of Segment 0806 that was a sufficient distance below the confluence of the Clear Fork and West Fork for mixing of these two streams to occur.

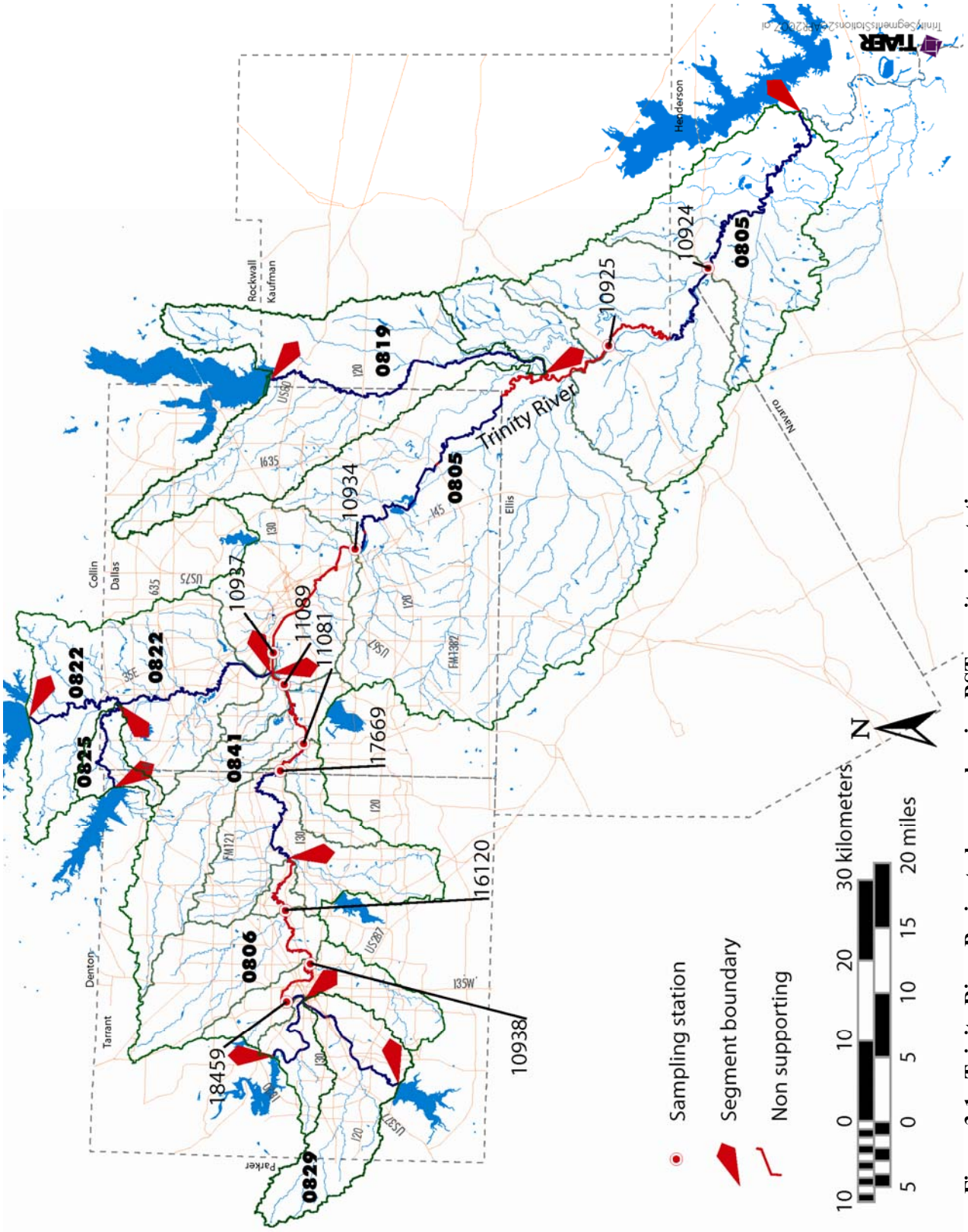

Figure 3-1. Trinity River Basin study area showing BST monitoring stations.

Station 10938 was located on the West Fork Trinity River at Beach Street in Fort Worth. USGS stream gauge 08048543 is located at this site. This station was located near the upstream end of the impaired assessment unit in Segment 0806.

Station 16120 was located on the West Fork Trinity River at Handley-Ederville Road approximately 0.55 km upstream of IH 820 in Fort Worth. This station was located near the middle of the impaired assessment unit in Segment 0806.

Segment 0841 - Lower West Fork Trinity River

Station 17669 was located on the Lower West Fork Trinity River at Roy Orr Blvd. in Grand Prairie. USGS stream gauge 08049500 is located at this site. This station was located immediately upstream of an assessment unit that showed nonsupport of contact recreation, and recent bacteria samples from 2000-2004 showed concentrations exceeding pertinent criteria.

Station 11081 was located on the Lower West Fork Trinity River at Beltline Road in Grand Prairie. This station was located in an assessment unit that showed nonsupport of bacteria criteria.

Station 11089 was located on the Lower West Fork Trinity River at West Loop 12 in Irving. This station was located near the downstream end of an assessment unit that showed nonsupport of bacteria criteria.

Segment 0805 - Upper Trinity River

Station 10937 was located on the Upper Trinity River at Mockingbird Lane southwest of downtown Dallas. This station was located in an assessment unit that showed nonsupport of bacteria criteria.

Station 10934 was located on the Upper Trinity River at South Loop 12 below Dallas. USGS stream gauge 08057410 is located at this site. This station was located in an assessment unit that showed nonsupport of bacteria criteria.

Station 10925 was located on the Upper Trinity River at State Highway (SH) 34 at the Ellis/Kaufman County line northeast of Ennis. USGS stream gauge 08062500 is located at this site. This station was located in an assessment unit that showed nonsupport of bacteria criteria.

Station 10924 was located on the Upper Trinity River at Farm Road (FM) 85 along the Henderson/Navarro County line west of Seven Points. This station was selected because it is the most downstream station of Segment 0805 that is accessible for monitoring.

3.1.2.2 BST Water Sampling

Water sampling for bacteria had two purposes: 1) collect quantitative data for *E. coli* concentrations in the Trinity River, and 2) primarily to collect *E. coli* isolates for subsequent BST analysis.

3.1.2.3 BST Water Sample Collection and Laboratory Procedures

BST water sampling events for *E. coli* were conducted on approximately a two per month basis beginning in March 2005 and lasting through August 2005. These samples were collected at 10 main-stem stations from the West Fork of the Trinity (3 stations each for stream Segments 0806 and 0841) and the Upper Trinity River (4 stations from stream Segment 0805) basins**.** Because *E. coli* populations have been found to vary on fine spatial and temporal scales, sampling representativeness during BST water sampling was increased by collecting five independent water samples equally spaced across the stream, one to five minutes apart, at each of the 10 main-stem stations. This sampling was performed on 11 separate events for a total of 550 water samples. Two *E. coli* isolates per sample were then submitted for to IEH for ribotyping, for a total of 1,100 isolates.

The Project Team followed the field sampling procedures documented in the TCEQ *Surface Water Quality Monitoring (SWQM) Procedures Volume 1: Physical and Chemical Monitoring Methods for Water, Sediment and Tissue* (December 2003). Bacteria water samples were collected directly from the stream (up to one-foot below the surface) into reusable sterile polypropylene bottles, in which 0.25 ml of 10% solution of sodium thiosulfate (per 250 ml of sample collected) was previously added to be used where chlorination was suspected. Care was exercised during sample collection 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, the Project Team sampled from a bridge using a weighted PVC sampler that was designed to hold a sample container. After collection each sample container was then labeled with an indelible, waterproof marker. Label information included station identification, date, and time of sample collection. Field sampling personnel wore clean, disposable gloves when they were likely to come in contact with samples that may become contaminated.

Following sample collection, samples were placed into Ziploc® style bags, in order to further prevent contamination, and carried on ice in ice chests from the point of collection to the TIAER mobile laboratory, which was located in a central location of the study area[2]. The TIAER lab staff received the samples, a copy of the chain of custody, and copies of the field data sheets. The lab staff then logged the individual sample information into the laboratory log book. This information included a unique sample ID, test group code, station name, date of collection, time of collection, project name, collector's name(s), and receiver's name. After logging the sample information into the logbook, the samples were checked for proper temperature. The acceptable temperature range was 0-6 °C. If the temperature exceeded 6 ^{o}C, the lab documented whether or not wet ice was present. If ice was present, the temperature variation was considered to be attributed to a short holding time that did not allow the samples to cool to between 0°C and 6 ^{o}C. Samples were considered acceptable if they were placed on ice immediately after collection, remained on ice upon receipt by the laboratory, sample preparation was initiated within six hours after the sample was collected, and sample preparation was completed within eight hours of collection.

[2] The TRA allowed TIAER to locate its mobile laboratory at a secure location of an abandoned pump station near monitoring station 11089.

The TIAER lab staff utilized the membrane filter technique for *E. coli* using modified mTEC agar. Upon sample preparation 0.1, 1.0, 10.0, and 100 ml of the sample solution were filtered through a 0.45 micron nitrocellulose filter. The filter was then transferred to a Petri dish containing modified mTEC agar, inverted and incubated for 2 hours at 35.0 +/- 0.2 °C to rehabilitate injured colonies, then an additional 22-24 hours at 44.5 +/- 0.2 °C. Following the 22-24 hour culture incubation and subsequent concentration enumeration, one Petri dish per sample, containing approximately 20-80 *E. coli* colonies, was chosen for BST analysis. The cultures were labeled appropriately and transferred to an insulated shipping container with blue-ice cold packs for cooling. A member of the TIAER lab staff then enclosed the sample chain of custody in the shipping container and sent it via overnight courier to IEH in Seattle, WA for ribotyping and comparison to known source samples.

3.1.3 Known Source Fecal and Sewage Ribotype Library Development

3.1.3.1 Sanitary Survey

A key component of the monitoring plan was preparation of a sanitary survey for the West Fork Trinity River and Upper Trinity River watersheds. Through the sanitary survey potential sources and general categories of fecal contamination within the watershed were identified and listed, thus ensuring that collection and analysis of resident *E. coli* strains from each known contributing source was accomplished. Identified sources included various wildlife, livestock, avian, and pet species, as well as human influences. Based on information obtained from the sanitary survey, a field collection strategy was defined for collecting known fecal source samples throughout the watershed, including a list of target species and a recommended number of fecal samples to collect from each species (Table 3-1).

In addition to the sanitary survey, the Project Team reviewed available literature, data, and information pertinent to describing the contributions and defining sources of bacterial loading in the watersheds. Special emphasis was placed on acquiring land use/land cover, human/agricultural census data, and wastewater/ storm water infrastructure. 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. These data included:

- reported wastewater permit information, including permit limits, self-reported effluent quality data, violations, and inspection reports;
- hydrologic and meteorological data;
- the extent to which on-site sewage systems (septic tanks) are used in the watershed;
- estimated populations of domestic pets; and
- special studies and published reports for the study area.

Table 3-1. Summary of target and realized fecal source sampling for library development.

Major Category	Minor Category	Target No. Samples to Collect	Total Samples Collected	Total Percentage of Target Sampled
Avian	Pigeon	20	17	
	Swallow	20	14	
	Other	20		
	(Heron)	-----	1	
	(Grackle)	-----	21	
	(Egret)	-----	10	
	(Kingbird)	-----	1	
	(Sparrow)	-----	4	
	(Dove)	-----	8	
	(Red-winged Blackbird)	-----	1	
	(Flycatcher)	-----	1	
	(Starling)	-----	3	
	(Vulture)	-----	3	
	(Killdeer)	-----	2	
	(Seagull)	-----	2	
	Roadrunner	-----	1	
	Guinea	-----	2	
	Total	**60**	**91**	**152%**
Human	Human (Raw Sewage	35	58	
	Human (Septage)	35	20	
	Human (WWTF Effluent)	0	10	
	Total	**70**	**88**	**126%**
Mammalian Wildlife	Armadillo	0	1	
	Bobcat	0	2	
	Deer	10	0	
	Mouse	5	0	
	Opossum	5	7	
	Rabbit	5	5	
	Raccoon	10	5	
	Rat	5	12	
	Squirrel	5	5	
	Other	15	0	
	Total	**60**	**37**	**62%**
Livestock	Cattle (Dairy)	15	14	
	Cattle (Beef)	45	65	
	Bison	0	6	
	Poultry	45	59	
	Horse/Donkey	10	25	
	Goat	5	19	
	Sheep	5	6	
	Llamas	0	3	
	Pig (Domestic)	5	9	
	Total	**130**	**206**	**158%**
Pets	Cat / Feline	30	23	
	Dog / Canine	30	61	
	Other	10	16	
	Total	**70**	**100**	**143%**
Petting Zoo	Various Species	10	0	
	Total	**10**	**0**	**0%**
All Species	**Grand Total**	**400**	**522**	**131%**

3.1.3.2 Known Source Fecal and Sewage Ribotype Library Sample Collection

For the known source fecal and sewage sampling, the Project Team field staff collected specimens directly from the source feces, with the exception of human samples, which were collected from WWTF influent**.** 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**.** In cases of uncertainty regarding its source, the sample was not used for library development. No more than 15 samples were collected from the members of the same animal species from a given location, unless those animals did not normally comprise a distinct population of low diversity, but were assembled temporarily (e.g., a livestock show, animal shelter, or migrating waterfowl). Only a single sample was collected from an individual animal. The overall source-sampling objective is to collect several, representative samples from every warm-blooded species or groups of related species (e.g., heron, egret, rat) known to populate the watersheds in sufficient numbers to be a potential source of the documented bacterial contamination.

Fresh animal fecal samples were collected aseptically, using a sterile spatula or swab, into sterile, screw-cap polypropylene specimen tubes, which were then capped and sealed. All sample containers were then labeled with the following information:

- sample type,
- host species,
- collection date,
- collection time,
- sample location, and
- sampler's initials.

All of the sample information was logged into a field logbook or noted on field data sheets. Samples were immediately placed into a cooler on wet ice in double zip lock bags and later transferred to a shipping container with blue-ice cold packs and shipped via overnight courier to IEH for ribotyping. Human wastewater samples were first plated for growth of *E. coli* colonies and then shipped (using the same cooling protocols) to IEH for ribotyping.

3.1.3.3 Ribotyping of BST Water and Known Source Fecal and Sewage Samples

Upon receipt of the known source fecal and sewage samples by IEH, one *E. coli* isolate from each Petri dish sample was scraped and prepared for DNA extraction. Following DNA extraction, the DNA samples were digested using *Eco*R1 and *Pvu*II endonuclease restriction enzymes. The resulting DNA fragments were then run on a 0.8% agarose gel and subsequently stained using ethidium bromide. The gel was then photographed and labeled. Label information included the isolate numbers loaded on each lane, the enzyme used to cut the DNA, date, gel number, voltage, current, gel strength, buffer strength, and electrophoresis time information.
The gel was then processed for Southern Blot Hybridization. The resulting ribotype was then analyzed based on the distance between the DNA bands. The ribotypes were then entered into a Microsoft Access® database and compared to ribotypes of known source (Complete IEH Ribotyping Protocol may be found in Appendix A).

3.1.4 Additional Data Collection

3.1.4.1 Anecdotal Record

The anecdotal record consists of a written log of field observations made at each station on the segment during monitoring activities. This record describes the physical stream characteristics noted by the Project Team field staff. At the time of water sample collection, all field observations were recorded in a field data logbook or on field data sheets. The data included, but were not be limited to: the name of sampler(s), date, time, station identification, depth of sample, qualitative estimation of flow severity, water body type, water appearance, weather conditions, days since last significant rainfall, stream uses, unusual riparian conditions, odors and any other significant sample information (as applicable). (Selected anecdotal and *E. coli* quantification data may be found in Appendix B.)

3.1.5 Schedule of Sampling Events

3.1.5.1 BST Water Sampling

BST water sampling occurred on each of the following dates:

- 23 March 05 (all stations; event 1)
- 05 April 05 (all stations; event 2)
- 19 April 05 (all stations; event 3)
- 04 May 05 (all stations; event 4)
- 17 May 05 (all stations; event 5)
- 01 June 05 (all stations; event 6)
- 14 June 05 (all stations; event 7)
- 28 June 05 (all stations; event 8)
- 12 July 05 (all stations; event 9)
- 27 July 05 (all stations; event 10)
- 08 August 05 (Stations 10937, 10934, 10925, and 10924; event 11)
- 16 August 05 (Stations 18459, 10938, 16120, 17669, 11081, and 11089; event 11)

3.1.5.2 BST Water Sampling Event Summary

Using data from the anecdotal record, a sampling event summary was developed in order to provide information concerning atmospheric, hydrologic, or other site specific information. This summary provides additional data in order to help explain any potential anomalies that may be discovered at a later date. The sampling event summary includes the following events:

Event 1

The first water sampling event occurred on March 23, 2005. The weather was clear to partly cloudy with a slight to moderate breeze, generally out of the north. Hydrologic conditions at each of the stations appeared to be normal since no significant rainfall had fallen for over a

week. With the exception of a slight chlorine odor and some patches of foam at station 11089, there were no particularly unusual conditions to report.

Event 2

The second sampling event took place on April 5, 2005. The weather on this particular day was cloudy early in the morning; changing to clear to partly cloudy skies later in the morning and into the afternoon. The wind was a slight to strong southerly breeze and the stream hydrologic conditions were found to be normal, as there were no significant rainfall accumulations during the previous seven days. With the exception of swallows present under the bridge at station 10925, there were no remarkable conditions to report.

Event 3

The third sampling event occurred on April 19, 2005. The weather was found to be a cloudy day with slight to strong south/southwest winds. Streamflow conditions were generally normal since no significant rain had fallen during the previous seven days. Station 10924 in Segment 0805 had a slight sheen present on the surface of the water and the water was notably turbid during this sampling event. Swallows were found to be present under the bridges at most of the stations in Segments 0806 and 0841.

Event 4

The fourth sampling event took place on May 04, 2005. The weather was cloudy with rain being observed at station 10924, and the wind was calm to slight. Despite the fact that significant rain was recorded during the previous 24 hours, the stream hydrologic conditions were still considered normal. No other remarkable conditions were observed at any of the stations.

Event 5

The fifth sampling event occurred on May 17, 2005. The weather was clear to partly cloudy with calm to moderate winds out of the south. Despite a significant rain event taking place three days prior to sampling, the hydrological stream conditions appeared normal. A large number of cliff swallows were observed at the bridges of stations 10938 and 17669.

Event 6

The sixth sampling event occurred on June 01, 2005. The weather on this day was clear to partly cloudy with a slight to moderate northwesterly wind. The last significant rainfall occurred within 24 hours of this sampling event, resulting in elevated flows and turbid water observed at many of the upper stations.

Event 7

The seventh sampling event took place on June 14, 2005. The weather was clear to partly cloudy with calm to moderate winds out of the northwest. The last significant rain event occurred over a week prior, and this coupled with warming temperatures resulted in low flows being observed in much of the Upper Trinity. No other remarkable conditions were observed during this sampling run.

Event 8

The eighth sampling event, on June 28, 2005, was conducted under clear to partly cloudy weather conditions with calm to slight southwesterly winds. Hydrologic conditions in the stream were found to be low to normal since a significant rainfall event had not taken place since June 1. A large number of swallows at station 10938 and a Jeep located in the river upstream of our sampling station at 16120 were the only remarkable conditions observed during this event.

Event 9

The ninth sampling event took place on July 12, 2005. The weather was clear to partly cloudy with calm to slight winds out of the south. Stream hydrologic conditions were low to normal. The last significant rain fell five days prior. No other remarkable conditions were noted.

Event 10

The tenth sampling event, occurring on July 27, 2005, took place during rainy weather, with a slight northwest wind. Stream conditions were found to be normal despite the rain. No other remarkable conditions were observed.

Event 11

The eleventh and last sampling event took place over two days, each about a week apart. On August 08, 2005, the stations in Segment 0805 were sampled. This day was cloudy with a moderate wind. Streamflow was found to be high since a significant rain had fallen less than 24 hours prior. No other remarkable conditions were noted. Segments 0806 and 0841 were sampled the following week on August 16, 2005. During this sampling event, the weather was found to be partly cloudy with a slight south wind. Since a significant rainfall event occurred less than 24 hours prior to this sampling event, the stream hydrologic conditions were found to be high. No other remarkable conditions were found to exist.

3.1.5.3 Known Source Fecal and Sewage Ribotype Library Sample Collection

Known source fecal and sewage ribotype library sample collection was also performed on approximately a two per month basis throughout the six-month study in order to ensure representative sampling of as many human, wildlife, and domestic animal sewage/fecal specimens as possible. Known source fecal and sewage ribotype library sample collection occurred on the following dates:

• 23 March 05	05 April 05
• 19 April 05	04 May 05
• 17 May 05	01 June 05
• 14 June 05	28 June 05
• 07 July 05	12 July 05
• 08 August 05	16 August 05

3.2 Results and Discussions

3.2.1 Quality Assurance/Quality Control Results

QA/QC measures utilized by TIAER 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*

TIAER laboratory personnel carried out QA/QC procedures in order to: 1) verify the sterility of the reusable *E. coli* collection containers, media, filters, glassware, and other supplies and equipment. through analysis of method blanks, 2) quantify any variation in the analytical process through analysis of laboratory duplicates, and, 3) determine the viability of the bacterial growth media by running a positive and negative control sample on each new batch of growth media that was produced.

The sterility of the reusable *E. coli* containers, media, filters, glassware, and other supplies and equipment was verified by analyzing a method blank. This procedure involved adding approximately 250 ml of sterile deionized water to a sterilized re-usable container before analysis on each day that project samples were collected and for every set of 20 samples that were processed, a 100 ml sample of water was pulled from the method blank and also processed by carrying it through the entire analytical procedure.

Laboratory duplicates were used in order to quantify any variation in the analytical process. This procedure involved analyzing an additional aliquot from a sample bottle for every 10 samples that were processed. This additional sample was then carried through the entire analytical procedure. (Data from culturing and enumeration QA/QC procedures may be found in Appendix C.)

Positive and negative control cultures were also processed with each batch of bacterial growth media that was produced. Positive controls involved inoculating a sterilized Petri dish containing the fresh sterilized media with a positive *E. coli* sample in order to verify that it would grow on the media. Negative controls involved inoculating a sterilized Petri dish containing the fresh sterilized media with a bacterial species other that *E. coli* (usually *Pseudomonas sp.*) in order to verify that it would not grow on the media. All positive controls were positive for the growth of *E. coli* and all negative controls were negative for the growth of any extraneous species.

3.2.1.2 Ribotyping QA/QC Results

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.

IEH prepared triplicate cultures of 30 *E. coli* isolates from known sources collected from the Trinity River segments of interest. These isolates were selected by Parsons and TIAER from a variety of species in the known source library. The 90 (30 x 3) cultures were then placed in 90 identical culture tubes, each with a removable label indicating their source and the isolate number. These tubes were mailed to the Parsons Project Manager (PM). The Parsons PM prepared and sent a list of the 30 isolate sources to the TIAER PM, who selected, from the list, 10 isolates to be blind QC test samples. By selecting a subset of only 33% of the prepared cultures, the laboratory had no basis for anticipating the identity of the unmarked samples that they received. The Parsons PM then identified the 30 culture tubes associated with those 10 isolates, replaced each label with a new label, numbered them from 1 to 30 in random fashion, and recorded those numbers on a key with the isolate number and source. The Parsons PM then sent those 30 culture tubes back to IEH after verifying that there was no way for their source to be identified. The Parsons PM sent the key to the TIAER QAO and PM. The samples were processed through the ribotyping procedures in a blind fashion; that is the laboratory did not know the sources. IEH then sent the results to the TIAER PM, who made a copy of the key and results and provided it to IEH and the Project Team QAO. IEH successfully ribotyped and identified 100% of the isolates in the double blind QA/QC study. (Data from ribotyping QA/QC study can be found in Appendix D.)

3.2.2 BST Results

For purposes of data analysis, organization, and presentation, the ribotyped ambient water samples are grouped by source categories. 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, goat and horse have some biological similarity but even greater similarity from a management viewpoint where they can be grouped into a livestock category that tend to occur on farms and ranches.

One source category is from samples that can not be identified with any known source. This category is referred to as "unknown" source. One cause of "unknowns" is the *E. coli* strains that occur in more than one source type and are, therefore, considered transient strains. For the ribotyping technique used in this study, about 4% of *E. coli* strains would be anticipated to be transient (see Section 3.1.1). Dr. Mansour Samadpour, the principal of IEH, indicated he would anticipate that these transient strains comprise 5 to 10% of the total *E. coli* population found in ambient water samples (Samadpour, 2006). The second cause of "unknowns" is *E. coli* isolates from water samples that do not match any *E. coli* in the known source library. In ribotyping, with the inherent high precision and accuracy of the rRNA methods, data completeness is most affected by the number of ribotypes found that match ribotypes in the known source library. Thus, a large library is important. For this project, in addition to the known source library collected specifically in the Trinity River watershed, the entire IEH library of multiple tens of thousands of library samples were used. But even with the watershed specific library and the

large library of IEH, transient strains and unidentified strains are anticipated to comprise 5 to 30% of the *E. coli* in ambient water samples for a typical study (Samadpour, 2006).

Following the ambient water sampling and the known source fecal and sewage ribotype library sampling, the results from each were analyzed and the ribotypes were matched to the project library and to IEH's larger library. Sources were then grouped into six separate categories, which included avian, human, mammalian wildlife, unknown, pet, and livestock. (Results from ribotyping may be found in Appendix E.) Categories were chosen based on similarity of co-occurrence and management practices (Table 3-2).

The avian category included all bird species, wild and domestic that are generally identified under the two sources of waterfowl and avian[3]; the human category included *E. coli* found in raw sewage collected from WWTF influent, WWTF effluent and septage collected from septic service trucks; mammalian wildlife included deer, raccoons, opossums, rabbits, and positive identification of wild canine or feline species, such as coyotes or bobcats; unknown species were those contributing *E. coli* that could not be traced back to any particular source; pets included cats, dogs, and any feline or canine species that could not be definitively identified; and livestock included cows, bison, horses, donkeys, sheep, and pigs. Of note, no large pig or poultry operations were observed in the watershed during library sample collection, and these observations are corroborated by the National Agricultural Statistics data summarized in Table 2-5 that indicate only small numbers of pigs and poultry in the counties associated with the watershed. As will be shown subsequently in the presentation of BST results, pig (or porcine) was not identified in any ambient water samples. The porcine category includes both domestic and feral pigs. Poultry were also not identified as a contributor in any ambient water samples.

During this project, various factors contributed to an unequal number of isolates being ribotyped, on occasion, for the various stations and sampling events. To determine any potential bias during source analysis resulting from the unequal number of isolates, the source data were normalized by calculating the percent source contribution at each station for each sampling event, averaging the results for each station over all events, and finally calculating the overall average percent contribution of all stations per affected segment. The normalized results were then compared to the non-normalized results using the following formula to calculate confidence intervals (CI):

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

[3] More than one avian species can and often do harbor the same *E. coli* strain, which makes unique identification of specific avian species by ribotyping difficult. Waterfowl can, however, often be distinguished from other avian species, and both poultry and Guinea fowl can be characterized. In the present study neither poultry nor Guinea fowl were characterized from any ambient water sample isolates. Though the absence of any contributions from domestic avian species can not be concluded, the estimated livestock populations in Table 2-5 support a presumption that domestic avian species are a minor contributor of bacteria in the West Fork Trinity and Upper Trinity River watersheds.

Table 3-2. Descriptions of *E. coli* sources as they were categorized based on BST ribotyping results.

Source Category	Source	Description
Avian	Avian	Includes all non-waterfowl avian species; wild and domestic.
	Waterfowl	Includes all waterfowl species.
Human	Sewage	Sewage (Includes all raw sewage from WWTF influent and septage.)
	Wastewater	Wastewater (Includes all treated WWTF effluent.)
Livestock	Bison	
	Bovine	
	Donkey	
	Equine	Includes all equine species that could not be positively identified to the species level.
	Goat	
	Horse	
Mammalian Wildlife	Armadillo	
	Coyote	
	Deer	
	Opossum	
	Rabbit	
	Raccoon	
	Rodent	Includes all rodents that could not be positively identified to the species level.
	Skunk	
	Squirrel	
Pet	Canine	Includes all canine species that could not be positively identified to the species level.
	Cat	
	Dog	
	Feline	Includes all feline species that could not be positively identified to the species level.
Unknown	Unknown	Includes all other species that could not be positively identified.

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.

The results from the normalized and non-normalized data analysis for Segments 0806, 0841, and 0805 were found to be very similar and no sources were found to be statistically different at the 95 percent confidence level (Tables 3-3, 3-4, and 3-5). Therefore, due to the simplicity of working with non-normalized data compared to normalized data, the non-normalized data has been used for all remaining analyses.

Table 3-3. Normalized and non-normalized *E. coli* source characterization data for Segment 0806. (CI = confidence interval)

Segment 0806			Non-Normalized Data			Normalized Data		
Category	**Source**	**Isolate #**	**Contribution (%)**	**95% CI Range**		**Contribution (%)**	**95% CI Range**	
Avian	Avian	81	23.4	15.11	31.71	23.6	15.3	31.9
Avian	Waterfowl	16	4.6	0.51	8.74	4.6	0.5	8.8
Avian	**Subtotal**	**97**	**28.0**	**19.23**	**36.84**	**28.2**	**19.4**	**37.0**
Human	Sewage	2	0.6	-0.91	2.06	0.6	-0.9	2.1
Human	Wastewater	37	10.7	4.64	16.75	10.6	4.5	16.6
Human	**Subtotal**	**39**	**11.3**	**5.07**	**17.47**	**11.2**	**5.0**	**17.3**
Livestock	Bison	0	0.0	0.00	0.00	0.0	0.0	0.0
Livestock	Bovine	5	1.4	-0.89	3.78	1.5	-0.9	3.8
Livestock	Donkey	0	0.0	0.00	0.00	0.0	0.0	0.0
Livestock	Equine	1	0.3	-0.76	1.34	0.3	-0.8	1.4
Livestock	Goat	1	0.3	-0.76	1.34	0.3	-0.8	1.4
Livestock	Horse	6	1.7	-0.82	4.29	1.7	-0.8	4.2
Livestock	**Subtotal**	**13**	**3.8**	**0.03**	**7.48**	**3.8**	**0.0**	**7.5**
Mammalian Wildlife	Armadillo	2	0.6	-0.91	2.06	0.6	-0.9	2.1
Mammalian Wildlife	Coyote	0	0.0	0.00	0.00	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.00	0.00	0.0	0.0	0.0
Mammalian Wildlife	Opossum	6	1.7	-0.82	4.29	1.8	-0.8	4.3
Mammalian Wildlife	Rabbit	1	0.3	-0.76	1.34	0.3	-0.8	1.4
Mammalian Wildlife	Raccoon	23	6.6	1.76	11.53	6.7	1.8	11.7
Mammalian Wildlife	Rodent	40	11.6	5.29	17.83	11.1	4.9	17.2
Mammalian Wildlife	Skunk	3	0.9	-0.95	2.68	0.8	-0.9	2.6
Mammalian Wildlife	Squirrel	4	1.2	-0.94	3.25	1.2	-0.9	3.3
Mammalian Wildlife	**Subtotal**	**79**	**22.8**	**14.61**	**31.06**	**22.5**	**14.3**	**30.7**
Pet	Canine	7	2.0	-0.74	4.78	2.0	-0.7	4.8
Pet	Cat	6	1.7	-0.82	4.29	1.8	-0.8	4.3
Pet	Dog	31	9.0	3.36	14.56	9.2	3.5	14.9
Pet	Feline	2	0.6	-0.91	2.06	0.7	-0.9	2.3
Pet	**Subtotal**	**46**	**13.3**	**6.64**	**19.95**	**13.7**	**7.0**	**20.4**
Unknown	Unknown	72	20.8	12.85	28.77	20.7	12.7	28.6
Unknown	**Subtotal**	**72**	**20.8**	**12.85**	**28.77**	**20.7**	**12.7**	**28.6**
	Total	**346**	**100.0**			**100.00**		

Table 3-4. Normalized and non-normalized *E. coli* source characterization data for Segment 0841. (CI = confidence interval)

Segment 0841			Non-Normalized Data			Normalized Data		
Category	**Source**	**Isolate #**	**Contribution (%)**	**95% CI Range**		**Contribution (%)**	**95% CI Range**	
Avian	Avian	78	22.8	14.58	31.03	22.6	14.4	30.8
Avian	Waterfowl	17	5.0	0.71	9.23	4.9	0.7	9.1
Avian	**Subtotal**	**95**	**27.8**	**19.00**	**36.56**	**27.5**	**18.7**	**36.2**
Human	Sewage	0	0.0	0.00	0.00	0.0	0.0	0.0
Human	Wastewater	70	20.5	12.56	28.38	20.5	12.6	28.5
Human	**Subtotal**	**70**	**20.5**	**12.56**	**28.38**	**20.5**	**12.6**	**28.5**
Livestock	Bison	0	0.0	0.00	0.00	0.0	0.0	0.0
Livestock	Bovine	6	1.8	-0.82	4.33	1.7	-0.8	4.3
Livestock	Donkey	0	0.0	0.00	0.00	0.0	0.0	0.0
Livestock	Equine	3	0.9	-0.95	2.70	0.9	-0.9	2.7
Livestock	Goat	0	0.0	0.00	0.00	0.0	0.0	0.0
Livestock	Horse	4	1.2	-0.94	3.28	1.2	-0.9	3.3
Livestock	**Subtotal**	**13**	**3.8**	**0.05**	**7.55**	**3.8**	**0.0**	**7.5**
Mammalian Wildlife	Armadillo	0	0.0	0.00	0.00	0.0	0.0	0.0
Mammalian Wildlife	Coyote	2	0.6	-0.91	2.08	0.6	-0.9	2.1
Mammalian Wildlife	Deer	1	0.3	-0.77	1.35	0.3	-0.8	1.4
Mammalian Wildlife	Opossum	3	0.9	-0.95	2.70	0.9	-1.0	2.8
Mammalian Wildlife	Rabbit	0	0.0	0.00	0.00	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	24	7.0	2.01	12.02	7.0	2.0	12.0
Mammalian Wildlife	Rodent	25	7.3	2.21	12.41	7.3	2.2	12.5
Mammalian Wildlife	Skunk	3	0.9	-0.95	2.70	0.9	-1.0	2.7
Mammalian Wildlife	Squirrel	0	0.0	0.00	0.00	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**58**	**17.0**	**9.60**	**24.31**	**17.0**	**9.7**	**24.4**
Pet	Canine	5	1.5	-0.89	3.81	1.5	-0.9	3.9
Pet	Cat	4	1.2	-0.94	3.28	1.2	-0.9	3.4
Pet	Dog	34	9.9	4.08	15.81	10.1	4.2	16.0
Pet	Feline	1	0.3	-0.77	1.35	0.3	-0.8	1.3
Pet	**Subtotal**	**44**	**12.9**	**6.30**	**19.43**	**13.0**	**6.4**	**19.7**
Unknown	Unknown	62	18.1	10.58	25.68	18.1	10.6	25.7
Unknown	**Subtotal**	**62**	**18.1**	**10.58**	**25.68**	**18.1**	**10.6**	**25.7**
	Total	**342**	**100.0**			**100.00**		

Table 3-5. Normalized and non-normalized *E. coli* source characterization data for Segment 0805. (CI = confidence interval)

Segment 0805			Non-Normalized Data			Normalized Data		
Category	**Source**	**Isolate #**	**Contribution (%)**	**95% CI Range**		**Contribution (%)**	**95% CI Range**	
Avian	Avian	99	22.1	14.01	30.29	23.2	15.0	31.5
Avian	Waterfowl	17	3.8	0.05	7.55	3.6	0.0	7.3
Avian	**Subtotal**	**116**	**26.0**	**17.36**	**34.54**	**26.9**	**18.2**	**35.6**
Human	Sewage	0	0.0	0.00	0.00	0.0	0.0	0.0
Human	Wastewater	106	23.7	15.38	32.05	23.5	15.2	31.8
Human	**Subtotal**	**106**	**23.7**	**15.38**	**32.05**	**23.5**	**15.2**	**31.8**
Livestock	Bison	1	0.2	-0.70	1.15	0.2	-0.7	1.2
Livestock	Bovine	29	6.5	1.66	11.32	6.5	1.7	11.3
Livestock	Donkey	3	0.7	-0.93	2.27	0.6	-0.9	2.2
Livestock	Equine	1	0.2	-0.70	1.15	0.2	-0.7	1.2
Livestock	Goat	3	0.7	-0.93	2.27	0.6	-0.9	2.2
Livestock	Horse	12	2.7	-0.48	5.85	2.8	-0.4	6.0
Livestock	**Subtotal**	**49**	**11.0**	**4.84**	**17.09**	**11.0**	**4.9**	**17.1**
Mammalian Wildlife	Armadillo	3	0.7	-0.93	2.27	0.6	-0.9	2.2
Mammalian Wildlife	Coyote	0	0.0	0.00	0.00	0.0	0.0	0.0
Mammalian Wildlife	Deer	1	0.2	-0.70	1.15	0.2	-0.7	1.2
Mammalian Wildlife	Opossum	2	0.4	-0.86	1.76	0.4	-0.8	1.7
Mammalian Wildlife	Rabbit	1	0.2	-0.70	1.15	0.2	-0.7	1.2
Mammalian Wildlife	Raccoon	27	6.0	1.37	10.71	6.0	1.3	10.6
Mammalian Wildlife	Rodent	29	6.5	1.66	11.32	6.4	1.6	11.2
Mammalian Wildlife	Skunk	0	0.0	0.00	0.00	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.00	0.00	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**63**	**14.1**	**7.27**	**20.91**	**13.9**	**7.1**	**20.6**
Pet	Canine	6	1.3	-0.91	3.60	1.3	-0.9	3.5
Pet	Cat	9	2.0	-0.74	4.77	2.0	-0.7	4.7
Pet	Dog	36	8.1	2.72	13.39	8.0	2.7	13.3
Pet	Feline	0	0.0	0.00	0.00	0.0	0.0	0.0
Pet	**Subtotal**	**51**	**11.4**	**5.18**	**17.64**	**11.2**	**5.1**	**17.4**
Unknown	Unknown	62	13.9	7.10	20.64	13.5	6.8	20.2
Unknown	**Subtotal**	**62**	**13.9**	**7.10**	**20.64**	**13.5**	**6.8**	**20.2**
	Total	**447**	**100.0**			**100.00**		

E. coli results for each of the segments were distributed and analyzed based on overall *E. coli* source distribution, runoff vs. non-runoff events, samples containing *E. coli* concentrations ≤394 org/100ml vs. those with >394 org/100ml (the single sample criterion), temporal differences between sampling events, and overall *E. coli* source contributions for the individual stations.

During runoff vs. non-runoff analyses, it was determined that a number of sampling events could not be placed into either category due to low rainfall amounts in certain areas or time of sampling relative to the beginning of the storm event. Therefore the isolates were separated and placed into one of the following categories for comparison purposes: 1) definitely runoff influenced, 2) definitely non-runoff influenced, or 3) potentially runoff influenced. The following analyses were then made between the categories: 1) the definite non-runoff isolates vs. the definite runoff isolates, 2) the definite non-runoff isolates vs. the definite runoff isolates (with potential event isolates added), and 3) the definite non-runoff isolates (with potential event isolates added) vs. the definite runoff isolates. Following the comparisons, it was concluded that there was no significant difference (α=0.05) between the three analyses. Thus for brevity of presentation herein the analysis with potential event isolates excluded is provided. This analysis reduces bias by avoiding possibly placing the potentially runoff influence isolates in a category where they may not belong.

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3.2.2.1 Trinity Segment 0806

The West Fork Trinity below Lake Worth (Segment 0806) results were based on 346 isolates collected from stations 18459, 10938, and 16120.

The overall *E. coli* source contribution for Segment 0806 was led by the avian category, with 28.0% of the total contribution (Figure 3-2; Table 3-6). Within the avian category, the major source was found to be the non-waterfowl species, which contributed 23.4% of the total *E. coli* to the affected segment (Table 3-6). Mammalian wildlife was found to be the second highest contributor with 22.8%, followed by the unknown category with 20.8%. Within the mammalian wildlife category, the rodent population contributed the most with 11.6%. The top three categories were followed by the pet, human, and livestock categories, respectively. These categories were led by dogs (9.0%) and wastewater (10.7%), while the livestock category's largest sources were horses (1.7%) and bovine (1.4%).

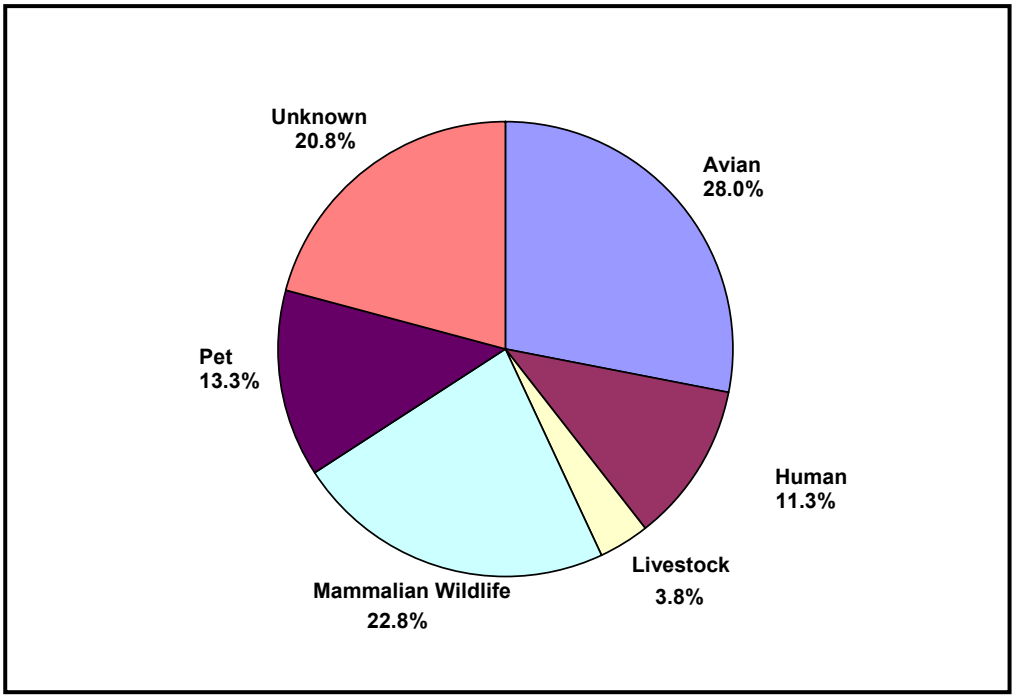

Figure 3-2. *E. coli* source characterization for Segment 0806 under all conditions.

Runoff vs. non-runoff events were not found to be significantly different (α=0.05) based on *E. coli* source contributions (Table 3-7). While not statistically significant, avian contribution was greater for non-runoff events than for runoff events, and both pet and livestock contributions were less for non-runoff events than for runoff events. Segment 0806 had a total of 212 non-runoff influenced isolates and 82 runoff influenced isolates, for a total of 294 isolates. The remaining 52 isolates were collected during events that could not be placed, definitively, in either the non-runoff or runoff categories; therefore they were excluded from the presented analysis.

Table 3-6. Overall *E. coli* source characterization and 95% confidence interval (CI) range for Segment 0806.

Segment 0806					
Category	**Source**	**Isolate #**	**Contribution (%)**	**95% CI Range**	
Avian	Avian	81	23.4	15.11	31.71
Avian	Waterfowl	16	4.6	0.51	8.74
Avian	**Subtotal**	**97**	**28.0**	**19.23**	**36.84**
Human	Sewage	2	0.6	-0.91	2.06
Human	Wastewater	37	10.7	4.64	16.75
Human	**Subtotal**	**39**	**11.3**	**5.07**	**17.47**
Livestock	Bison	0	0	0	0
Livestock	Bovine	5	1.4	-0.89	3.78
Livestock	Donkey	0	0	0	0
Livestock	Equine	1	0.3	-0.76	1.34
Livestock	Goat	1	0.3	-0.76	1.34
Livestock	Horse	6	1.7	-0.82	4.29
Livestock	**Subtotal**	**13**	**3.8**	**0.03**	**7.48**
Mammalian Wildlife	Armadillo	2	0.6	-0.91	2.06
Mammalian Wildlife	Coyote	0	0	0	0
Mammalian Wildlife	Deer	0	0	0	0
Mammalian Wildlife	Opossum	6	1.7	-0.82	4.29
Mammalian Wildlife	Rabbit	1	0.3	-0.76	1.34
Mammalian Wildlife	Raccoon	23	6.6	1.76	11.53
Mammalian Wildlife	Rodent	40	11.6	5.29	17.83
Mammalian Wildlife	Skunk	3	0.9	-0.95	2.68
Mammalian Wildlife	Squirrel	4	1.2	-0.94	3.25
Mammalian Wildlife	**Subtotal**	**79**	**22.8**	**14.61**	**31.06**
Pet	Canine	7	2	-0.74	4.78
Pet	Cat	6	1.7	-0.82	4.29
Pet	Dog	31	9	3.36	14.56
Pet	Feline	2	0.6	-0.91	2.06
Pet	**Subtotal**	**46**	**13.3**	**6.64**	**19.95**
Unknown	Unknown	72	20.8	12.85	28.77
Unknown	**Subtotal**	**72**	**20.8**	**12.85**	**28.77**
	Total	**346**	**100**		

Table 3-7. Runoff vs. non-runoff influenced *E. coli* source characterization for Segment 0806. (CI = confidence interval)

Segment 0806		Non-Runoff				Runoff			
Category	Source	Isolate #	Contribution (%)	95% CI Range		Isolate #	Contribution (%)	95% CI Range	
Avian	Avian	51	24.1	15.7	32.4	13	15.9	8.7	23.0
Avian	Waterfowl	11	5.2	0.8	9.5	3	3.7	0.0	7.3
Avian	**Subtotal**	**62**	**29.2**	**20.3**	**38.2**	**16**	**19.5**	**11.7**	**27.3**
Human	Sewage	0	0.0	0.0	0.0	1	1.2	-0.9	3.4
Human	Wastewater	26	12.3	5.8	18.7	9	11.0	4.8	17.1
Human	**Subtotal**	**26**	**12.3**	**5.8**	**18.7**	**10**	**12.2**	**5.8**	**18.6**
Livestock	Bison	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Bovine	5	2.4	-0.6	5.3	0	0.0	0.0	0.0
Livestock	Donkey	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Equine	1	0.5	-0.9	1.8	0	0.0	0.0	0.0
Livestock	Goat	0	0.0	0.0	0.0	1	1.2	-0.9	3.4
Livestock	Horse	2	0.9	-1.0	2.8	4	4.9	0.7	9.1
Livestock	**Subtotal**	**8**	**3.8**	**0.0**	**7.5**	**5**	**6.1**	**1.4**	**10.8**
Mammalian Wildlife	Armadillo	2	0.9	-1.0	2.8	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	2	0.9	-1.0	2.8	3	3.7	0.0	7.3
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	11	5.2	0.8	9.5	9	11.0	4.8	17.1
Mammalian Wildlife	Rodent	27	12.7	6.2	19.3	8	9.8	3.9	15.6
Mammalian Wildlife	Skunk	1	0.5	-0.9	1.8	2	2.4	-0.6	5.5
Mammalian Wildlife	Squirrel	4	1.9	-0.8	4.6	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**47**	**22.2**	**14.0**	**30.3**	**22**	**26.8**	**18.1**	**35.5**
Pet	Canine	4	1.9	-0.8	4.6	3	3.7	0.0	7.3
Pet	Cat	2	0.9	-1.0	2.8	4	4.9	0.7	9.1
Pet	Dog	20	9.4	3.7	15.2	7	8.5	3.1	14.0
Pet	Feline	1	0.5	-0.9	1.8	1	1.2	-0.9	3.4
Pet	**Subtotal**	**27**	**12.7**	**6.2**	**19.3**	**15**	**18.3**	**10.7**	**25.9**
Unknown	Unknown	42	19.8	12.0	27.6	14	17.1	9.7	24.4
Unknown	**Subtotal**	**42**	**19.8**	**12.0**	**27.6**	**14**	**17.1**	**9.7**	**24.4**
	Total	**212**	**100**			**82**	**100**		

E. coli source contributions for samples containing ≤394 org/100ml were not found to be significantly different (α=0.05) from samples containing >394 org/100 ml (Table 3-8).

Table 3-8. *E. coli* source characterization for samples containing ≤394 org/100 ml vs. samples containing >394 org/100ml for Segment 0806. (CI = confidence interval)

Segment 0806		Samples ≤ 394 org / 100ml				Samples > 394 org / 100ml			
Category	Source	Isolate #	Contribution (%)	95% CI Range		Isolate #	Contribution (%)	95% CI Range	
Avian	Avian	67	26.0	17.4	34.6	14	15.9	8.7	23.1
Avian	Waterfowl	13	5.0	0.8	9.3	3	3.4	-0.1	7.0
Avian	Subtotal	80	31.0	21.9	40.1	17	19.3	11.6	27.1
Human	Sewage	1	0.4	-0.8	1.6	1	1.1	-0.9	3.2
Human	Wastewater	28	10.9	4.8	16.9	9	10.2	4.3	16.2
Human	Subtotal	29	11.2	5.0	17.4	10	11.4	5.1	17.6
Livestock	Bison	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Bovine	5	1.9	-0.8	4.6	0	0.0	0.0	0.0
Livestock	Donkey	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Equine	0	0.0	0.0	0.0	1	1.1	-0.9	3.2
Livestock	Goat	0	0.0	0.0	0.0	1	1.1	-0.9	3.2
Livestock	Horse	2	0.8	-0.9	2.5	4	4.5	0.5	8.6
Livestock	Subtotal	7	2.7	-0.5	5.9	6	6.8	1.9	11.8
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0	2	2.3	-0.6	5.2
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	3	1.2	-0.9	3.3	3	3.4	-0.1	7.0
Mammalian Wildlife	Rabbit	1	0.4	-0.8	1.6	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	14	5.4	1.0	9.9	9	10.2	4.3	16.2
Mammalian Wildlife	Rodent	31	12.0	5.6	18.4	9	10.2	4.3	16.2
Mammalian Wildlife	Skunk	1	0.4	-0.8	1.6	2	2.3	-0.6	5.2
Mammalian Wildlife	Squirrel	4	1.6	-0.9	4.0	0	0.0	0.0	0.0
Mammalian Wildlife	Subtotal	54	20.9	13.0	28.9	25	28.4	19.6	37.2
Pet	Canine	4	1.6	-0.9	4.0	3	3.4	-0.1	7.0
Pet	Cat	1	0.4	-0.8	1.6	5	5.7	1.1	10.2
Pet	Dog	24	9.3	3.6	15.0	7	8.0	2.7	13.3
Pet	Feline	1	0.4	-0.8	1.6	1	1.1	-0.9	3.2
Pet	Subtotal	30	11.6	5.3	17.9	16	18.2	10.6	25.7
Unknown	Unknown	58	22.5	14.3	30.7	14	15.9	8.7	23.1
Unknown	Subtotal	58	22.5	14.3	30.7	14	15.9	8.7	23.1
	Total	**258**	**100.0**			**88**	**100.0**		

Largely similar to the comparisons of runoff and non-runoff events, avian contribution was greater for *E. coli* isolates from samples containing ≤394 org/100 ml than for samples containing >394 org/100 ml, and mammalian wildlife, pet, and livestock contribution were less for samples containing ≤394 org/100 ml than for samples containing >394 org/100 ml. But as with runoff vs. non-runoff analysis, the differences were not statistically significant for α=0.05. Segment 0806 had a total of 258 *E. coli* isolates from samples with ≤394 org/100 ml and 88 isolates from samples with >394 org/100ml, for a total of 346 isolates.

Temporal contributions of *E. coli* isolates by the various categories were analyzed and graphed in order to identify differences between sampling events and possibly determine whether or not there were temporal patterns present (Figure 3-3.). The categorical contributions results for Segment 0806 did not appear to contain any strong seasonal patterns and variations appeared to be more random than systematically associated with time.

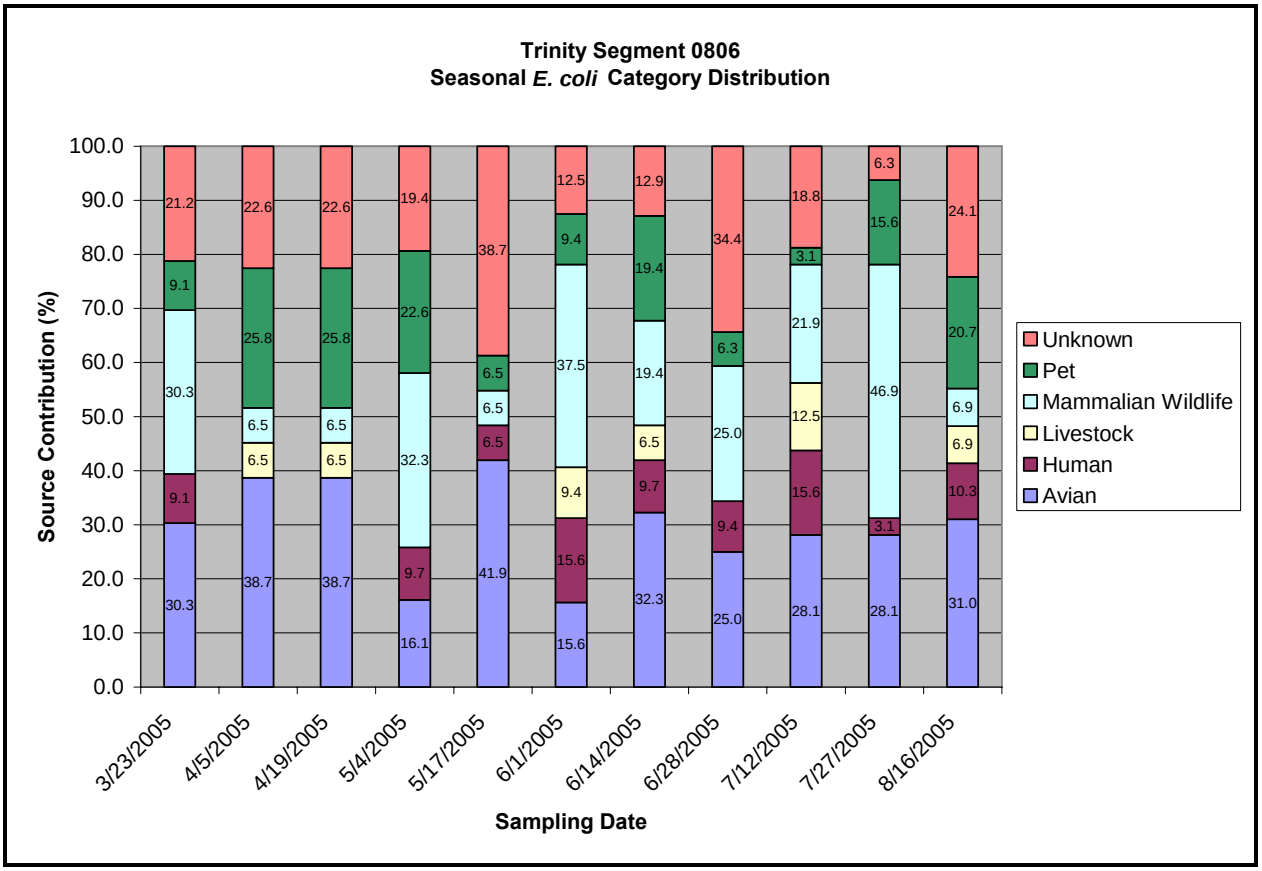

Figure 3-3. Segment 0806 temporal *E. coli* category distribution.

3.2.2.1.1 Station 18459- Northside Drive (Tarrant County)

Station 18459 results were based on 116 isolates. The highest contributor of *E. coli* contamination at the uppermost station, 18459, was found to be avian in nature with a 25.0% contribution (Figure 3-4; Table 3-9). Mammalian wildlife was the next highest contributor at 23.3%, followed by the unknown category with 19.8%. The human, pet, and livestock categories made up the remaining 32%. The source results for station 18459 were found to be similar to the overall segment distribution. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

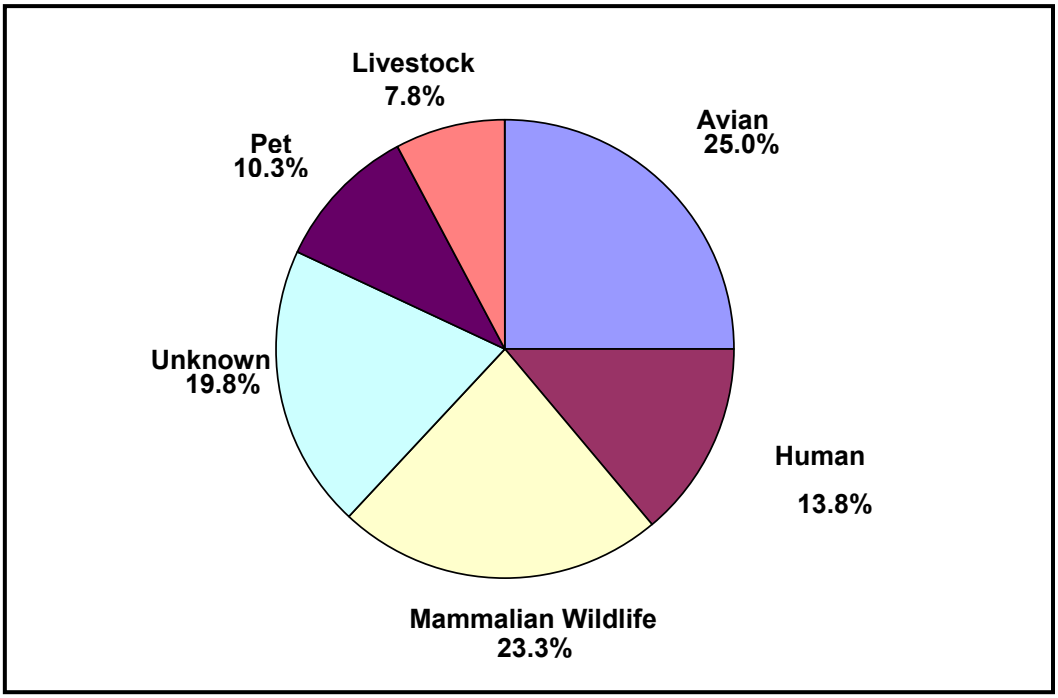

Figure 3-4. *E. coli* source characterization for station 18459 under all conditions.

Table 3-9. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 18459.

Station 18459					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	22	19.0	11.3	26.6
Avian	Waterfowl	7	6.0	1.4	10.7
Avian	**Subtotal**	**29**	**25.0**	**16.5**	**33.5**
Human	Sewage	2	1.7	-0.8	4.3
Human	Wastewater	14	12.1	5.7	18.5
Human	**Subtotal**	**16**	**13.8**	**7.0**	**20.6**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	4	3.4	-0.1	7.0
Livestock	Donkey	0	0.0	0.0	0.0
Livestock	Equine	1	0.9	-0.9	2.7
Livestock	Goat	1	0.9	-0.9	2.7
Livestock	Horse	3	2.6	-0.5	5.7
Livestock	**Subtotal**	**9**	**7.8**	**2.5**	**13.0**
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	0	0.0	0.0	0.0
Mammalian Wildlife	Rabbit	1	0.9	-0.9	2.7
Mammalian Wildlife	Raccoon	8	6.9	1.9	11.9
Mammalian Wildlife	Rodent	15	12.9	6.4	19.5
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	3	2.6	-0.5	5.7
Mammalian Wildlife	**Subtotal**	**27**	**23.3**	**15.0**	**31.6**
Pet	Canine	4	3.4	-0.1	7.0
Pet	Cat	0	0.0	0.0	0.0
Pet	Dog	8	6.9	1.9	11.9
Pet	Feline	0	0.0	0.0	0.0
Pet	**Subtotal**	**12**	**10.3**	**4.4**	**16.3**
Unknown	Unknown	23	19.8	12.0	27.6
Unknown	**Subtotal**	**23**	**19.8**	**12.0**	**27.6**
	Total	**116**	**100.0**		

3.2.2.1.2 Station 10938- Beach Street (Tarrant County)

Station 10938 results were based on 116 isolates. The highest contributors of *E. coli* contamination at station 10938 were the avian and unknown categories, both with 26.7% apiece (Figure 3-5; Table 3-10). Mammalian wildlife was next, representing 18.1% of the contribution. Following wildlife, the pet population was fourth in total contribution, with approximately 16% of the total. The human and livestock populations represented the lowest contributors, with 12.1% and 0.9%, respectively. Compared to the overall segment distribution, the results for station 10938 were again found to be similar. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

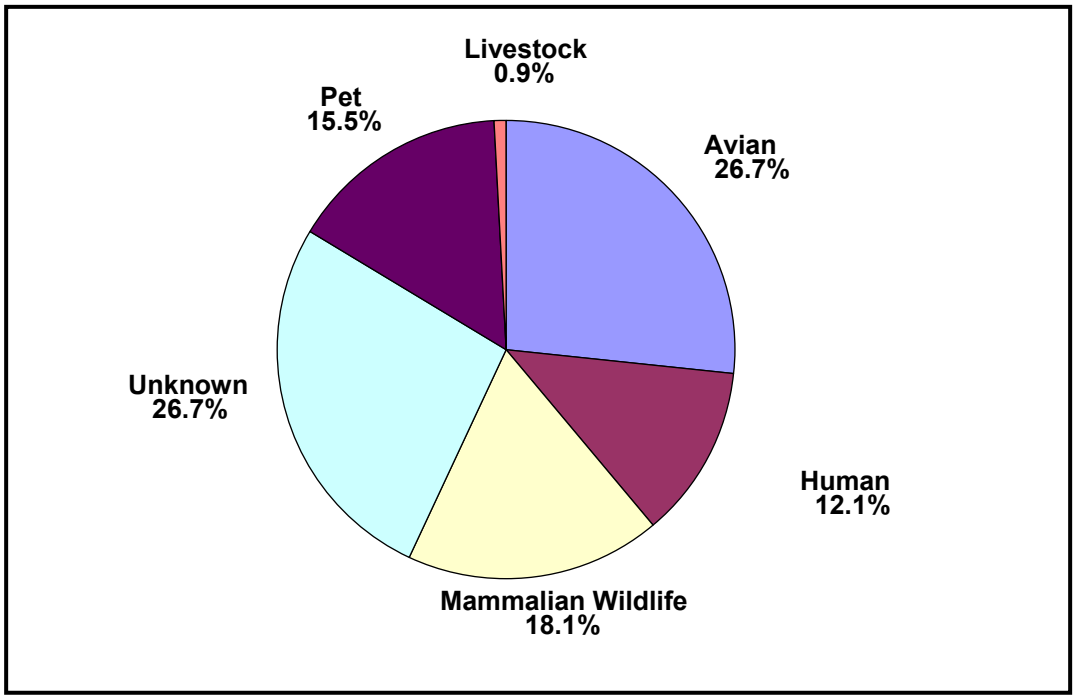

Figure 3-5. *E. coli* source characterization for station 10938 under all conditions.

Table 3-10. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 10938.

Station 10938					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	28	24.1	15.8	32.5
Avian	Waterfowl	3	2.6	-0.5	5.7
Avian	**Subtotal**	**31**	**26.7**	**18.1**	**35.4**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	14	12.1	5.7	18.5
Human	**Subtotal**	**14**	**12.1**	**5.7**	**18.5**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	1	0.9	-0.9	2.7
Livestock	Donkey	0	0.0	0.0	0.0
Livestock	Equine	0	0.0	0.0	0.0
Livestock	Goat	0	0.0	0.0	0.0
Livestock	Horse	0	0.0	0.0	0.0
Livestock	**Subtotal**	**1**	**0.9**	**-0.9**	**2.7**
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	2	1.7	-0.8	4.3
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	8	6.9	1.9	11.9
Mammalian Wildlife	Rodent	10	8.6	3.1	14.1
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	1	0.9	-0.9	2.7
Mammalian Wildlife	**Subtotal**	**21**	**18.1**	**10.6**	**25.7**
Pet	Canine	2	1.7	-0.8	4.3
Pet	Cat	2	1.7	-0.8	4.3
Pet	Dog	13	11.2	5.0	17.4
Pet	Feline	1	0.9	-0.9	2.7
Pet	**Subtotal**	**18**	**15.5**	**8.4**	**22.6**
Unknown	Unknown	31	26.7	18.1	35.4
Unknown	**Subtotal**	**31**	**26.7**	**18.1**	**35.4**
	Total	**116**	**100.0**		

3.2.2.1.3 Station 16120- Handley-Ederville (Tarrant County)

Station 16120 results were based on 114 isolates. The highest contributor of *E. coli* contamination at station 16120 was the avian category, representing 32.5 % of the total (Figure 3-6; Table 3-11). The non-waterfowl species contributed 27.2% of the total station concentration, equaling the mammalian wildlife, the second highest category. This category was also once again led by the rodent population, with a little over 13% of the total. The top two categorical contributors were followed by the unknown category with 15.8%. The pet, human, and livestock contributions, respectively, were the lowest contributors of *E. coli* at station 16120. Compared to the overall segment distribution, the results for station 16120 were very similar to the overall segment distribution. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

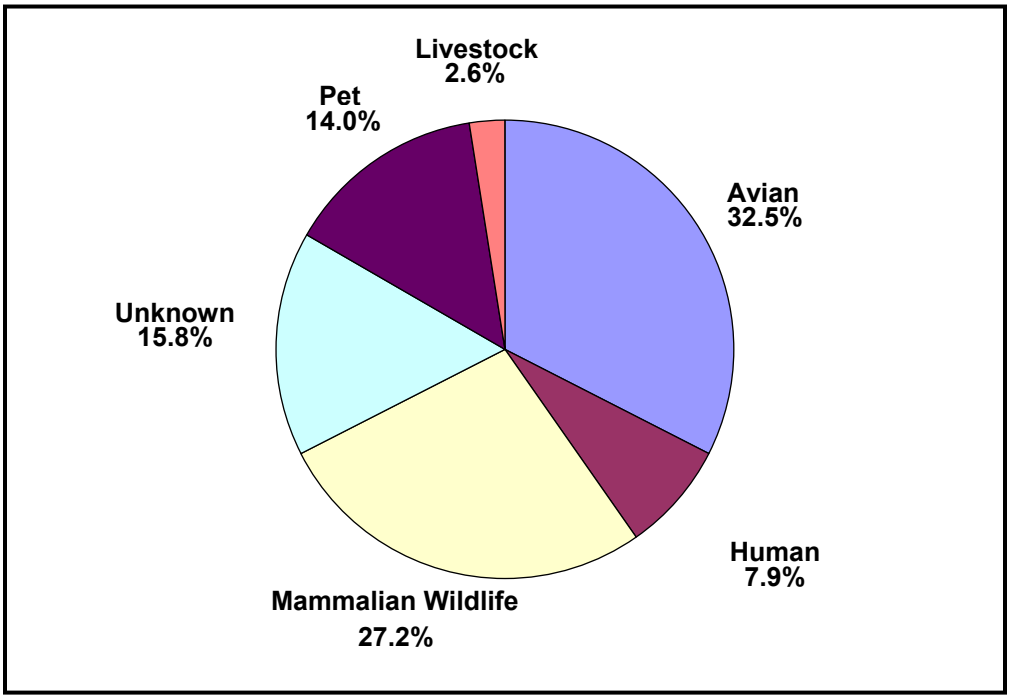

Figure 3-6. *E. coli* source characterization for station 16120 under all conditions.

Table 3-11. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 16120.

Station 16120					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	31	27.2	18.5	35.9
Avian	Waterfowl	6	5.3	0.9	9.6
Avian	**Subtotal**	**37**	**32.5**	**23.3**	**41.6**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	9	7.9	2.6	13.2
Human	**Subtotal**	**9**	**7.9**	**2.6**	**13.2**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	0	0.0	0.0	0.0
Livestock	Donkey	0	0.0	0.0	0.0
Livestock	Equine	0	0.0	0.0	0.0
Livestock	Goat	0	0.0	0.0	0.0
Livestock	Horse	3	2.6	-0.5	5.8
Livestock	**Subtotal**	**3**	**2.6**	**-0.5**	**5.8**
Mammalian Wildlife	Armadillo	2	1.8	-0.8	4.3
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	4	3.5	-0.1	7.1
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	7	6.1	1.4	10.8
Mammalian Wildlife	Rodent	15	13.2	6.5	19.8
Mammalian Wildlife	Skunk	3	2.6	-0.5	5.8
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**31**	**27.2**	**18.5**	**35.9**
Pet	Canine	1	0.9	-1.0	2.7
Pet	Cat	4	3.5	-0.1	7.1
Pet	Dog	10	8.8	3.2	14.3
Pet	Feline	1	0.9	-1.0	2.7
Pet	**Subtotal**	**16**	**14.0**	**7.2**	**20.8**
Unknown	Unknown	18	15.8	8.6	22.9
Unknown	**Subtotal**	**18**	**15.8**	**8.6**	**22.9**
	Total	**114**	**100.0**		

3.2.2.2 Trinity Segment 0841

The Lower West Fork Trinity River (Segment 0841) results were based on 342 isolates collected from stations 17669, 11081, and 11089. The overall *E. coli* source contribution for Segment 0841 was led by the avian category, representing 27.8% of the total, followed by the human contribution, which made up 20.5% (Figure 3-7; Table 3-12). The unknown category made up 18.1% of the total segment contribution, followed closely by mammalian wildlife. Within the wildlife category rodent and raccoon were the dominant contributors. The pet and livestock categories were found to be the lowest contributors of *E. coli* in this particular segment. Overall, sources of *E. coli* in Segment 0841 were found to be essentially the same as the results from upstream Segment 0806.

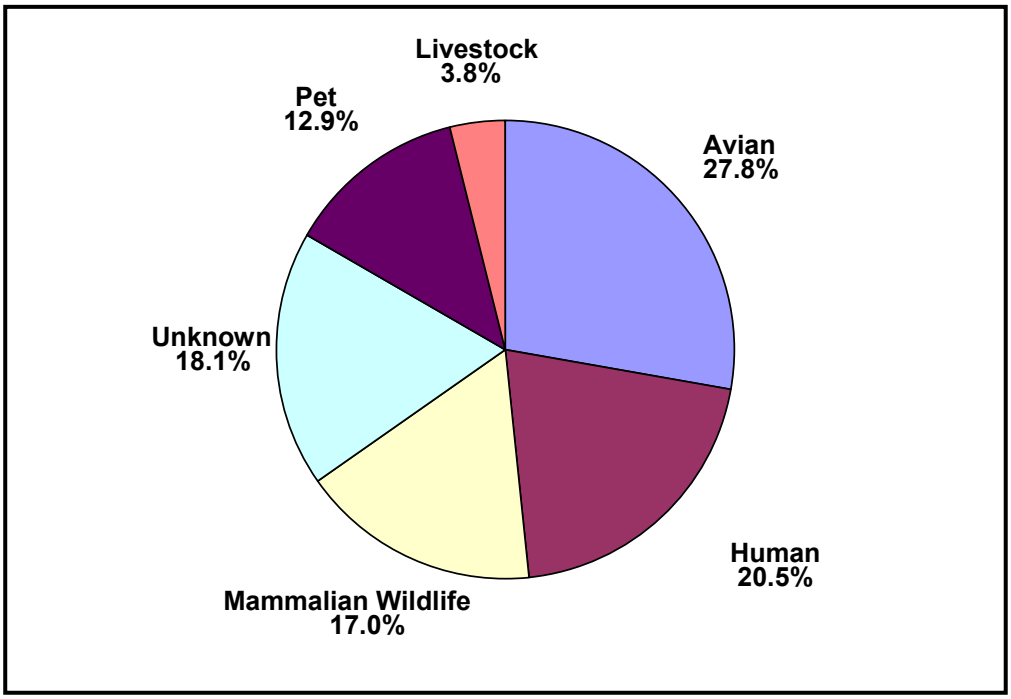

Figure 3-7. *E. coli* source characterization for Segment 0841 under all conditions.

Runoff vs. non-runoff source contributions were not found to be significantly different (α=0.05) based on *E. coli* source contributions (Table 3-13). As found in Segment 0806, some differences in source contributions that are not statistically significant can be observed in the data. Avian and pet contributions increased from non-runoff to runoff events, and mammalian wildlife and the unknown category decreased from non-runoff to runoff events. Segment 0841had a total of 187 non-runoff influenced isolates and 102 runoff influenced isolates, for a total of 289 isolates. The remaining 53 isolates were collected during events that could not be, definitively, placed in either the non-runoff or runoff categories. Therefore, as stated earlier in the results background information, the indefinite isolates were excluded from this particular analysis.

Table 3-12. Overall *E. coli* source characterization and 95% confidence interval (CI) range for Segment 0841.

Segment 0841					
Category	**Source**	**Isolate #**	**Contribution (%)**	**95% CI Range**	
Avian	Avian	78	22.8	14.58	31.03
Avian	Waterfowl	17	5.0	0.71	9.23
Avian	**Subtotal**	**95**	**27.8**	**19.00**	**36.56**
Human	Sewage	0	0.0	0.00	0.00
Human	Wastewater	70	20.5	12.56	28.38
Human	**Subtotal**	**70**	**20.5**	**12.56**	**28.38**
Livestock	Bison	0	0.0	0.00	0.00
Livestock	Bovine	6	1.8	-0.82	4.33
Livestock	Donkey	0	0.0	0.00	0.00
Livestock	Equine	3	0.9	-0.95	2.70
Livestock	Goat	0	0.0	0.00	0.00
Livestock	Horse	4	1.2	-0.94	3.28
Livestock	**Subtotal**	**13**	**3.8**	**0.05**	**7.55**
Mammalian Wildlife	Armadillo	0	0.0	0.00	0.00
Mammalian Wildlife	Coyote	2	0.6	-0.91	2.08
Mammalian Wildlife	Deer	1	0.3	-0.77	1.35
Mammalian Wildlife	Opossum	3	0.9	-0.95	2.70
Mammalian Wildlife	Rabbit	0	0.0	0.00	0.00
Mammalian Wildlife	Raccoon	24	7.0	2.01	12.02
Mammalian Wildlife	Rodent	25	7.3	2.21	12.41
Mammalian Wildlife	Skunk	3	0.9	-0.95	2.70
Mammalian Wildlife	Squirrel	0	0.0	0.00	0.00
Mammalian Wildlife	**Subtotal**	**58**	**17.0**	**9.60**	**24.31**
Pet	Canine	5	1.5	-0.89	3.81
Pet	Cat	4	1.2	-0.94	3.28
Pet	Dog	34	9.9	4.08	15.81
Pet	Feline	1	0.3	-0.77	1.35
Pet	**Subtotal**	**44**	**12.9**	**6.30**	**19.43**
Unknown	Unknown	62	18.1	10.58	25.68
Unknown	**Subtotal**	**62**	**18.1**	**10.58**	**25.68**
	Total	**342**	**100.0**		

Table 3-13. Runoff vs. non-runoff influenced *E. coli* source characterization for Segment 0841. (CI = confidence interval)

Segment 0841		Non-Runoff				Runoff			
Category	Source	Isolate #	Contribution (%)	95% CI Range		Isolate #	Contribution (%)	95% CI Range	
Avian	Avian	37	19.8	12.0	27.6	28	27.5	18.7	36.2
Avian	Waterfowl	9	4.8	0.6	9.0	5	4.9	0.7	9.1
Avian	**Subtotal**	**46**	**24.6**	**16.2**	**33.0**	**33**	**32.4**	**23.2**	**41.5**
Human	Sewage	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Human	Wastewater	40	21.4	13.4	29.4	20	19.6	11.8	27.4
Human	**Subtotal**	**40**	**21.4**	**13.4**	**29.4**	**20**	**19.6**	**11.8**	**27.4**
Livestock	Bison	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Bovine	2	1.1	-0.9	3.1	4	3.9	0.1	7.7
Livestock	Donkey	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Equine	3	1.6	-0.9	4.1	0	0.0	0.0	0.0
Livestock	Goat	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Horse	3	1.6	-0.9	4.1	1	1.0	-1.0	2.9
Livestock	**Subtotal**	**8**	**4.3**	**0.3**	**8.2**	**5**	**4.9**	**0.7**	**9.1**
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	2	1.1	-0.9	3.1	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0	1	1.0	-1.0	2.9
Mammalian Wildlife	Opossum	1	0.5	-0.9	2.0	0	0.0	0.0	0.0
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	15	8.0	2.7	13.3	4	3.9	0.1	7.7
Mammalian Wildlife	Rodent	17	9.1	3.5	14.7	7	6.9	1.9	11.8
Mammalian Wildlife	Skunk	2	1.1	-0.9	3.1	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**37**	**19.8**	**12.0**	**27.6**	**12**	**11.8**	**5.4**	**18.1**
Pet	Canine	2	1.1	-0.9	3.1	2	2.0	-0.8	4.7
Pet	Cat	1	0.5	-0.9	2.0	2	2.0	-0.8	4.7
Pet	Dog	17	9.1	3.5	14.7	13	12.7	6.2	19.3
Pet	Feline	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Pet	**Subtotal**	**20**	**10.7**	**4.6**	**16.8**	**17**	**16.7**	**9.4**	**24.0**
Unknown	Unknown	36	19.3	11.5	27.0	15	14.7	7.8	21.6
Unknown	**Subtotal**	**36**	**19.3**	**11.5**	**27.0**	**15**	**14.7**	**7.8**	**21.6**
	Total	**187**	**100**			**102**	**100**		

E. coli source contributions for samples containing ≤394 org/100ml were not found to be significantly different (α=0.05) from samples containing >394 org/100ml (Table 3-14). Again, some non-statistically significant differences may be observed. Avian contributions are higher for the samples containing >394 org/100ml, while mammalian wildlife and unknown source contributions are higher for samples containing ≤394 org/100ml. Segment 0841 had a total of 225 isolates from samples with ≤394 org/100ml and 117 isolates from samples with >394 org/100ml, for a total of 342 isolates.

Table 3-14. *E. coli* source characterization for samples containing ≤394 org/100ml vs. those with >394 org/100ml for Segment 0841. (CI = confidence interval)

Segment 0841		Samples ≤ 394 org / 100ml				Samples > 394 org / 100ml			
Category	Source	Isolate #	Contribution (%)	95% CI Range		Isolate #	Contribution (%)	95% CI Range	
Avian	Avian	45	20.0	12.2	27.8	33	28.2	19.4	37.0
Avian	Waterfowl	11	4.9	0.7	9.1	6	5.1	0.8	9.5
Avian	**Subtotal**	**56**	**24.9**	**16.4**	**33.4**	**39**	**33.3**	**24.1**	**42.6**
Human	Sewage	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Human	Wastewater	47	20.9	12.9	28.9	23	19.7	11.9	27.4
Human	**Subtotal**	**47**	**20.9**	**12.9**	**28.9**	**23**	**19.7**	**11.9**	**27.4**
Livestock	Bison	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Bovine	2	0.9	-1.0	2.7	4	3.4	-0.1	7.0
Livestock	Donkey	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Equine	3	1.3	-0.9	3.6	0	0.0	0.0	0.0
Livestock	Goat	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Livestock	Horse	3	1.3	-0.9	3.6	1	0.9	-0.9	2.7
Livestock	**Subtotal**	**8**	**3.6**	**-0.1**	**7.2**	**5**	**4.3**	**0.3**	**8.2**
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	2	0.9	-1.0	2.7	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0	1	0.9	-0.9	2.7
Mammalian Wildlife	Opossum	3	1.3	-0.9	3.6	0	0.0	0.0	0.0
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	17	7.6	2.4	12.7	7	6.0	1.3	10.6
Mammalian Wildlife	Rodent	18	8.0	2.7	13.3	7	6.0	1.3	10.6
Mammalian Wildlife	Skunk	3	1.3	-0.9	3.6	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**43**	**19.1**	**11.4**	**26.8**	**15**	**12.8**	**6.3**	**19.4**
Pet	Canine	3	1.3	-0.9	3.6	2	1.7	-0.8	4.2
Pet	Cat	2	0.9	-1.0	2.7	2	1.7	-0.8	4.2
Pet	Dog	22	9.8	4.0	15.6	12	10.3	4.3	16.2
Pet	Feline	0	0.0	0.0	0.0	1	0.9	-0.9	2.7
Pet	**Subtotal**	**27**	**12.0**	**5.6**	**18.4**	**17**	**14.5**	**7.6**	**21.4**
Unknown	Unknown	44	19.6	11.8	27.3	18	15.4	8.3	22.5
Unknown	**Subtotal**	**44**	**19.6**	**11.8**	**27.3**	**18**	**15.4**	**8.3**	**22.5**
	Total	**225**	**100.0**			**117**	**100.0**		

Temporal contributions of *E. coli* isolates by the various categories were analyzed and graphed in order to identify differences between sampling events and possibly determine whether or not there were temporal patterns present (Figure 3-8). The categorical contributions for Segment 0841 did not exhibit any strong seasonal patterns, and variations appear to be more random than systematically associated with time.

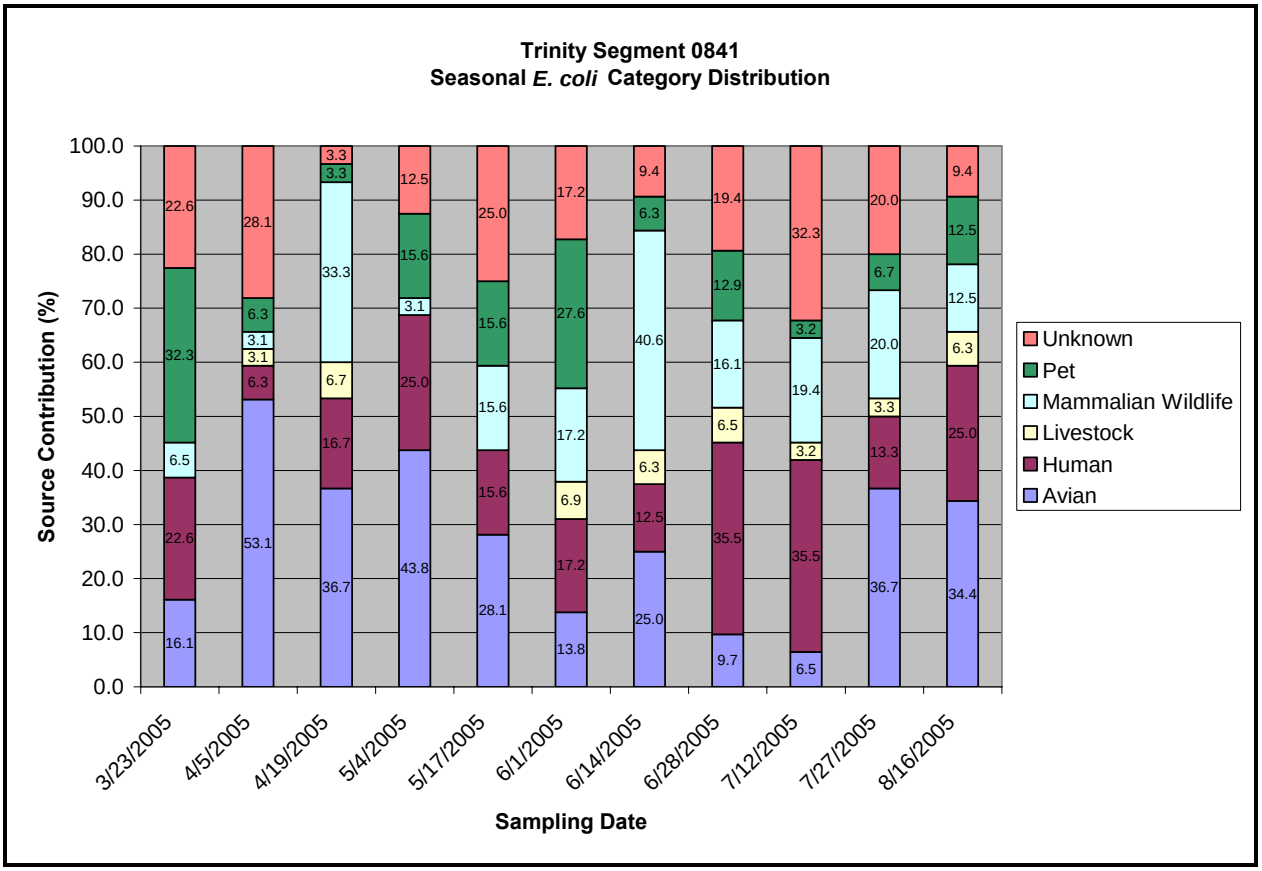

Figure 3-8. Segment 0841 temporal *E. coli* category distribution.

3.2.2.2.1 Station 17669- Roy Orr (Dallas County)

Station 17669 results were based on 113 isolates. The largest contributor of *E. coli* at station 17669 was due to avian influence, which made up 28.3% of the total (Figure 3-9; Table 3-15). Human influence was next with 19.5%, while mammalian wildlife contributed 18.6%.At station 17669, the raccoon contribution, 8.0%, surpassed the rodent contribution, which contributed 7.1%. The unknown category was the fourth highest contributor, followed by pets and livestock, respectively. The pet category was once again led by the dogs with 10.6%, and the livestock category was found to be co-dominated again by bovine and equine species. The results for station 17669 were found to be very similar to the overall segment findings. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

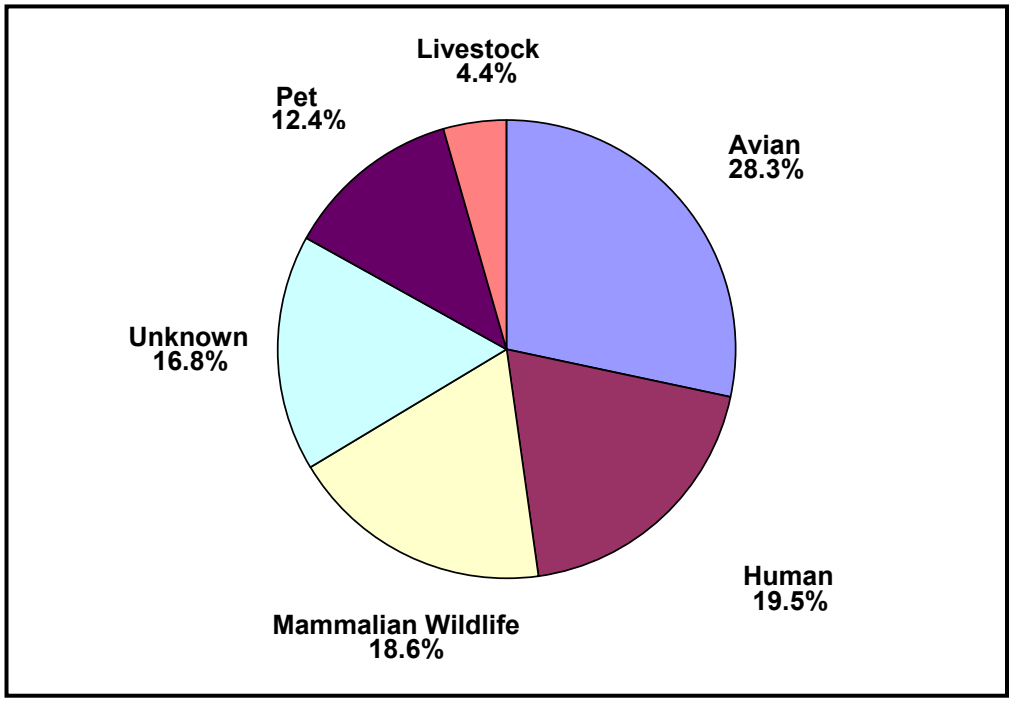

Figure 3-9. *E. coli* source characterization for station 17669 under all conditions.

Table 3-15. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 17669.

Station 17669					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	25	22.1	14.0	30.3
Avian	Waterfowl	7	6.2	1.5	10.9
Avian	**Subtotal**	**32**	**28.3**	**19.5**	**37.1**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	22	19.5	11.7	27.2
Human	**Subtotal**	**22**	**19.5**	**11.7**	**27.2**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	2	1.8	-0.8	4.4
Livestock	Donkey	0	0.0	0.0	0.0
Livestock	Equine	2	1.8	-0.8	4.4
Livestock	Goat	0	0.0	0.0	0.0
Livestock	Horse	1	0.9	-1.0	2.7
Livestock	**Subtotal**	**5**	**4.4**	**0.4**	**8.5**
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	1	0.9	-1.0	2.7
Mammalian Wildlife	Deer	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	1	0.9	-1.0	2.7
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	9	8.0	2.7	13.3
Mammalian Wildlife	Rodent	8	7.1	2.1	12.1
Mammalian Wildlife	Skunk	2	1.8	-0.8	4.4
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**21**	**18.6**	**11.0**	**26.2**
Pet	Canine	0	0.0	0.0	0.0
Pet	Cat	1	0.9	-1.0	2.7
Pet	Dog	12	10.6	4.6	16.7
Pet	Feline	1	0.9	-1.0	2.7
Pet	**Subtotal**	**14**	**12.4**	**5.9**	**18.8**
Unknown	Unknown	19	16.8	9.5	24.1
Unknown	**Subtotal**	**19**	**16.8**	**9.5**	**24.1**
	Total	**113**	**100.0**		

3.2.2.2.2 Station 11081- Belt Line Road (Dallas County)

Station 11081 results were based on 115 isolates. At station 11081, avian population was once again the highest contributor of *E. coli* bacteria, representing 31.3% of the total contribution (Figure 3-10; Table 3-16). The next highest source of contamination came from the unknown category with 20.0%. Human addition to the concentration of *E. coli* was third highest with 18.3%. The mammalian wildlife, pet, and livestock contributions represented the three lowest contributors of *E. coli* at this particular station. There were no substantial differences between the overall segment distribution and station 11081. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

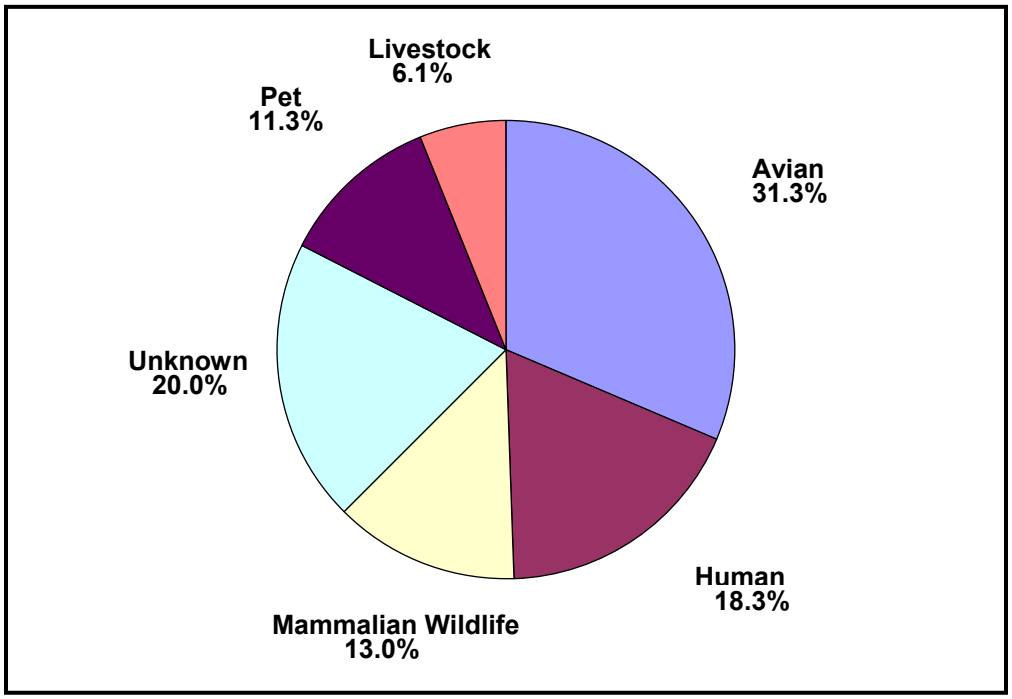

Figure 3-10. *E. coli* source characterization for station 11081 under all conditions.

Table 3-16. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 11081.

Station 11081					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	30	26.1	17.5	34.7
Avian	Waterfowl	6	5.2	0.9	9.6
Avian	**Subtotal**	**36**	**31.3**	**22.2**	**40.4**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	21	18.3	10.7	25.8
Human	**Subtotal**	**21**	**18.3**	**10.7**	**25.8**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	4	3.5	-0.1	7.1
Livestock	Donkey	0	0.0	0.0	0.0
Livestock	Equine	0	0.0	0.0	0.0
Livestock	Goat	0	0.0	0.0	0.0
Livestock	Horse	3	2.6	-0.5	5.7
Livestock	**Subtotal**	**7**	**6.1**	**1.4**	**10.8**
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	1	0.9	-1.0	2.7
Mammalian Wildlife	Deer	1	0.9	-1.0	2.7
Mammalian Wildlife	Opossum	0	0.0	0.0	0.0
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	6	5.2	0.9	9.6
Mammalian Wildlife	Rodent	7	6.1	1.4	10.8
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**15**	**13.0**	**6.4**	**19.6**
Pet	Canine	2	1.7	-0.8	4.3
Pet	Cat	3	2.6	-0.5	5.7
Pet	Dog	8	7.0	2.0	11.9
Pet	Feline	0	0.0	0.0	0.0
Pet	**Subtotal**	**13**	**11.3**	**5.1**	**17.5**
Unknown	Unknown	23	20.0	12.2	27.8
Unknown	**Subtotal**	**23**	**20.0**	**12.2**	**27.8**
	Total	**115**	**100.0**		

3.2.2.2.3 Station 11089- West Loop 12 (Dallas County)

Station 11089 results were based on 114 isolates. Avian and human populations shared the largest contribution of *E. coli* at station 11089 with 23.7% each, while the mammalian wildlife contribution represented 19.3% (Figure 3-11; Table 3-17). The unknown, pet, and livestock populations, respectively, represented the lowest contributors. Compared to the overall segment, the results for this station were found to be similar. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

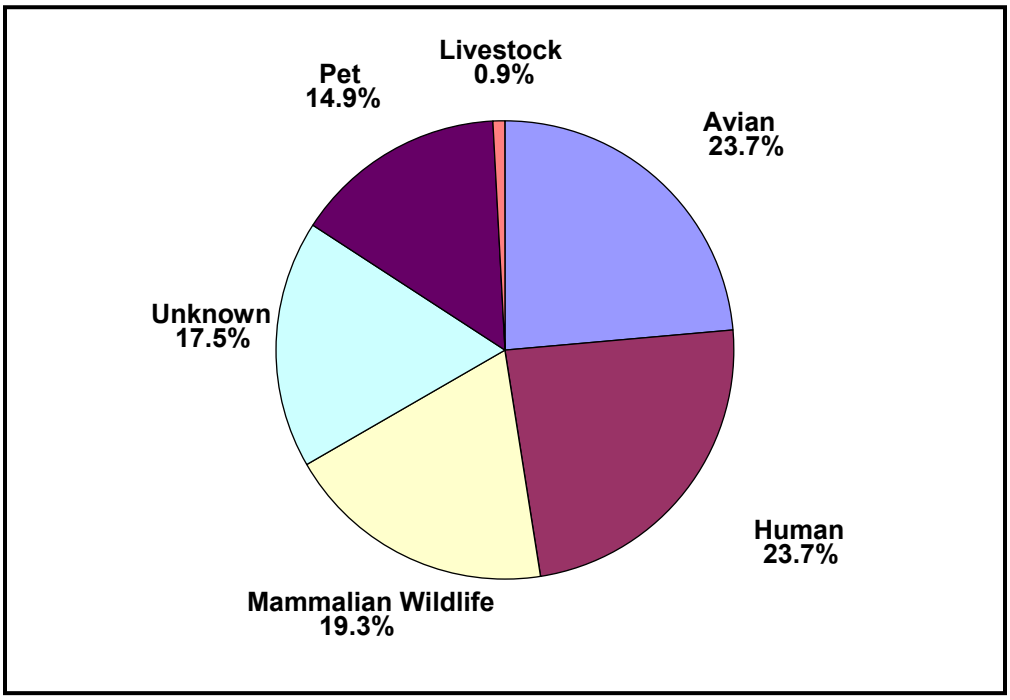

Figure 3-11. *E. coli* source characterization for station 11089 under all conditions.

Table 3-17. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 11089.

Station 11089					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	23	20.2	12.3	28.0
Avian	Waterfowl	4	3.5	-0.1	7.1
Avian	**Subtotal**	**27**	**23.7**	**15.4**	**32.0**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	27	23.7	15.4	32.0
Human	**Subtotal**	**27**	**23.7**	**15.4**	**32.0**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	0	0.0	0.0	0.0
Livestock	Donkey	0	0.0	0.0	0.0
Livestock	Equine	1	0.9	-1.0	2.7
Livestock	Goat	0	0.0	0.0	0.0
Livestock	Horse	0	0.0	0.0	0.0
Livestock	**Subtotal**	**1**	**0.9**	**-1.0**	**2.7**
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	2	1.8	-0.8	4.3
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	9	7.9	2.6	13.2
Mammalian Wildlife	Rodent	10	8.8	3.2	14.3
Mammalian Wildlife	Skunk	1	0.9	-1.0	2.7
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**22**	**19.3**	**11.6**	**27.0**
Pet	Canine	3	2.6	-0.5	5.8
Pet	Cat	0	0.0	0.0	0.0
Pet	Dog	14	12.3	5.8	18.7
Pet	Feline	0	0.0	0.0	0.0
Pet	**Subtotal**	**17**	**14.9**	**7.9**	**21.9**
Unknown	Unknown	20	17.5	10.1	25.0
Unknown	**Subtotal**	**20**	**17.5**	**10.1**	**25.0**
	Total	**114**	**100.0**		

3.2.2.3 Trinity Segment 0805

The Upper Trinity River (Segment 0805) results were based on 447 isolates collected from stations 10937, 10934, 10925, and 10924. Overall *E. coli* source contributions for Segment 0805 was led by avian species with 26.0% of the total (Figure 3-12; Table 3-18). Following avian species, the human category was found to contribute 23.7%, while mammalian wildlife contributed 14.3%. The unknown, pet, and livestock species contributions were the lowest in Segment 0805. Because of the length of Segment 0805 (100 miles) and the upstream to downstream transition from urban to rural land use/land cover, only within this segment was there found to be a statistically significant spatial variability in source contributions. Most notably, livestock contributions are significantly greater for the two downstream stations (10925 and 10924) than the two upstream stations (10937 and 10934), while other categories show much smaller, statistically non-significant changes. (The differences in livestock contribution are provided in more detail under individual station discussions.) Overall, sources of *E. coli* in Segment 0805 were found to be essentially the same as the results from upstream Segments 0806 and 0841.

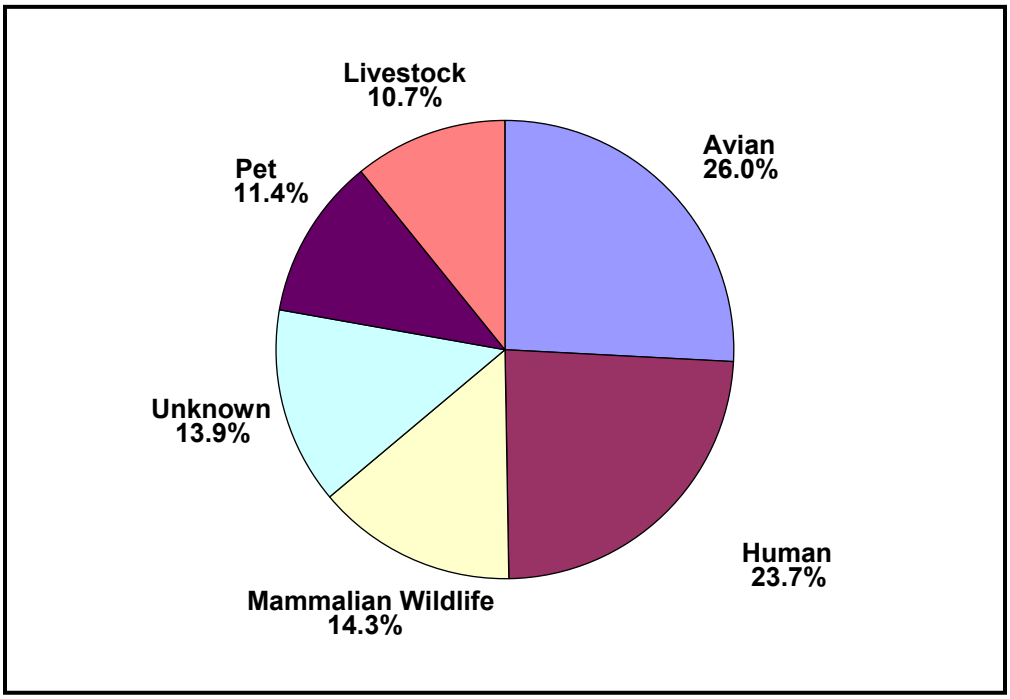

Figure 3-12. *E. coli* source characterization for Segment 0805 under all conditions.

Runoff vs. non-runoff events were not found to be significantly different (α=0.05) based on *E. coli* source contributions (Table 3-19). While not statistically significant, mammalian wildlife contribution appeared to decrease from non-runoff to runoff events, while pet contribution increased. Segment 0805 had a total of 282 non-runoff influenced isolates and 102 runoff influenced isolates for a total of 384 isolates. The remaining 63 isolates were collected

Table 3-18. Overall *E. coli* source characterization and 95% confidence interval (CI) range for Segment 0805.

Segment 0805					
Category	**Source**	**Isolate #**	**Contribution (%)**	**95% CI Range**	
Avian	Avian	99	22.1	14.01	30.29
Avian	Waterfowl	17	3.8	0.05	7.55
Avian	**Subtotal**	**116**	**26.0**	**17.36**	**34.54**
Human	Sewage	0	0.0	0.00	0.00
Human	Wastewater	106	23.7	15.38	32.05
Human	**Subtotal**	**106**	**23.7**	**15.38**	**32.05**
Livestock	Bison	1	0.2	-0.70	1.15
Livestock	Bovine	29	6.5	1.66	11.32
Livestock	Donkey	3	0.7	-0.93	2.27
Livestock	Equine	1	0.2	-0.70	1.15
Livestock	Goat	3	0.7	-0.93	2.27
Livestock	Horse	12	2.7	-0.48	5.85
Livestock	**Subtotal**	**49**	**11.0**	**4.84**	**17.09**
Mammalian Wildlife	Armadillo	3	0.7	-0.93	2.27
Mammalian Wildlife	Coyote	0	0.0	0.00	0.00
Mammalian Wildlife	Deer	1	0.2	-0.70	1.15
Mammalian Wildlife	Opossum	2	0.4	-0.86	1.76
Mammalian Wildlife	Rabbit	1	0.2	-0.70	1.15
Mammalian Wildlife	Raccoon	27	6.0	1.37	10.71
Mammalian Wildlife	Rodent	29	6.5	1.66	11.32
Mammalian Wildlife	Skunk	0	0.0	0.00	0.00
Mammalian Wildlife	Squirrel	0	0.0	0.00	0.00
Mammalian Wildlife	**Subtotal**	**63**	**14.1**	**7.27**	**20.91**
Pet	Canine	6	1.3	-0.91	3.60
Pet	Cat	9	2.0	-0.74	4.77
Pet	Dog	36	8.1	2.72	13.39
Pet	Feline	0	0.0	0.00	0.00
Pet	**Subtotal**	**51**	**11.4**	**5.18**	**17.64**
Unknown	Unknown	62	13.9	7.10	20.64
Unknown	**Subtotal**	**62**	**13.9**	**7.10**	**20.64**
	Total	**447**	**100.0**		

Table 3-19. Runoff vs. non-runoff influenced *E. coli* source characterization for Segment 0805. (CI = confidence interval)

Segment 0805		Non-Runoff				Runoff			
Category	Source	Isolate #	Contribution (%)	95% CI Range		Isolate #	Contribution (%)	95% CI Range	
Avian	Avian	65	23.0	14.8	31.3	20	19.6	11.8	27.4
Avian	Waterfowl	6	2.1	-0.7	5.0	6	5.9	1.3	10.5
Avian	**Subtotal**	**71**	**25.2**	**16.7**	**33.7**	**26**	**25.5**	**16.9**	**34.0**
Human	Sewage	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Human	Wastewater	68	24.1	15.7	32.5	21	20.6	12.7	28.5
Human	**Subtotal**	**68**	**24.1**	**15.7**	**32.5**	**21**	**20.6**	**12.7**	**28.5**
Livestock	Bison	1	0.4	-0.8	1.5	0	0.0	0.0	0.0
Livestock	Bovine	17	6.0	1.4	10.7	8	7.8	2.6	13.1
Livestock	Donkey	3	1.1	-0.9	3.1	0	0.0	0.0	0.0
Livestock	Equine	1	0.4	-0.8	1.5	0	0.0	0.0	0.0
Livestock	Goat	3	1.1	-0.9	3.1	0	0.0	0.0	0.0
Livestock	Horse	6	2.1	-0.7	5.0	3	2.9	-0.4	6.3
Livestock	**Subtotal**	**31**	**11.0**	**4.9**	**17.1**	**11**	**10.8**	**4.7**	**16.9**
Mammalian Wildlife	Armadillo	2	0.7	-0.9	2.4	1	1.0	-1.0	2.9
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	1	0.4	-0.8	1.5	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	2	0.7	-0.9	2.4	0	0.0	0.0	0.0
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0	1	1.0	-1.0	2.9
Mammalian Wildlife	Raccoon	23	8.2	2.8	13.5	3	2.9	-0.4	6.3
Mammalian Wildlife	Rodent	16	5.7	1.1	10.2	6	5.9	1.3	10.5
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**44**	**15.6**	**8.5**	**22.7**	**11**	**10.8**	**4.7**	**16.9**
Pet	Canine	4	1.4	-0.9	3.7	2	2.0	-0.8	4.7
Pet	Cat	5	1.8	-0.8	4.4	4	3.9	0.1	7.7
Pet	Dog	21	7.4	2.3	12.6	10	9.8	4.0	15.6
Pet	Feline	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Pet	**Subtotal**	**30**	**10.6**	**4.6**	**16.7**	**16**	**15.7**	**8.6**	**22.8**
Unknown	Unknown	38	13.5	6.8	20.2	17	16.7	9.4	24.0
Unknown	**Subtotal**	**38**	**13.5**	**6.8**	**20.2**	**17**	**16.7**	**9.4**	**24.0**
	Total	**282**	**100**			**102**	**100**		

during events that could not be placed, definitively, in either the non-runoff or runoff categories; therefore, those isolates were excluded from this particular analysis as explained earlier in the introductory material for the results section.

Avian, pet and unknown contributions were higher for samples containing >394 org/ 100ml than samples containing ≤394 org/ 100ml, and human, livestock and mammalian wildlife were higher for samples containing ≤394 org/ 100ml (Table 3-20). None of these differences, however, were statistically significant at α=0.05. Segment 0805 had a total of 350 *E. coli* isolates from samples with ≤394 org/ 100ml and 97 isolates from samples with >394 org/ 100ml, for a total of 447 isolates.

Table 3-20. *E. coli* source characterization for samples containing ≤394 org/100ml vs. those with >394 org/100ml for Segment 0841. (CI = confidence interval)

Segment 0805		Samples ≤ 394 org / 100ml				Samples > 394 org / 100ml			
Category	Source	Isolate #	Contribution (%)	95% CI Range		Isolate #	Contribution (%)	95% CI Range	
Avian	Avian	71	20.3	12.4	28.2	28	28.9	20.0	37.7
Avian	Waterfowl	12	3.4	-0.1	7.0	5	5.2	0.8	9.5
Avian	**Subtotal**	**83**	**23.7**	**15.4**	**32.1**	**33**	**34.0**	**24.7**	**43.3**
Human	Sewage	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Human	Wastewater	89	25.4	16.9	34.0	17	17.5	10.1	25.0
Human	**Subtotal**	**89**	**25.4**	**16.9**	**34.0**	**17**	**17.5**	**10.1**	**25.0**
Livestock	Bison	1	0.3	-0.8	1.3	0	0.0	0.0	0.0
Livestock	Bovine	26	7.4	2.3	12.6	3	3.1	-0.3	6.5
Livestock	Donkey	3	0.9	-0.9	2.7	0	0.0	0.0	0.0
Livestock	Equine	1	0.3	-0.8	1.3	0	0.0	0.0	0.0
Livestock	Goat	3	0.9	-0.9	2.7	0	0.0	0.0	0.0
Livestock	Horse	9	2.6	-0.5	5.7	3	3.1	-0.3	6.5
Livestock	**Subtotal**	**43**	**12.3**	**5.9**	**18.7**	**6**	**6.2**	**1.5**	**10.9**
Mammalian Wildlife	Armadillo	2	0.6	-0.9	2.0	1	1.0	-0.9	3.0
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	1	0.3	-0.8	1.3	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	2	0.6	-0.9	2.0	0	0.0	0.0	0.0
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0	1	1.0	-0.9	3.0
Mammalian Wildlife	Raccoon	24	6.9	1.9	11.8	3	3.1	-0.3	6.5
Mammalian Wildlife	Rodent	23	6.6	1.7	11.4	6	6.2	1.5	10.9
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**52**	**14.9**	**7.9**	**21.8**	**11**	**11.3**	**5.1**	**17.6**
Pet	Canine	5	1.4	-0.9	3.8	1	1.0	-0.9	3.0
Pet	Cat	5	1.4	-0.9	3.8	4	4.1	0.2	8.0
Pet	Dog	27	7.7	2.5	12.9	9	9.3	3.6	15.0
Pet	Feline	0	0.0	0.0	0.0	0	0.0	0.0	0.0
Pet	**Subtotal**	**37**	**10.6**	**4.5**	**16.6**	**14**	**14.4**	**7.5**	**21.3**
Unknown	Unknown	46	13.1	6.5	19.8	16	16.5	9.2	23.8
Unknown	**Subtotal**	**46**	**13.1**	**6.5**	**19.8**	**16**	**16.5**	**9.2**	**23.8**
	Total	**350**	**100.0**			**97**	**100.0**		

Temporal contributions of *E. coli* isolates by the various categories were analyzed and graphed in order to identify differences between sampling events and possibly determine whether or not there were temporal patterns present (Figure 3-13). The categorical contributions for Segment 0805 did not exhibit any strong seasonal patterns, and variations appear to be more random than systematically associated with time.

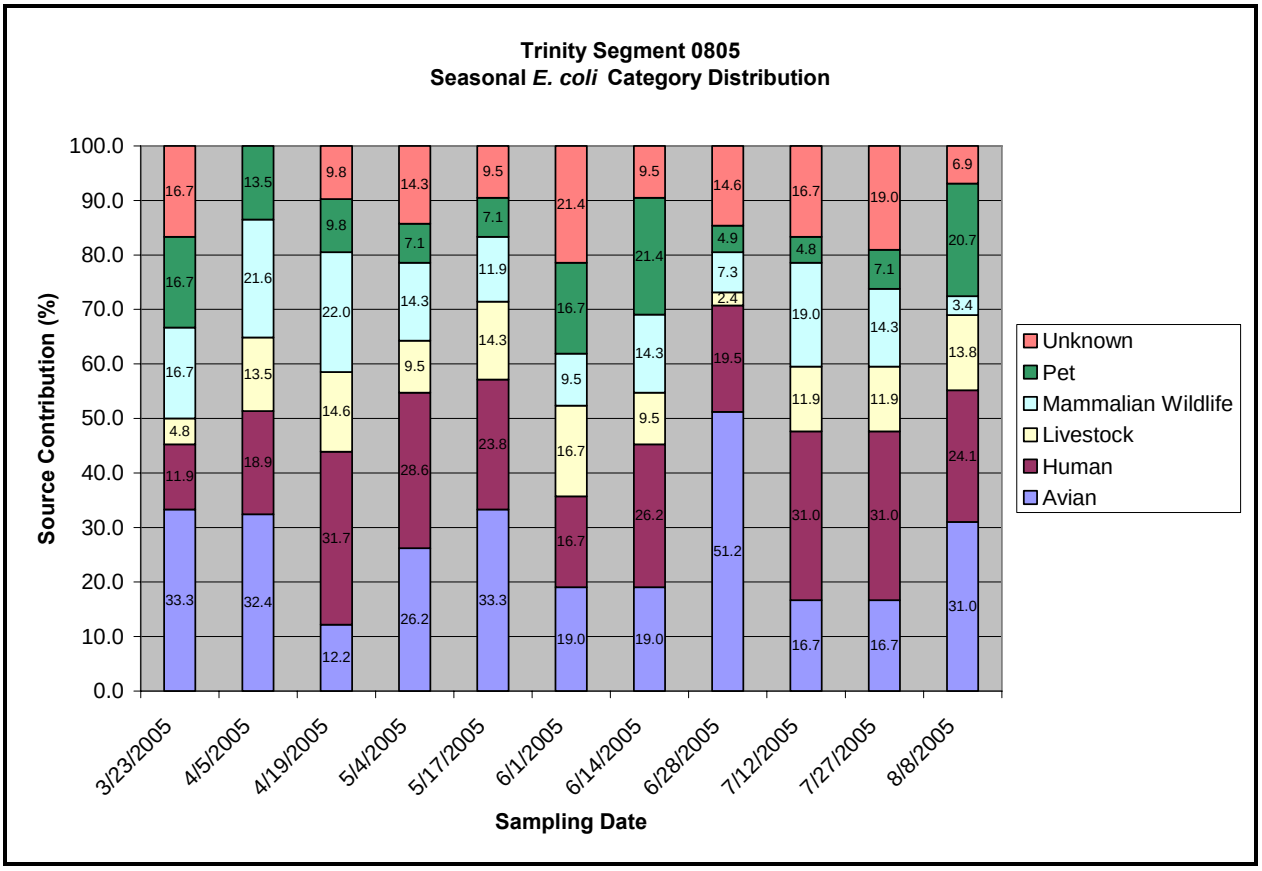

Figure 3-13. Segment 0805 temporal *E. coli* category distribution.

3.2.2.3.1 Station 10937- Mockingbird Lane (Dallas County)

Station 10937 results were based on 116 isolates. The largest contributor of *E. coli* contamination at station 10937 was from the human category, representing 28.4% of the total contribution (Figure 3-14; Table 3-21). Avian species contributed 25.0%, followed by mammalian wildlife with 18.1%. Unknown and pet categories were found to be the lowest contributors at this station 10937. Livestock were not represented at this particular station. When compared to the overall segment distribution, the results for station 10937 were substantially lower for the livestock category, which failed to be represented. The result is a 10.7% decrease from the average segment livestock contribution. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

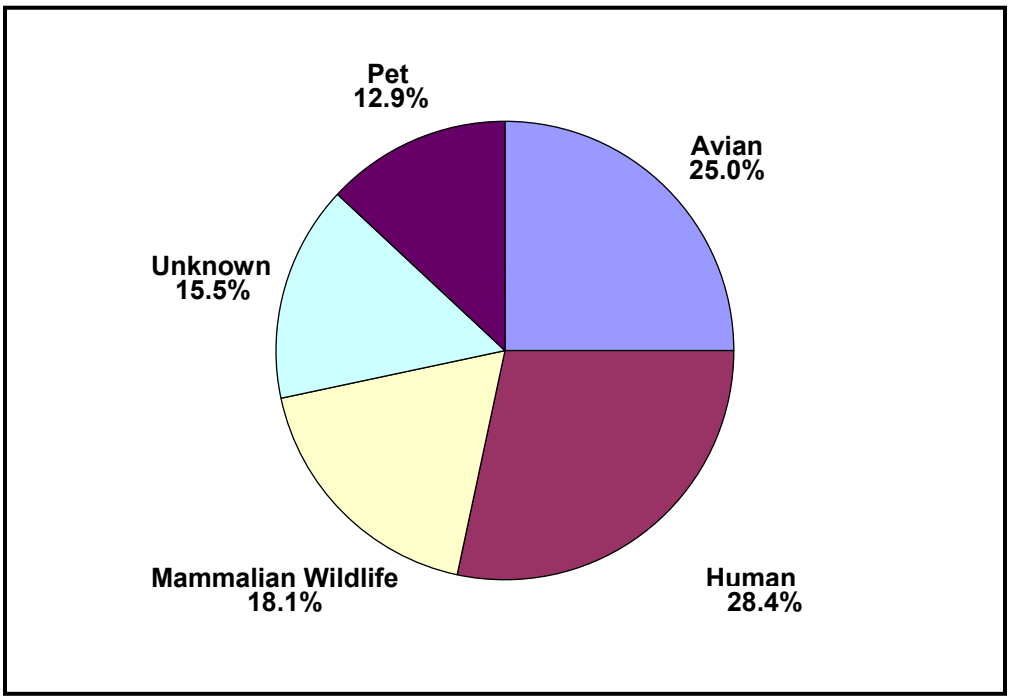

Figure 3-14. *E. coli* category characterization for station 10937 under all conditions.

Table 3-21. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 10937.

Station 10937					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	24	20.7	12.8	28.6
Avian	Waterfowl	5	4.3	0.3	8.3
Avian	**Subtotal**	**29**	**25.0**	**16.5**	**33.5**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	33	28.4	19.6	37.3
Human	**Subtotal**	**33**	**28.4**	**19.6**	**37.3**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	0	0.0	0.0	0.0
Livestock	Donkey	0	0.0	0.0	0.0
Livestock	Equine	0	0.0	0.0	0.0
Livestock	Goat	0	0.0	0.0	0.0
Livestock	Horse	0	0.0	0.0	0.0
Livestock	**Subtotal**	**0**	**0.0**	**0.0**	**0.0**
Mammalian Wildlife	Armadillo	1	0.9	-0.9	2.7
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	0	0.0	0.0	0.0
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	8	6.9	1.9	11.9
Mammalian Wildlife	Rodent	12	10.3	4.4	16.3
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**21**	**18.1**	**10.6**	**25.7**
Pet	Canine	1	0.9	-0.9	2.7
Pet	Cat	1	0.9	-0.9	2.7
Pet	Dog	13	11.2	5.0	17.4
Pet	Feline	0	0.0	0.0	0.0
Pet	**Subtotal**	**15**	**12.9**	**6.4**	**19.5**
Unknown	Unknown	18	15.5	8.4	22.6
Unknown	**Subtotal**	**18**	**15.5**	**8.4**	**22.6**
	Total	**116**	**100.0**		

3.2.2.3.2 Station 10934- South Loop 12 (Dallas County)

Station 10934 results were based on 116 isolates. Thirty-one percent contribution of avian *E. coli* represented the highest percentage at station 10934 (Figure 3-15; Table 3-22). The next highest percentage was from the human category with 21.6%, while the unknown category was the third highest contributor with an average of 18.1%. Pet, mammalian wildlife, and livestock populations contributed the least.

Compared with the overall segment, the avian contribution was slightly higher at station 10934, 31.0% compared to the overall segment average of 26.0%. Also, the livestock contribution was 5.5% lower than the overall segment average. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

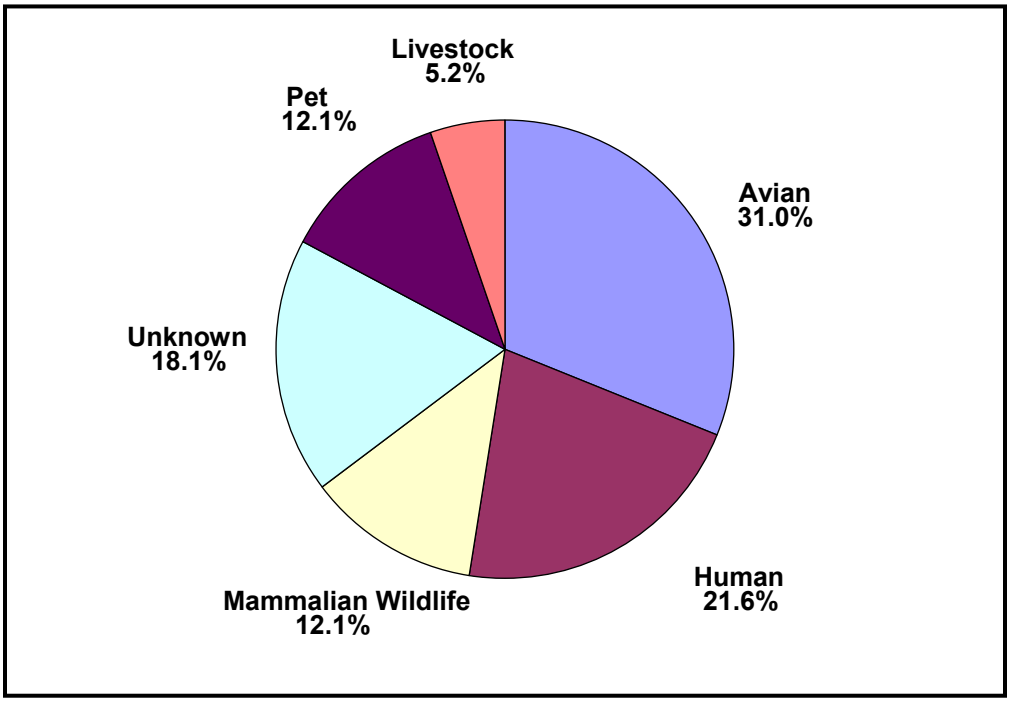

Figure 3-15. *E. coli* category characterization for station 10934 under all conditions.

Table 3-22. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 10934.

Station 10934					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	30	25.9	17.3	34.4
Avian	Waterfowl	6	5.2	0.8	9.5
Avian	**Subtotal**	**36**	**31.0**	**22.0**	**40.1**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	25	21.6	13.5	29.6
Human	**Subtotal**	**25**	**21.6**	**13.5**	**29.6**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	2	1.7	-0.8	4.3
Livestock	Donkey	0	0.0	0.0	0.0
Livestock	Equine	0	0.0	0.0	0.0
Livestock	Goat	0	0.0	0.0	0.0
Livestock	Horse	4	3.4	-0.1	7.0
Livestock	**Subtotal**	**6**	**5.2**	**0.8**	**9.5**
Mammalian Wildlife	Armadillo	1	0.9	-0.9	2.7
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	0	0.0	0.0	0.0
Mammalian Wildlife	Rabbit	1	0.9	-0.9	2.7
Mammalian Wildlife	Raccoon	5	4.3	0.3	8.3
Mammalian Wildlife	Rodent	7	6.0	1.4	10.7
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**14**	**12.1**	**5.7**	**18.5**
Pet	Canine	2	1.7	-0.8	4.3
Pet	Cat	4	3.4	-0.1	7.0
Pet	Dog	8	6.9	1.9	11.9
Pet	Feline	0	0.0	0.0	0.0
Pet	**Subtotal**	**14**	**12.1**	**5.7**	**18.5**
Unknown	Unknown	21	18.1	10.6	25.7
Unknown	**Subtotal**	**21**	**18.1**	**10.6**	**25.7**
	Total	**116**	**100.0**		

3.2.2.3.3 Station 10925- SH 34 (Ellis County)

Station 10925 results were based on 103 isolates. The *E. coli* population at station 10925 was led by an avian contribution of 24.3% (Figure 3-16; Table 3-23). The human category contribution represented 22.3% of the *E. coli* input, and the livestock contribution averaged 18.4%. Mammalian wildlife, unknown category, and pet population, respectively, were found to be the lowest *E. coli* contributors at station 10925. When compared with the overall segment, the largest difference was found to be associated with the livestock contribution, which was 7.7% greater at station 10925 than the overall segment average. This increase is probably a result of the largely rural area surrounding this station, resulting in an increased number of livestock present in the immediate watershed. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

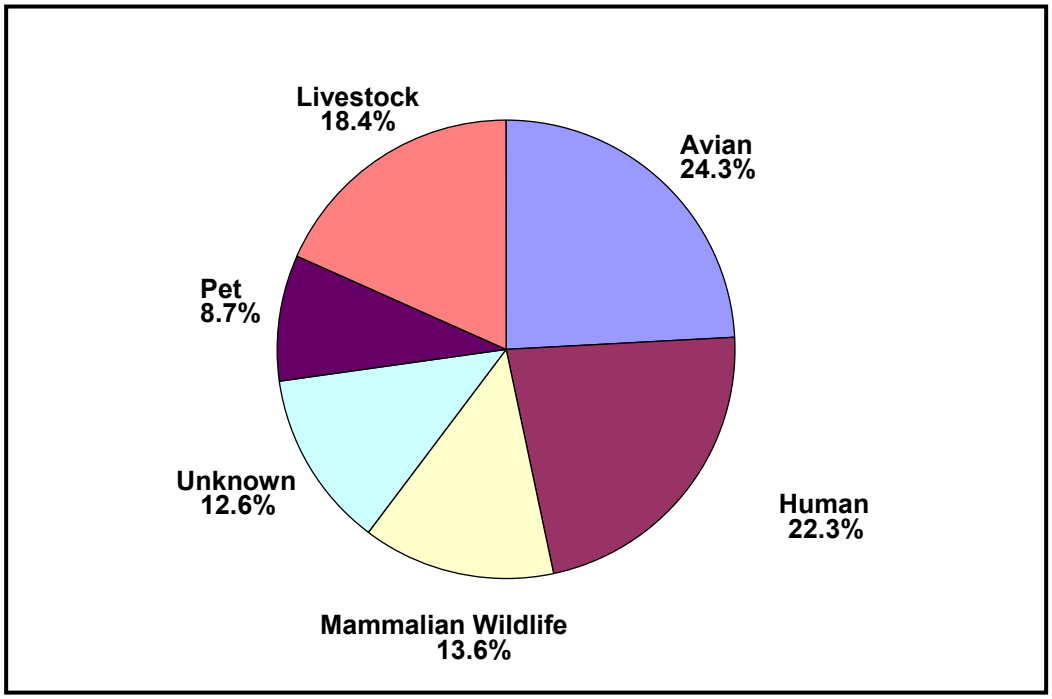

Figure 3-16. *E. coli* source characterization for station 10925 under all conditions.

Table 3-23. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 10925.

Station 10925					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	22	21.4	13.3	29.4
Avian	Waterfowl	3	2.9	-0.4	6.2
Avian	**Subtotal**	**25**	**24.3**	**15.9**	**32.7**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	23	22.3	14.2	30.5
Human	**Subtotal**	**23**	**22.3**	**14.2**	**30.5**
Livestock	Bison	1	1.0	-1.0	2.9
Livestock	Bovine	14	13.6	6.9	20.3
Livestock	Donkey	2	1.9	-0.8	4.6
Livestock	Equine	1	1.0	-1.0	2.9
Livestock	Goat	0	0.0	0.0	0.0
Livestock	Horse	2	1.9	-0.8	4.6
Livestock	**Subtotal**	**20**	**19.4**	**11.7**	**27.2**
Mammalian Wildlife	Armadillo	1	1.0	-1.0	2.9
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	0	0.0	0.0	0.0
Mammalian Wildlife	Opossum	1	1.0	-1.0	2.9
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	7	6.8	1.9	11.7
Mammalian Wildlife	Rodent	4	3.9	0.1	7.7
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**13**	**12.6**	**6.1**	**19.1**
Pet	Canine	0	0.0	0.0	0.0
Pet	Cat	1	1.0	-1.0	2.9
Pet	Dog	8	7.8	2.5	13.0
Pet	Feline	0	0.0	0.0	0.0
Pet	**Subtotal**	**9**	**8.7**	**3.2**	**14.3**
Unknown	Unknown	13	12.6	6.1	19.1
Unknown	**Subtotal**	**13**	**12.6**	**6.1**	**19.1**
	Total	**103**	**100.0**		

3.2.2.3.4 Station 10924- FM 85 (Navarro County)

Station 10924 results were based on 112 isolates. Avian population led the contribution of *E. coli* at station 10924, with 23.2% (Figure 3-17; Table 3-24). Human addition was second highest with 22.3%. Livestock were once again high with 20.5% of the total contribution, while the mammalian wildlife, pet, and unknown categories contributed the least to the overall *E. coli* concentration.

When compared with the overall segment, the livestock and unknown categories showed the highest percent difference. The livestock contribution was found to be 9.8% higher for station 10924 than for the combined segment, and unknowns were lower. This station, like 10925, is largely rural in nature and has a higher density of livestock than station 10937 and 10934. The limited number of isolates at any one station precluded performance of any statistically meaningful analysis that involved further separation of the data, such as was performed on the aggregated data for the segment.

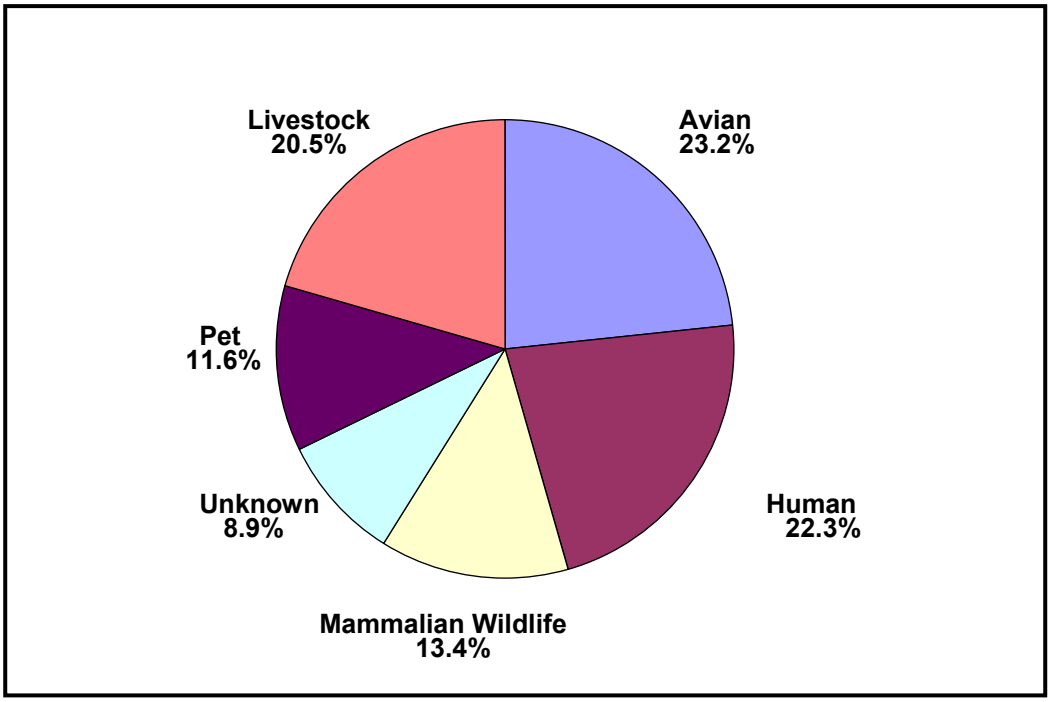

Figure 3-17. *E. coli* source characterization for station 10924 under all conditions.

Table 3-24. Overall *E. coli* source characterization and 95% confidence interval (CI) range for station 10924.

Station 10924					
Category	**Source**	**Isolate #**	**% Contribution**	**95% CI Range**	
Avian	Avian	23	20.5	12.6	28.5
Avian	Waterfowl	3	2.7	-0.5	5.8
Avian	**Subtotal**	**26**	**23.2**	**14.9**	**31.5**
Human	Sewage	0	0.0	0.0	0.0
Human	Wastewater	25	22.3	14.2	30.5
Human	**Subtotal**	**25**	**22.3**	**14.2**	**30.5**
Livestock	Bison	0	0.0	0.0	0.0
Livestock	Bovine	13	11.6	5.3	17.9
Livestock	Donkey	1	0.9	-1.0	2.7
Livestock	Equine	0	0.0	0.0	0.0
Livestock	Goat	3	2.7	-0.5	5.8
Livestock	Horse	6	5.4	0.9	9.8
Livestock	**Subtotal**	**23**	**20.5**	**12.6**	**28.5**
Mammalian Wildlife	Armadillo	0	0.0	0.0	0.0
Mammalian Wildlife	Coyote	0	0.0	0.0	0.0
Mammalian Wildlife	Deer	1	0.9	-1.0	2.7
Mammalian Wildlife	Opossum	1	0.9	-1.0	2.7
Mammalian Wildlife	Rabbit	0	0.0	0.0	0.0
Mammalian Wildlife	Raccoon	7	6.3	1.5	11.0
Mammalian Wildlife	Rodent	6	5.4	0.9	9.8
Mammalian Wildlife	Skunk	0	0.0	0.0	0.0
Mammalian Wildlife	Squirrel	0	0.0	0.0	0.0
Mammalian Wildlife	**Subtotal**	**15**	**13.4**	**6.7**	**20.1**
Pet	Canine	3	2.7	-0.5	5.8
Pet	Cat	3	2.7	-0.5	5.8
Pet	Dog	7	6.3	1.5	11.0
Pet	Feline	0	0.0	0.0	0.0
Pet	**Subtotal**	**13**	**11.6**	**5.3**	**17.9**
Unknown	Unknown	10	8.9	3.3	14.5
Unknown	**Subtotal**	**10**	**8.9**	**3.3**	**14.5**
	Total	**112**	**100.0**		

3.2.3 Summary and Conclusions

During this study water samples were collected from Segments 0806, 0841, and 0805 of the Trinity River in order to quantify the *E. coli* concentrations in the waterbodies, and primarily to isolate representative colonies from the samples and track their sources through BST. BST is a process in which bacteria may be linked to their source hosts through their DNA by molecular tools, in this study, ribotyping. The study was initiated by the Texas Commission for Environmental Quality (TCEQ) in order to determine the extent and sources of bacteria contamination.

Water samples were collected during 11 events, between 23 March 2005 and 16 August 2005, while the known source fecal and sewage ribotype library sample collection occurred over 12 sampling events during the same period. Overall, 550 water samples were collected from 10 different stations along the West Fork and the Trinity River. Approximately two bacterial colonies (isolates) were isolated from each water sample, for a total of 1,135 isolates.

Following unknown isolate and known source ribotyping, the results were identified, matched, assigned to the proper category. The isolates for each segment were analyzed based on their relative contribution, runoff vs. non-runoff influenced, whether they were isolated from samples containing ≤394 org/ 100ml or from samples containing >394 org/ 100ml, and based on temporal differences.

The *E. coli* sources were relatively diverse in each of the three segments, with no one category dominating any of the stations or segments (Tables 3-25, 3-26, and 3-27). Avian species were the highest contributors of *E. coli* in each of the three segments; with the highest concentration associated with the uppermost segment, 0806, and progressively falling in each of the next two segments. However, there was less than a 2% difference between the avian contribution in Segment 0806 and Segment 0805. Human contribution was relatively low in Segment 0806, while it was relatively high in Segments 0841 and 0805. The human contribution rose steadily from Segment 0806 to Segment 0805. Mammalian wildlife was found to be a relatively high contributor in Segment 0806, falling steadily through Segment 0841 into Segment 0805. The unknown sources contributed a relatively large percentage in Segment 0806, but dropped steadily from Segment 0806 to Segment 0805. The pet contribution was found to be somewhat low and stable, with less than a 2% change between Segments 0806 and 0805, even though it did show a consistent drop from the uppermost site to the lowermost site. Livestock were consistently low in the upper two segments, each with 3.8%; however, their contribution rose dramatically to 10.7% in Segment 0805 and to an average of about 19% at the two most downstream and rural stations. Overall, each of the source contributors showed a definite trend, whether positive or negative, as one moves downstream from Segment 0806, through Segment 0841, and into Segment 0805. The categories did show consistencies in source species. The avian category was consistently dominated by non-waterfowl species, while the livestock category's contribution was shared by bovine and horses. Mammalian wildlife was found to be high in rodent species and raccoons, while the pet category was found to be consistently led by dogs.

Table 3-25. Summary *E. coli* source characterization summary for stations associated with Segment 0806.

Source	18459	10938	16120	Segment 0806 Total
Avian (%)	25.0	26.7	32.5	28.0
Human (%)	13.8	12.1	7.9	11.3
Mammalian Wildlife (%)	23.3	18.1	27.2	22.8
Unknown (%)	19.8	26.7	15.8	20.8
Pet (%)	10.3	15.5	14.0	13.3
Livestock (%)	7.8	0.9	2.6	3.8
Total	100.0	100.0	100.0	100.0

Table 3-26. Summary *E. coli* source characterization summary for stations associated with Segment 0841.

Source	17669	11081	11089	Segment 0841 Total
Avian (%)	28.3	31.3	23.7	27.8
Human (%)	19.5	18.3	23.7	20.5
Mammalian Wildlife (%)	18.6	13.0	19.3	17.0
Unknown (%)	16.8	20.0	17.5	18.1
Pet (%)	12.4	11.3	14.9	12.9
Livestock (%)	4.4	6.1	0.9	3.8
Total	100.0	100.0	100.0	100.0

Table 3-27. Summary *E. coli* source characterization summary for stations associated with Segment 0805.

Source	10937	10934	10925	10924	Segment 0805 Total
Avian (%)	25.0	31.0	24.3	23.2	26.0
Human (%)	28.4	21.6	22.3	22.3	23.7
Mammalian Wildlife (%)	18.1	12.1	12.6	13.4	14.1
Unknown (%)	15.5	18.1	12.6	8.9	13.9
Pet (%)	12.9	12.1	8.7	11.6	11.4
Livestock (%)	0.0	5.2	19.4	20.5	11.0
Total	100.0	100.0	100.0	100.0	100.0

The remaining analyses, runoff vs. non-runoff influence and isolates from samples with ≤394 org/ 100ml vs. isolates from samples with >394 org/ 100ml, showed no statistically significant differences in sources when evaluated by segment. In addition, normalization of the data showed no significant difference from non-normalized data. Also, there were no temporal patterns in source contributions evident in any of the three segments.

In conclusion, the *E. coli* sources that were encountered were found to be diverse and non-dominating.

Section 4

BACTERIA ALLOCATION TOOL DEVELOPMENT

This report section provides the basis for the bacteria allocation tool used to assist in developing the TMDL load allocation (or load reduction). First, the reason will be discussed for selecting an empirical based approach, commonly referred to as the load duration curve method. Next the methodology is provided for developing load duration curves and their associated flow exceedance curves. This section concludes with presentation of the flow exceedance and load duration curves developed for relevant monitoring stations in Segments 0806, 0841, 0822, and 0805 of the Trinity River basin.

4.1 Model Selection

The TMDL allocation process for bacteria involves assigning bacteria, i.e., *E. coli*, loads to their sources such that the total loads do not result in violations of pertinent numeric criteria protecting contact recreation use. To perform the allocation process, a tool must be applied to assist in allocating bacteria loads and determining required reductions to existing loadings. The decision on the appropriate bacteria allocation tool to apply was informed by the data requirements of each tool, the complexity of potential sources in the watersheds, and the availability of those watershed-specific data for segments 0806, 0841, 0822, and 0805. In general, two tools are in common usage for bacteria TMDLs—mechanistic computer models and an empirical approach referred to as the load duration curve.

Mechanistic computer models provide analytical abstractions of a real or prototype system—for this situation the West Fork Trinity River, Elm Fork Trinity River, and the Upper Trinity River watersheds. 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. Mechanistic models are typically very data intensive to operate requiring large amounts of information for setup and calibration.

The load duration curve method allows for estimation of existing and TMDL loads by utilizing the cumulative frequency distribution of streamflow and measured pollutant concentration data (Cleland, 2003). In addition to estimating stream loads, the load duration curve method allows for the determination of the hydrologic conditions under which impairments are typically occurring. The load duration curve method 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 method further recognizes the frequent information limitations with bacteria TMDLs that constrain use of the more powerful mechanistic models. Data requirements for the load duration curve are minimal consisting of continuous daily streamflow records and historical bacteria data. The load duration curve method has no capabilities to evaluate alternative allocation approaches

to reach TMDL goals nor can it be used to quantify source contributions and instream fate and transport processes. The method does, however, provide a means to estimate the amount of bacteria reduction required, can give indications of the broad origins of the bacteria, i.e., point source and nonpoint source, and provides a means to allocate allowable loadings.

4.1.1 Situational Limitations of Mechanistic Modeling

Because the present surface water bacteria standards for Segments 0806, 0841, 0822 and 0805, as most Texas waters, do not restrict under what streamflow conditions the contact recreation criteria should be met, the allocation process must consider all streamflow conditions ranging from low flows to high flows except for critical low flows as defined by the State of Texas.[4] The allocation tool, therefore, must be capable of characterizing streamflows and bacteria loads at desired locations under the wide variety of environmental conditions experienced in the impaired segments of the West Fork Trinity River, Elm Fork Trinity River, and Upper Trinity River. If a mechanistic modeling tool is applied, it must be capable of simulating response of 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's land uses and land covers to rainfall, route runoff water through the conveyance channels of the watershed, add in point source contributions, and may 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. Streamflow transport of the bacteria in tributaries and in the mainstem river 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

[4] Present State of Texas surface water quality standards do <u>not</u> require that the criteria to protect contact recreation use be met when streamflow conditions are below the 7-day, 2-year low-flow for waters listed in Appendix A, which includes Segments 0806, 0841, 0822, and 0806 (TNRCC, 2000).

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 models to most watersheds.

Mechanistic bacteria modeling has evolved over the last several decades beginning in the late 1960s to early 1970s as increasing computer resources 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 West Fork Trinity River, Elm Fork Trinity River, and Upper Trinity River watersheds are no exception, only very limited watershed-specific information is available to define 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 may not be known within a reasonable range of certainty. Compounding implications of these data limitations, 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 that protect the contact recreation use.

4.1.2 West Fork Trinity River, Elm Fork Trinity River, and Upper Trinity River 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 West Fork Trinity River, Elm Fork Trinity River and Upper Trinity River to allow adequate definition of many of the physical and biological processes influencing in-stream bacteria concentrations for mechanistic model application, and these limitations became an important consideration in the allocation tool selection process.

Hydrologic data in the form of daily streamflow records are in relatively high abundance for the West Fork Trinity River, Elm Fork Trinity River, and Upper Trinity River. These data are collected and made readily available by the U.S. Geological Survey (USGS), which operates several streamflow gauges in the Trinity River basin (Table 4-1; Figure 4-1).

Seven major municipal wastewater treatment facilities (WWTFs) with permitted annual average discharges of over one million gallons per day (MGD) discharge into the West Fork Trinity River, Elm Fork Trinity River, and Upper Trinity River (Table 4-2; Figure 4-1). Monthly average discharge information from each WWTFs self-reporting data was available for use in this project for a period of over 25 years.

As mentioned in Section 2, two major sources of ambient *E. coli* data existed for developing the TMDL load allocation. One source was data obtained from the routine ambient collection of *E. coli* and other water quality data in the project area under the TCEQ Surface Water Quality Monitoring Program by the TCEQ Field Operations Division and the Clean

Rivers Program by the Trinity River Authority, Tarrant Regional Water District, City of Fort Worth, City of Arlington, City of Grand Prairie, and City of Irving. These data are periodically sent to the TCEQ Regulatory Activities and Compliance System (TRACS) database (recently

Table 4-1 Basic information on USGS streamflow gauges in project area

Gauge No.	Site Description	Segment Location	Drainage Area (sq. mi.)	Daily Streamflow Record (beginning & end date)*
08047500	Clear Fork Trinity River at Fort Worth, TX	0829	518	Mar. 1924 – present
08048000	West Fork Trinity River at Fort Worth, TX	0806	2,615	Mar. 1920 – present
08048543	W. Fk Trin. Rv at Beach St., Fort Worth, TX	0806	2,685	Oct. 1976 – present
08049500	West Fork Trinity River at Grand Prairie, TX	0841	3,065	Apr. 1925 – present
08050100	Mountain Creek at Grand Prairie, TX	0841	298	Oct. 1960 – present
08055500	Elm Fork Trinity River near Carrolton, TX	0822	2,459	Jan. 1907 – present
08061700	Duck Creek near Garland, TX	0822	31.6	Jan. 1958 – Dec. 1992
08057200	White Rock Creek at Greenville Ave, Dallas, TX	0822	66.4	Apr. 1984 – present
08057000	Trinity River at Dallas, TX	0805	6,106	Oct. 1902 – present
08057410	Trinity River below Dallas, TX	0805	6,279	Nov. 1956 – present
08062000	East Fork Trinity River near Crandall, TX	0819	1,256	Jul. 1949 – present
08062500	Trinity River near Rosser, TX	0805	8,147	Aug. 1924 – present

* At some gauges there are missing periods of record within the total time span encompassed by the streamflow record.

Table 4-2 Municipal WWTFs with permitted annual average discharges exceeding 5 MGD

Permit Id (TCEQ/EPA)	Permittee	Facility Name	Segment Number	Permitted Annual Average Flow (MGD)
WQ0010494-13 TX0047295	City of Fort Worth	Village Creek WWTF	0841	166
WQ0010303-001 TX0022802	Trinity River Authority	Central Regional WWTF	0841	162
WQ0010662-001 TX0052892	City of Lewisville	City of Lewisville WWTF	0822	18.0
WQ0010060-001 TX0047830	City of Dallas	Central WWTF	0805	150
WQ0010060-006 TX0047848	City of Dallas	Southside WWTF	0805	110
WQ0013415-001 TX0104345	Trinity River Authority	Red Oak Creek Regional WWTF	0805	6.0
WQ0010984-001 TX0022811	Trinity River Authority	Ten Mile Creek WWTF	0805	24.0

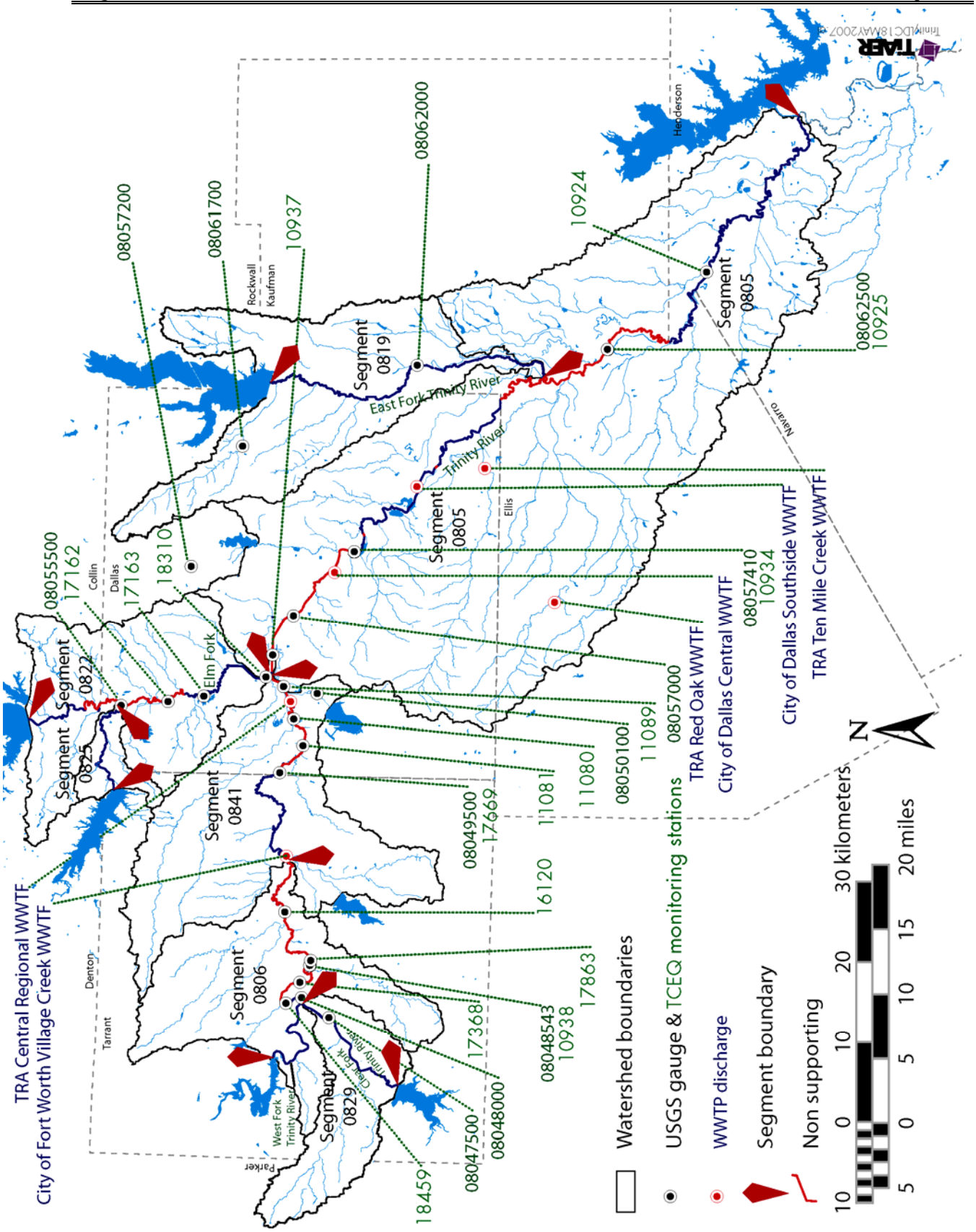

Figure 4-1 Trinity River Basin study area showing locations of monitoring stations, large WWTFs, and USGS streamflow gauges.

updated into SWQMIS or Surface Water Quality Monitoring Information System) and were provided to TIAER for the specific purposes of this project. Routine ambient data from September 2000 through January 2006 were available at the time the load allocation was performed. The other major source of ambient *E. coli* data was collected by the TIAER Project Team at selected stream stations within the West Fork Trinity River and Upper Trinity River for the bacterial source tracking (BST) study and also to provide information to assist in the load allocation process. As discussed previously in this report, the BST monitoring consisted of 5 samples per station per event collected for 11 events between March 2005 and August 2005. The Project Team's bacteria monitoring supporting the allocation process consisted of base-flow and wet-weather sampling for nine events between April 2005 and January 2006. Collectively the data obtained from both routine ambient and TMDL development bacteria monitoring are referred to as the historical data set and provide a data set containing a substantial amount of *E. coli* data at several locations in each segment (Table 4-3; Figure 4-1).

4.1.3 Allocation Tool Selection

Based on good availability of historical daily streamflow records, discharge information for large municipal WWTFs, and ambient *E. coli* data and deficiencies in data to describe bacterial landscape and in-stream processes, the decision was made to use the load duration curve method as opposed to a mechanistic watershed loading and hydrologic/water quality model.

4.2 Methodology for Flow Duration & Load Duration Curve Development

To develop the load duration curves, the previously discussed data resources were used in the following series of sequential steps.

- **Step 1:** Determine the hydrologic period of record to be used in developing the flow duration curves.
- **Step 2:** Determine desired stream locations for which flow and load duration curves will be developed. (The stream locations will be at monitoring stations in or near the impaired portions of Segments 0806, 0841, 0822, and 0806 for which adequate *E. coli* data are available.)
- **Step 3:** Develop daily streamflow records at desired stream locations using the daily gauged streamflow records and municipal WWTF self-reporting data.
- **Step 4:** Develop streamflow duration curves at desired stream locations, segmented into discreet flow regimes.
- **Step 5:** Develop the allowable bacteria load duration curves at the same stream locations based on the relevant criteria and the data from the streamflow duration curve.
- **Step 6:** Superpose historical bacteria data, in this situation *E. coli* data from September 2000–January 2006, on the allowable bacteria load duration curve.

Additional information explaining the load duration curve method may be found in Cleland (2003) and NDEP (2003).

Table 4-3 Summary of combined (historical) data set of TCEQ and CRP Partners and TIAER Project Team *E. coli* concentrations

TCEQ Station Id.	Segment Number	Routine Ambient Data	TMDL Development Data	Number of Data Values
18459	0806	No Data	23Mar05 – 24Jan06	29
17368	0806	09Jan01 – 10Jan06	No Data	77
10938*	0806	09Jan01 – 10Jan06	23Mar05 – 24Jan06	113
17863*	0806	13Jan03 – 09Jan06	No Data	36
16120	0806	09Jan01 – 10Jan06	23Mar05 – 24Jan06	96
17669	0841	10Dec01 – 19Jan06	23Mar05 – 24Jan06	78
11081	0841	18Sep00 – 09Jan06	23Mar05 – 24Jan06	72
11080	0841	11Dec01 – 20Oct04	No Data	33
11089	0841	03Oct00 (one data pt.)	23Mar05 – 24Jan06	30
17162	0822	05Dec01 – 09Nov05	No Data	34
17163	0822	05Dec01 – 18Oct04	No Data	33
18310	0822	05Dec01 – 10Aug05	No Data	39
10937	0805	20Feb01 – 09Jan06	23Mar05 – 24Jan06	80
10934	0805	10Feb01 – 09Jan06	23Mar05 – 25Jan06	80
10930	0805	21Feb01 – 04Jan06	No Data	48
10925	0805	01Feb01 – 10Jan06	23Mar05 – 26Jan06	90
10924	0805	26Feb01 – 11Jul02	23Mar05 – 26Jan06	37

* Stations 10938 and 17863 are in close proximity (see Figure 4-1). Hence the *E. coli* data from these two stations were combined for subsequent analysis and use in the allocation tool development.

4.2.1 Step 1: Determine Hydrologic Period

Daily hydrologic (streamflow) records were available for several key USGS gauge locations for periods as long as over 80 years to as short as about 50 years. Even the shorter of these two periods of record, 50 years, is more than adequate to capture a reasonable variation in meteorological patterns of high and low rainfall periods. Two important confounding factors, however, are present in the contributing drainage areas of Segments 0806, 0841, 0822, and 0805—rapid urbanization and development of large water storage reservoirs. Both of these factors will alter the hydrologic response of streams under base flow and stormwater runoff conditions. Over the past 50 years population growth has been great within the major metropolitan areas of Dallas and Tarrant counties (a three- to four-fold population increase) and within more recent decades increasing growth has also occurred in the more rural counties of Ellis and Kaufman (Table 4-4). Commensurate with this urban growth have been increases in the amount of impervious cover resulting in greater amounts of runoff from rainfall events and also increases in municipal WWTF discharges as service population increased. Several large reservoirs have also become operational within the drainage area of the project area; some within the last 40 years or less (Table 4-5). Because of the population growth, increased WWTF discharges, and development of reservoirs, the hydrology of the West Fork Trinity River, Elm Fork Trinity River, and Upper Trinity River has experienced changes. An anticipated trend of increasing base flow was borne out by plotting the time sequence of yearly minimum monthly flow at representative USGS gauges located across the study area (Figures 4-2 through 4-5).

Though the duration of the flow record varied from gauge to gauge, a strong positive trend in minimum monthly flows was indicated at each location.

Table 4-4 U.S. Census Bureau population data for relevant counties (1950-2000). Source: Texas Water Development Board

County	1950	1960	1970	1980	1990	2000
Dallas	614,799	951,527	1,327,321	1,556,390	1,852,810	2,218,774
Ellis	45,645	43,395	46,638	59,743	85,167	111,360
Kaufman	31,170	29,931	32,392	39,015	52,220	71,313
Tarrant	361,253	538,495	716,317	860,880	1,170,103	1,446,219

Table 4-5 Major reservoirs on tributaries to the Trinity River

Reservoir Name	Tributary	Year Impoundment Began	Conservation Pool Storage (Acre-Feet)
Lake Worth	West Fork Trinity River	1914	12,290
Lake Benbrook	Clear Fork Trinity River	1952	88,250
Lake Arlington	Village Creek	1957	39,930
Joe Pool Lake	Mountain Creek	1986	176,900
Mountain Cr. Lake	Mountain Creek	1937	22,840
Ray Roberts Lake	Elm Fork Trinity River	1986	799,600
Lake Lewisville	Elm Fork Trinity River	1954	457,600
Grapevine Lake	Denton Creek	1952	181,100
Lake Ray Hubbard	East Fork Trinity River	1978	489,900

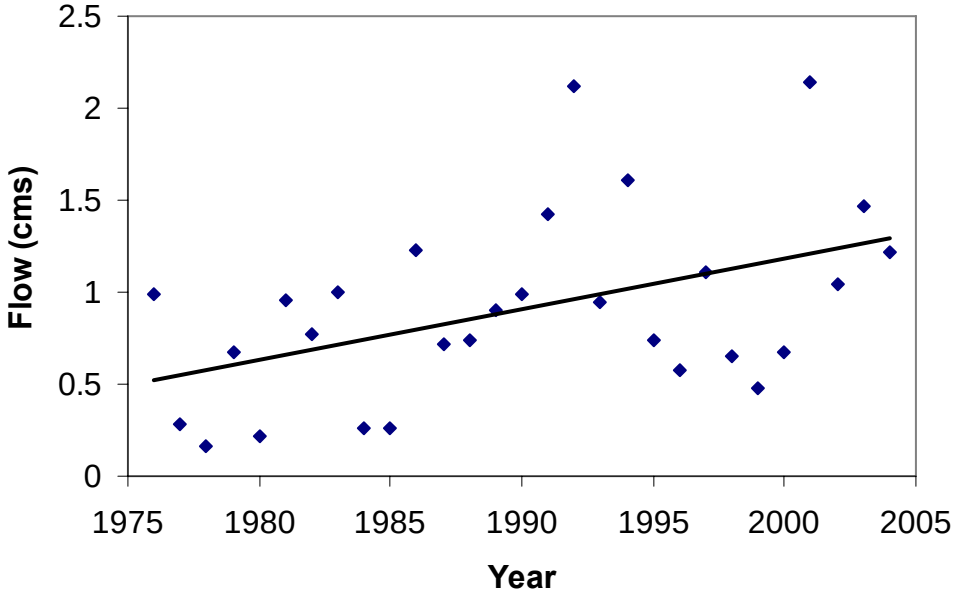

Figure 4-2 Yearly minimum monthly flow at USGS gauge 08048543, Segment 0806

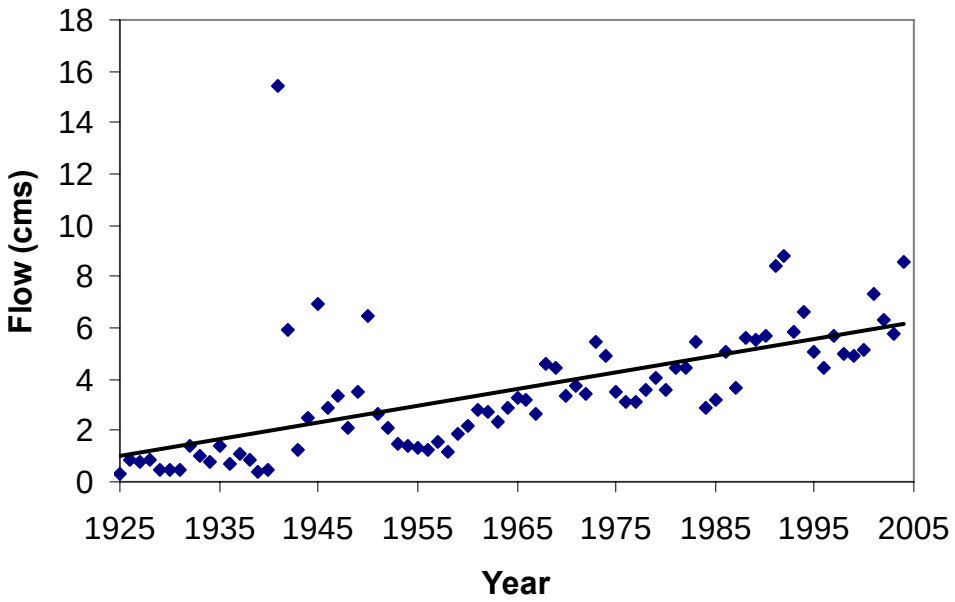

Figure 4-3 Yearly minimum monthly flow at USGS gauge 08049500, Segment 0841

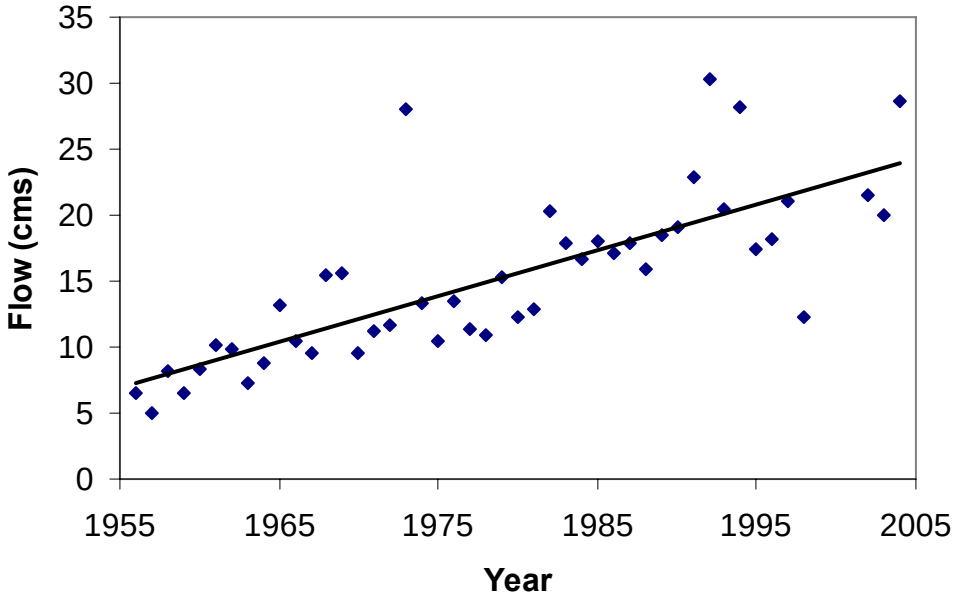

Figure 4-4 Yearly minimum monthly flow at USGS gauge 08057410, upper Segment 0805

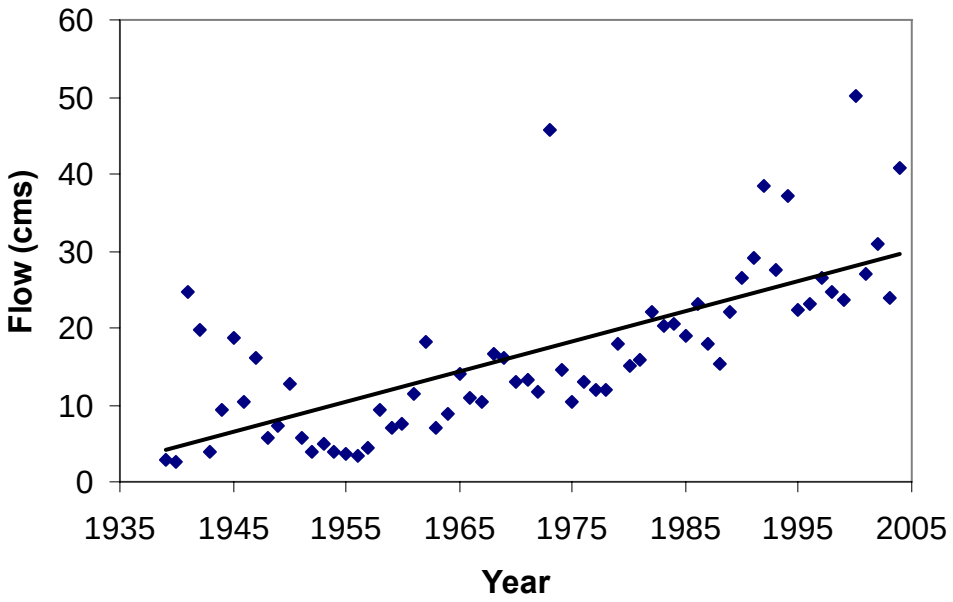

Figure 4-5 Yearly minimum monthly flow at USGS gauge 08062500, lower Segment 0805

Optimally the period of record to develop flow duration curves should include as much data as possible in order to capture extremes of high and low streamflows and hydrologic variability from high to low precipitation years, but the flow during the period of record selected should also be representative of conditions experienced when the *E. coli* data were collected. However, the positive trend in base flow indicated that a bias would be introduced into the flow duration curves if the selected period of record includes all possible historical data going back 50 or more years. Precipitation data for two weather stations, the Dallas/Fort Worth Airport (representing the northwest portion of the study area) and Rosser near USGS gauge 08062500 (representing the southeast portion of the study area) were analyzed to inform a decision on the minimum acceptable hydrologic period. Using 40-years of precipitation data for the period 1966 through 2005, basic statistics were determined for the annual data at each weather station (Table 4-6). The 25-year period was selected as the minimum length period that best represented the average, mean, and standard deviation of the 40-year period of data that was selected as the basis of comparison. The selection process was relatively subjective. Both the 20- or 25-year periods captured the 40-year average and mean precipitation adequately, but the 25-year period better matched the standard deviation. The 30-year period did not provide significant improvement over the 25-year period in representing the 40-year average statistics, especially when consideration was given to the upward base-flow trend, which supports selection of the shorter period. Therefore the 25-year records of daily streamflow from February 1, 1981 through January 31, 2006 were selected to develop the streamflow duration curves at each station. The month of January 2006 was included and January 1981 excluded, since the most recently available *E. coli* data for this analysis occurred in January 2006.

Table 4-6 Basic statistics of annual precipitation data for weather stations at DFW Airport and Rosser, TX (1966-2005)

	DFW Airport			Rosser, TX		
Period (years)	**Mean (in)**	**Median (in)**	**Standard Dev. (in)**	**Mean (in)**	**Median (in)**	**Standard Dev. (in)**
20 (1986-2005)	36.2	35.8	9.2	39.8	42.2	9.6
25 (1981-2005)	36.2	35.4	8.6	39.4	41.5	8.9
30 (1976-2005)	34.9	34.1	8.6	38.7	41.2	8.9
40 (1966-2005)	35.0	35.5	8.3	38.2	38.7	8.5

4.2.2 Step 2: Determine Desired Stream Locations

The stations for which adequate *E. coli* data were available (see Table 4-3) determined the stream locations for which flow and bacteria load duration curves would be developed. These stations were conveniently located either within or in close proximity to the impaired reaches within each segment with the notable exceptions of stations 17163 and 18310 in Segment 0822 and station 10924 in the lower portion of Segment 0805 (Figure 4-1). The purposes for including these three stations that are each located outside of the impaired reaches will be discussed in Section 5—TMDL Load Allocation Analysis. Also, because of immediate proximity, the *E. coli* data for stations 10938 and 17863 were combined for all subsequent analyses.

4.2.3 Step 3: Develop Daily Streamflow Records

Once the hydrologic period of record and station locations were determined, the next step was to develop the 25-year daily streamflow record for each station. The daily streamflow records were developed from extant USGS records modified by the imposition of certain rules necessitated by hydrologic complicating factors. The following factors complicate the use of USGS streamflow records for developing flow and load duration curves:

- The large reservoirs on several tributaries to the Upper Trinity River not only highly impact downstream hydrology, but also effectively reduce bacteria concentrations in releases as a result of their large detention times and enhanced conditions over typical run-of-river conditions for bacterial settling and die-off.
- Several large (i.e., greater than 5 MGD) WWTFs discharge into Segments 0822, 0841, and 0805 (Table 4-2), and these facilities should be evaluated at their full permitted daily average discharge limits within the TMDL allocation process.
- Large municipal drinking water intakes are present in the study area, especially in Segment 0822. The hydrology within Segment 0822 is often a response to controlled releases from Grapevine Lake and Lake Lewisville to meet municipal water demands and then downstream withdrawals at the points of intake.
- The calculated TMDL allocation for each segment needs to accumulate in the downstream direction and take into account classified stream segments that support the contact recreation use and are tributaries to nonsupporting segments. The TMDL allocation for Segment 0841, therefore, needs to take into account the upstream TMDL allocation from Segment 0806, and Segment 0805's allocation needs to take into account the upstream allocations from Segments 0822 and 0841. Also, the TMDL allocation for

Segment 0806 needs to take into account the allowable loading from tributary Segment 0829; Segment 0822's allocation needs to take into account the allowable loading from tributary Segment 0825; and Segment 0805's allocation needs to take into account the allowable loading from tributary Segment 0819. This accumulation results in the TMDL allocation being developed by considering the intervening drainage area of each segment (that is the drainage area at the outlet or most downstream point of the segment excluding the drainage area above large reservoirs and of upstream and tributary segments for which either bacteria TMDLs are being developed or the segments support the contact recreation use but still have allowable bacteria loadings).

Overall the method to develop the necessary streamflow record for each selected station involved a modified drainage-area ratio approach. With this basic approach, each daily streamflow value at the nearest representative USGS gauge is multiplied by a factor to estimate the flow at a station. The factor is determined by dividing the drainage area above the sampling station by the drainage area above the USGS gauge. To address the complications listed above the following modifications and rules were incorporated into this basic approach:

Action # 1: Calculate Appropriate Drainage Area Ratios (DARs) Considering Reservoirs

- To address the complications imposed by the presence of reservoirs, the drainage-area ratio approach was applied excluding the drainage area above major reservoirs from the computation, since these reservoirs substantively reduce immediately downstream flows under most hydrologic conditions. As labeled on Figure 2-1, the reservoirs impacting the ratios were Lake Worth, Benbrook Lake, Marine Creek Lake, Lake Arlington, Mountain Creek Lake, Lake Grapevine, Lake Lewisville, White Rock Lake and Lake Ray Hubbard. Drainage area computations were based on the Digital Elevation Models (DEM) data of the USGS (GeoCommunity™, 2006). Individual drainage areas were developed using the Geographic Information System (GIS) interface called AVSWATX (Di Luzio et al., 2004), and the areas with the drainage areas above the major reservoirs excluded are provided in Appendix F, Table F-2.
- To further address the complications imposed by the presence of reservoirs, the drainage-area ratio was employed, when possible, based on upstream and downstream USGS gauges with a sampling station located on the river between the two gauges. The streamflow record at the sampling station was then calculated by adding to the flow of the upstream gauge the difference in flow between the downstream and upstream gauges multiplied by the ratio of the drainage area between the upstream gauge and the sampling station to the total intervening drainage area between the two gauges. Using this intervening drainage-area ratio accomplished three desired hydrologic outcomes. First, releases from reservoirs, which should not be included in the flow that was multiplied by the drainage area ratio, were largely removed by the subtraction of flows of an upstream gauge or gauges from the flows of a downstream gauge. Second, the data from the upstream gauge or gauges were used intact, thus preserving and using unmodified data. Third, this drainage area ratio approach was more likely to be appropriate, because it was applied in a limited manner using only the intervening area between upstream and downstream gauges.

Action # 2: Correct Streamflow Records for Actual WWTF Discharges as Necessary

- To compensate for the complication from WWTF discharges into the streams, that portion of the streamflow originating from point sources was removed (subtracted) and an adjusted daily streamflow record was developed prior to applying the drainage area ratio. Because accuracy of the drainage area ratio is dependent upon similarity of hydrologic response based on similarity of landscape features such as geology, soils, and land use/land cover, point source derived flows should be removed from the flow record prior to application of the ratio. The daily streamflows for all gauges with upstream large WWTFs (defined as > 5 MGD permitted daily average flow) were adjusted by subtracting historical WWTF flows from the daily streamflow record. Typically only self-reported monthly average discharge values were available for most time periods for most WWTFs; however, some limited self-reported daily discharge data were available for some facilities in more recent years. Monthly self-reported data was obtained from the TCEQ TRACs database, and a small portion of self-reported daily discharge data were obtained from the EPA Enforcement and Compliance History Online database (http://www.epa-echo.gov/echo/). When only monthly discharge data were available, that average was applied to each day of the month. When the subtraction process resulted in negative numbers, that daily flow was set to zero.

Action # 3: Make Adjustments for Withdrawals in Segment 0822, Station 18310

- In Segment 0822 additional changes were necessary and the details are provided in Appendix F. As an overview, streamflow records in Segment 0822 were further adjusted for the large Dallas and Park Cities municipal water intakes present in the lower portion of the segment, and USGS gauge records from small urban watersheds east of Segment 0822 were used in the estimation of flow records at two of the stations in the segment.

Action # 4: Impose Conservation of Water Mass on Stations in Segment 0805

- A further compensation was necessary to ensure that the TMDL bacteria load allocation for upstream Segments 0841 and 0822 could be accounted for in downstream Segment 0805. This compensation in essence imposed a conservation of water mass approach on the streamflows in Segment 0805. Whenever the adjusted daily streamflow at any USGS gauge in Segment 0805 was less than the combined adjusted flows (i.e., with WWTF discharges removed) from the most downstream station on Segment 0841 (station 11089) and on Segment 0822 (station 18310), the flow for that day was set equal to the combined adjusted flow. This alteration was generally applied to all days, but most necessary under low streamflow conditions when upstream flows at times exceeded flows further downstream. This calculation ensured that the daily streamflow at downstream gauges at least equaled the combined flows entering from Segments 0841 and 0822. The necessity for this compensation was likely a combination of several factors including uncertainties in the measurement of daily streamflow at all USGS gauges and discharges at all WWTFs, channel losses, and small withdrawals along the segment. More details on this action are provided in Appendix F.

Action # 5: Apply DARs and Add Full Permitted WWTF Discharges

- To account for WWTFs at their daily permitted discharge limit, as required in the TMDL, the drainage area ratio approach was applied at each station and to that calculated streamflow record was added the summation of the permitted daily average discharges from upstream WWTFs.

The computations of the daily record for each station outlined above compensated in a consistent manner for large complexities that precluded calculation of consistent streamflows required for the TMDL allocations from a simpler application of the drainage-area ratio approach without any adjustments. The specific means of determining the flow at each sampling station is provided in Appendix F.

4.2.4 Step 4: Development of Streamflow Duration Curves

The daily flow data in units of cubic meters per second (cms) were used to develop a flow duration curve for each station. The flow duration curve was 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). Exceedance values along the x-axis represent the percent of days that flow was at or above the associated flow value on the y-axis. Exceedance values near 100% occur during low flow or drought conditions while values approaching 0% occur during periods of high flow or flood conditions. The flow duration curves for all segments indicated increasing flow overall from upstream to downstream between segments and by stations within each segment except station 18310 on the Elm Fork as a result of the large municipal intakes near that station.

Flow Duration Curves for Segments 0806 and 0829

The flow duration curves of sampling stations within West Fork Trinity River below Lake Worth (Segment 0806) indicated similar flow patterns between stations, which may be attributed to the absence of large WWTF discharges between any of the sampling stations within this segment (Figure 4-6). The flow duration curve at the downstream end of the Clear Fork Trinity River below Benbrook Lake (Segment 0829) is also provided on Figure 4-6, since Segment 0829 is a classified stream segment that enters into Segment 0806.

Flow Duration Curves for Segment 0841

The City of Fort Worth Village Creek WWTF is located above all four sampling stations in Segment 0841. The TRA Central Regional WWTF is located above station 11089. The influence of these WWTFs on the duration curves is apparent in the region of the nearly constant flows between 7 and 12 cms for stations 17669, 11081, and 11080, and between 16 and 21 cms for stations 11089 (Figure 4-7). The close proximity and absence of significant inflow between stations 11080 and 11081 resulted in very similar flow duration curves for both of these stations. Further, station 17669, while upstream of station 11081 and 11080, is located sufficiently close to these other stations that the calculated streamflow was essentially identical to that at those other two stations at the scale plotted in Figure 4-7.

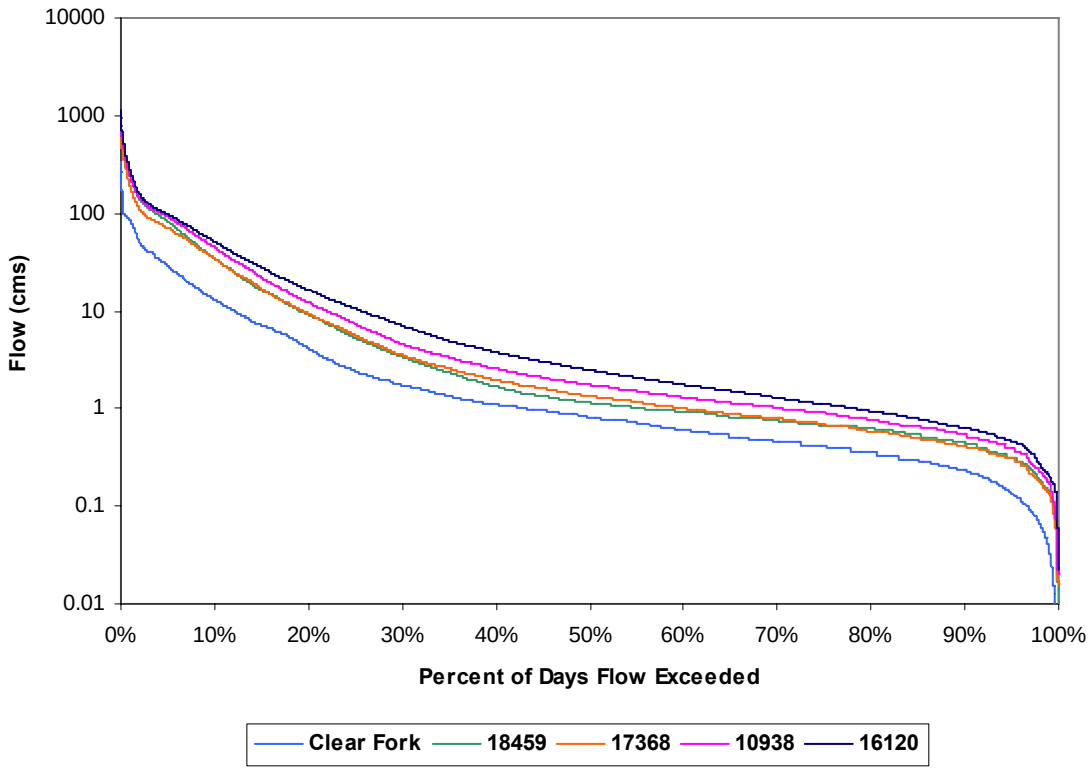

Figure 4-6 Flow duration curves for stations in Segment 0806

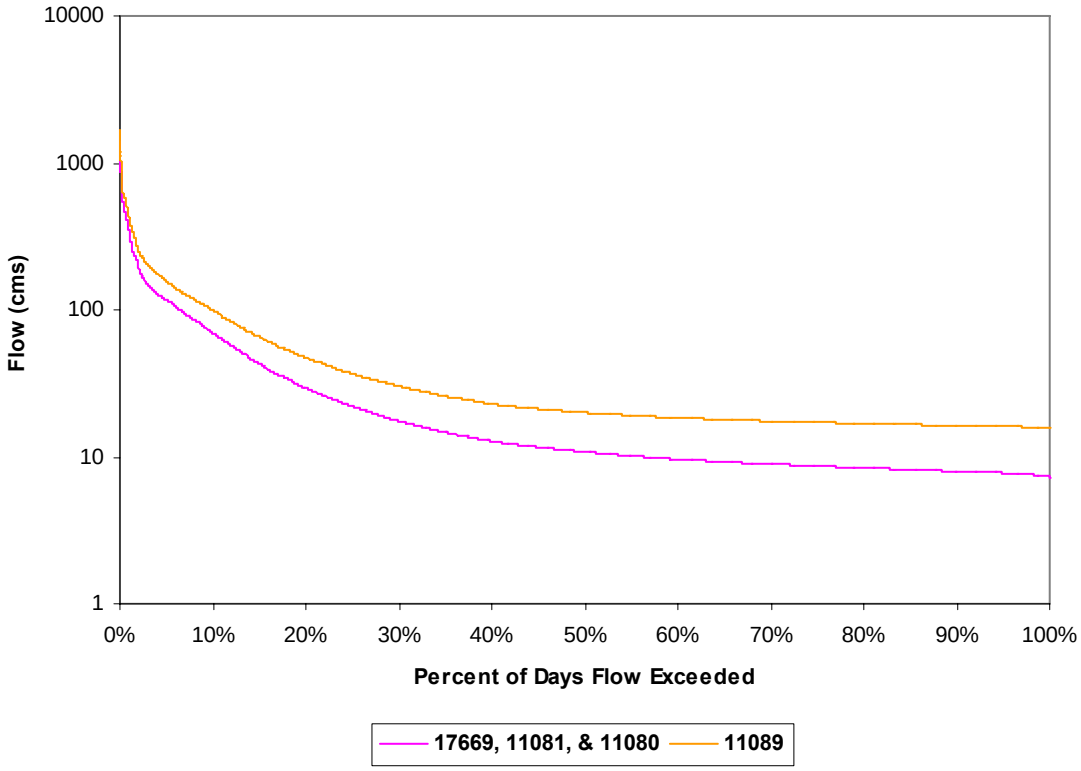

Figure 4-7 Flow duration curves for Segment 0841

Flow Duration Curves for Segments 0822 and 0825

The city of Dallas and Park Cities drinking water intakes are located downstream of stations 17162 and 17163, and upstream of station 18310. Though the city of Dallas also has a large water intake above all three stations and immediately upstream of USGS gauge 08055500. For the Elm Fork Trinity River below Lewisville Lake (Segment 0822), the influence of the drinking water intake withdrawals on the duration curves is apparent in the considerably lower flows at downstream station 18310 as compared to the upstream stations 17162 and 17163 (Figure 4-8). The lower flows at station 18310 become more apparent beginning at approximately 30% exceedance. This flow pattern can be explained since under high flow conditions (low exceedances) a smaller percentage of the total volume of the river is being removed by the drinking water intakes. As a classified stream segment and a tributary to Segment 0822, the flow duration curve at the outlet of Denton Creek (Segment 0825) is also shown on Figure 4-8.

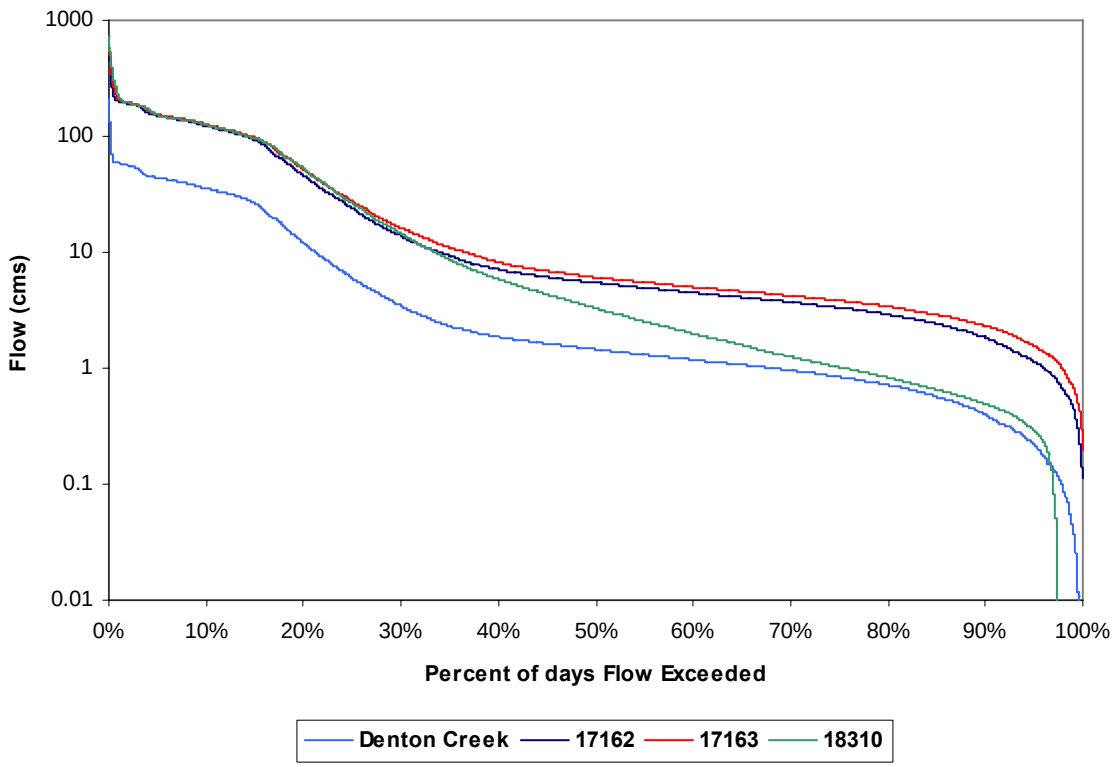

Figure 4-8 Flow duration curves for Segment 0822

Flow Duration Curves for Segments 0805 and 0819

The Dallas Central WWTF was located above all sampling stations on the Upper Trinity River (Segment 0805) with the exception of station 10937. The Dallas Southside WWTF is located above stations 10930, 10925, and 10924. The appreciably smaller TRA Red Oak Creek and Ten Mile Creek WWTFs are located above stations 10925 and 10924. The relatively constant flow between 22-35 cms at station 10934 and similarity of higher flows when compared

to the upstream station 10937 indicates the influence of the Dallas Central WWTF on the flow duration curve at station 10934 (Figure 4-9). An increase in flow was indicated in the flow duration curve for station 10930 when compared to station 10934, and this increase is mostly attributable to discharges from the Dallas Southside WWTF. A comparison of the flow duration curves of stations 10930 and 10925 indicates considerably higher flows at station 10925 when flow exceedance is less than approximately 50%. This relatively large difference under high flow conditions between stations 10930 and 10925 is due to the confluence of the East Fork Trinity River between the two stations. Stations 10925 and 10924 have similar flow exceedance patterns. As a classified stream segment and major tributary to Segment 0805, the flow duration curve at the outlet of the East Fork Trinity River (Segment 0819) is also shown on Figure 4-9.

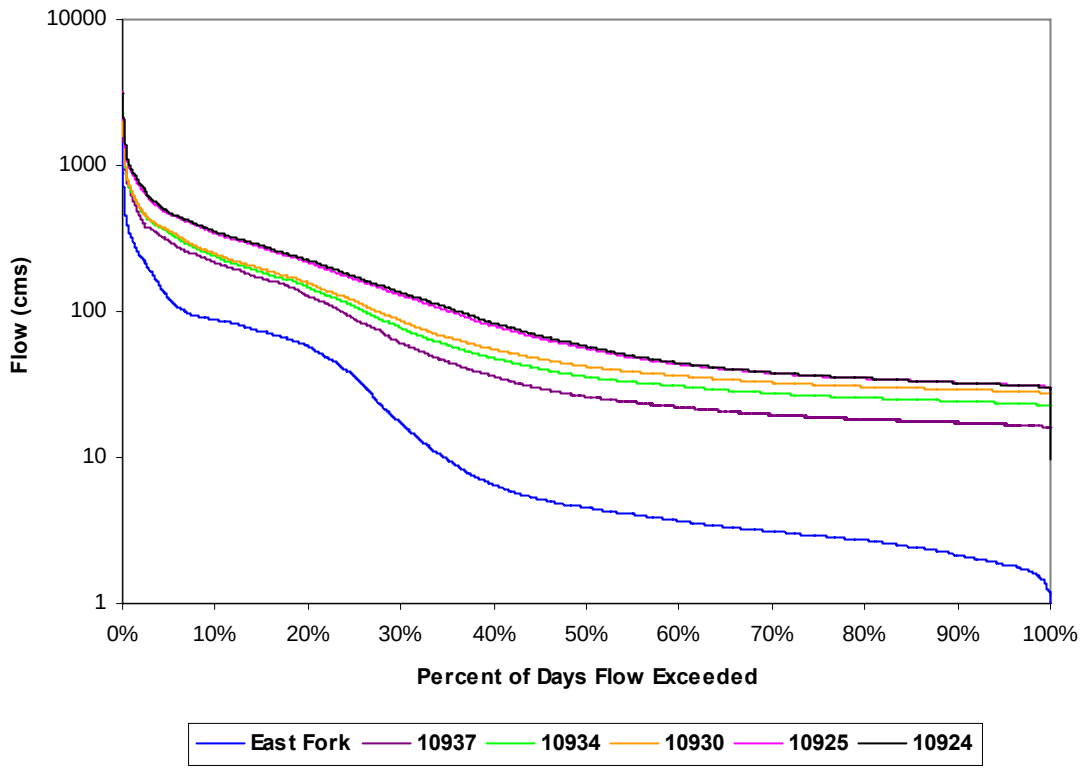

Figure 4-9 Flow duration curves for Segment 0805.

4.2.5 Steps: 5 and 6 Load Duration Curves and Bacteria Data

In Step 5, 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 colonies per 100 ml and a single sample *E. coli* concentration not to exceed 394 colonies per 100 ml. A load duration curve is developed by multiplying each streamflow value from Step 4 by the *E. coli* criterion (either 126 or 394 colonies per 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. For the tributary classified segments (0829, 0825, and 0819), which all support the contact recreation use, all necessary computations for the TMDL load allocation can be readily determined from the flow duration curves; therefore, load duration curves were not developed from their flow duration curves.

In Step 6, for each station, each historical *E. coli* measurement was associated with the streamflow on the day of measurement. The historical *E. coli* measurements are combined with the appropriate streamflow to give a loading as performed for the criterion in Step Five. The associated streamflow for each bacteria loading was 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 was then plotted on the load duration curve at its percent exceedance. This process was repeated for each *E. coli* measurement at each station. Points above a curve represent exceedances of that bacteria criterion and its associated allowable loadings. The streamflows and associated *E. coli* concentrations at each of the stations are provided in Appendix H.

The bacteria load duration curves for stations within Segment 0806 are presented in Figures 4-10 – 4-13, Segment 0841 in Figures 4-14 – 4-17, Segment 0822 in Figures 4-18 – 4-20 and Segment 0805 in Figures 4-21 – 4-25. The bacteria load duration curves for all stations indicate that bacteria single sample load exceedances are generally occurring during higher flows, while the exceedances for geometric mean standards are occurring at moderate to high flows. Actual interpretation of these curves in the context of the TMDL allocation process is reserved for the next report section. It may generally be observed, however, in all the bacteria load duration curves that a pattern of a greater frequency of exceedances of the criteria are apparent in the historical data with increasing flow (i.e., decreasing values of the percent of days loading exceeded on the x-axis of the figures).

It should be noted that flow duration curves and load duration curves were developed for all stations for which adequate historical *E. coli* data existed in order to present as complete a representation of conditions in each segment as possible. Not all these stations, however, were used in the TMDL allocation analysis (Section 5), because some stations either were not located in an impaired reach or did not represent a downstream location in a segment.

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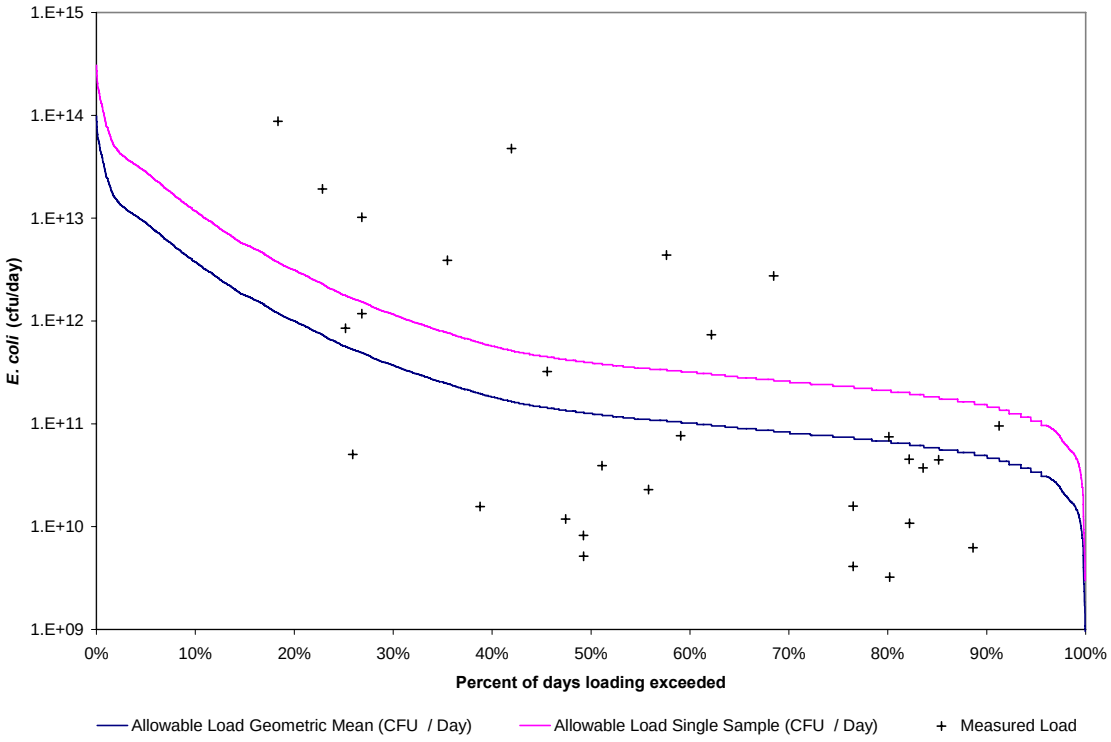

Figure 4-10 Bacteria load duration curve for station 18459, Segment 0806.

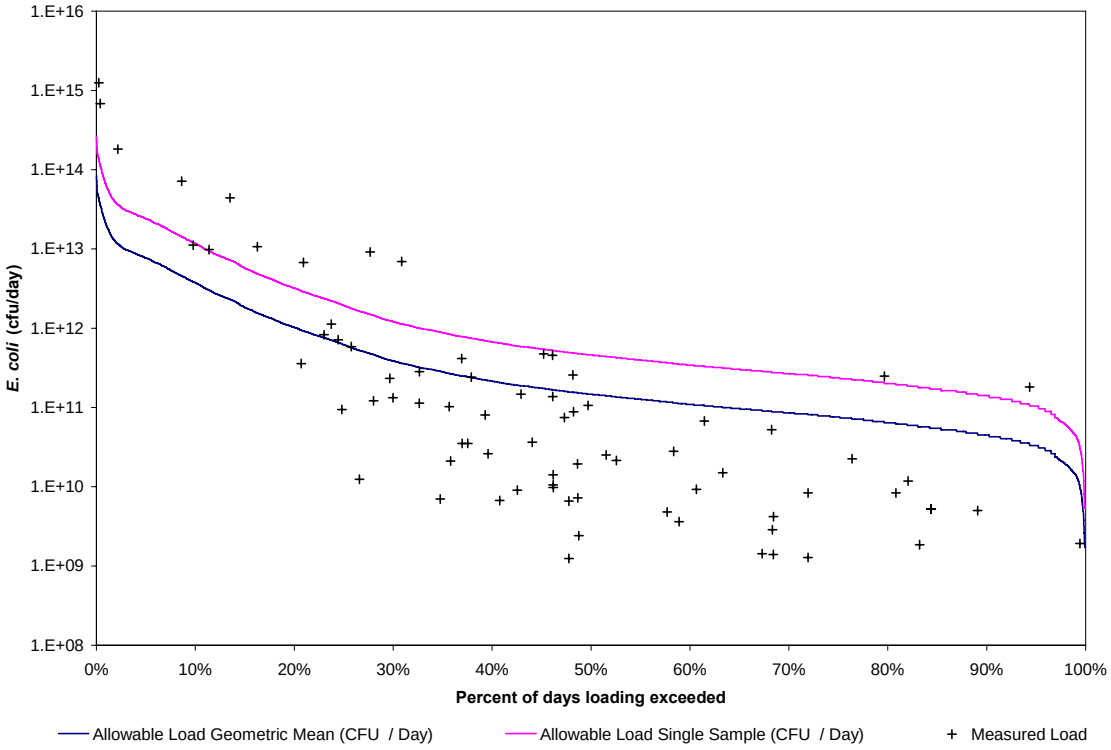

Figure 4-11 Bacteria load duration curve for station 17368, Segment 0806.

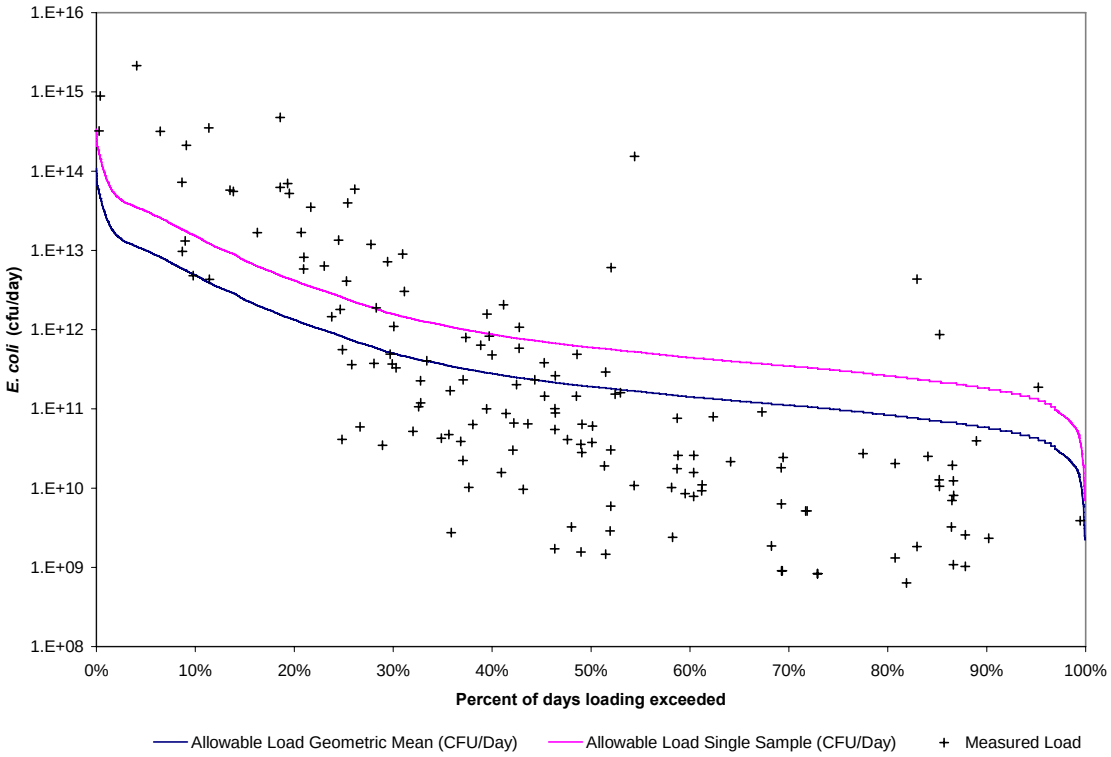

Figure 4-12 Bacteria load duration curve for station 10938, Segment 0806.

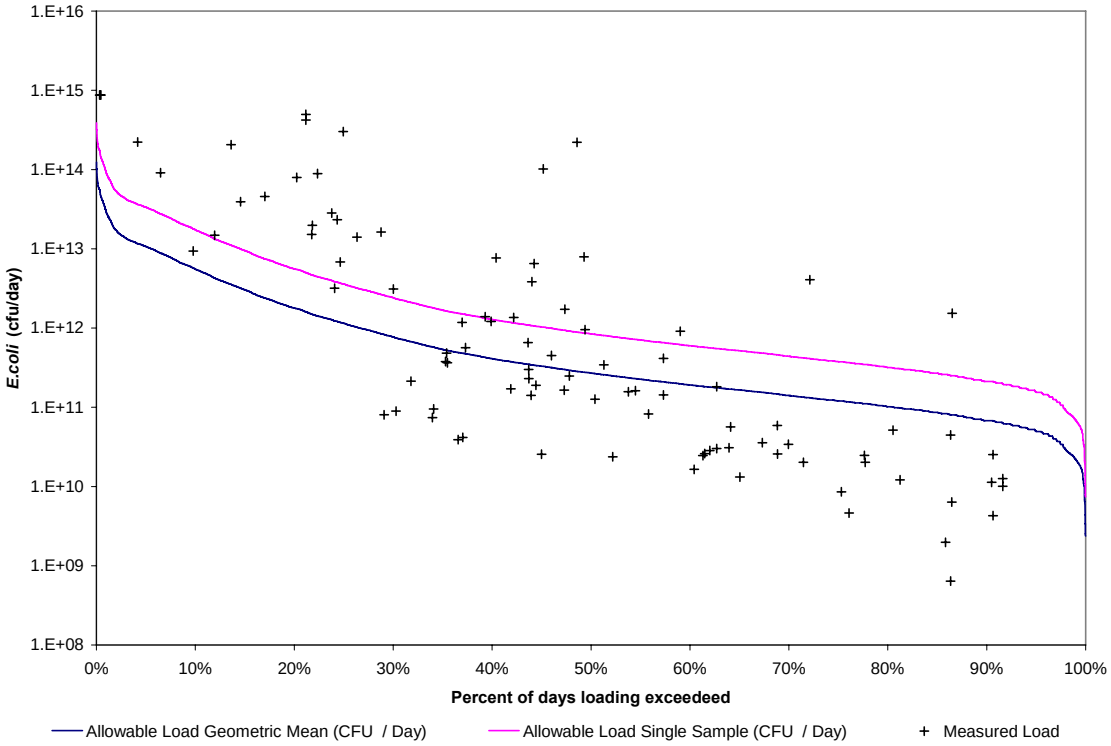

Figure 4-13 Bacteria load duration curve for station 16120, Segment 0806.

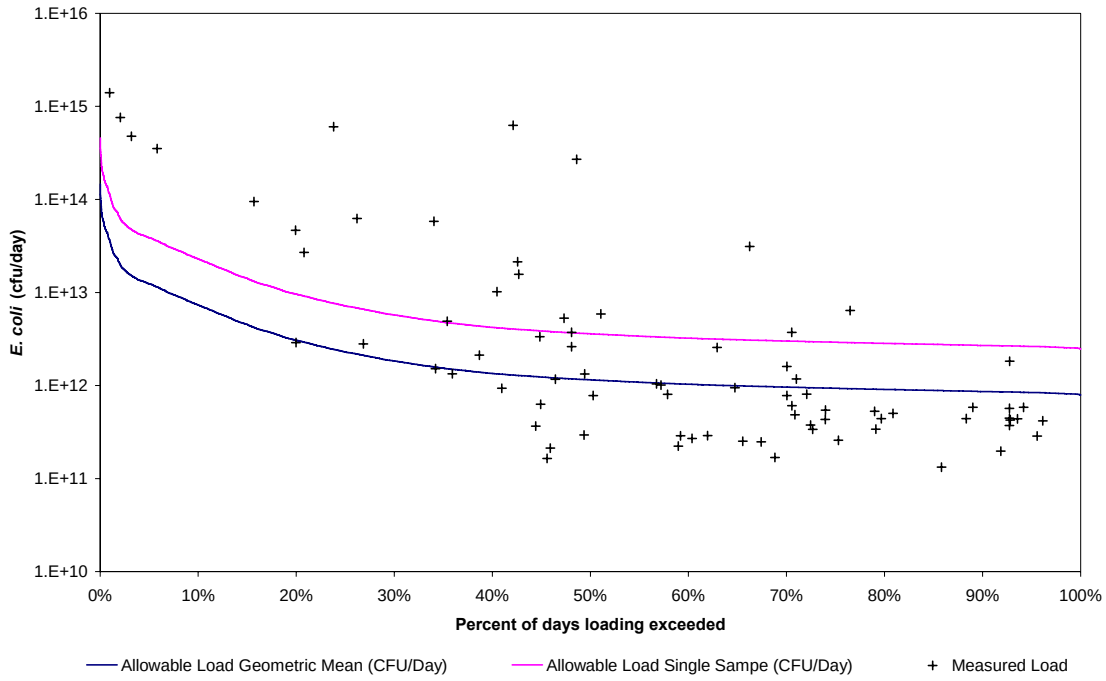

Figure 4-14 Bacteria load duration curve for station 17669, Segment 0841.

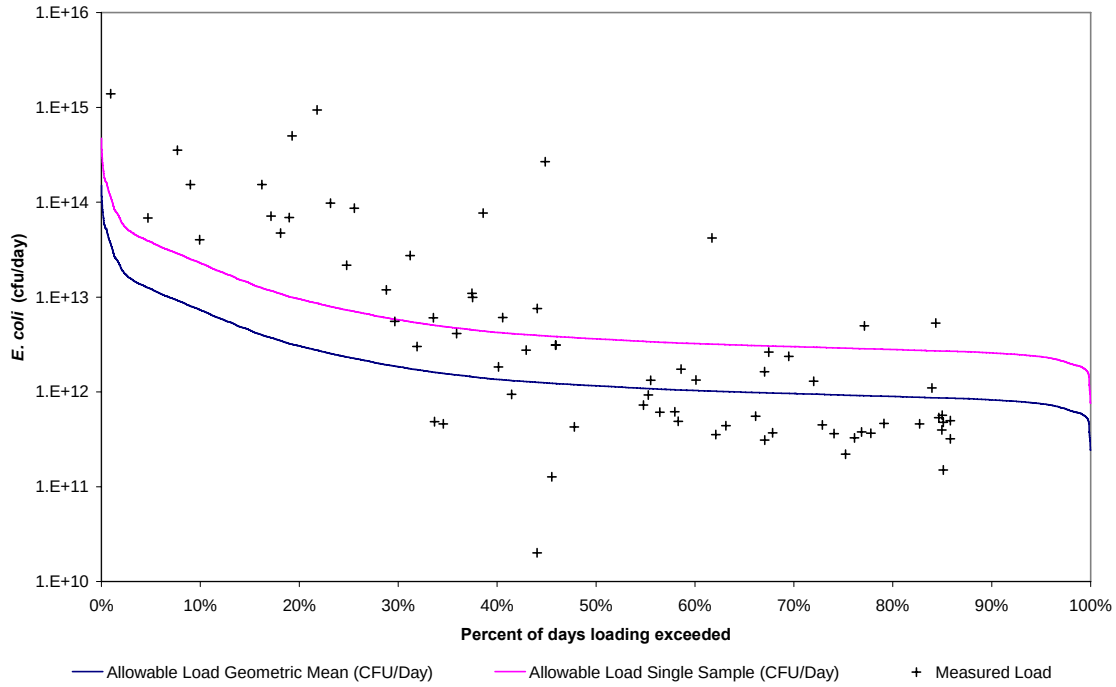

Figure 4-15 Bacteria load duration curve for station 11081, Segment 0841.

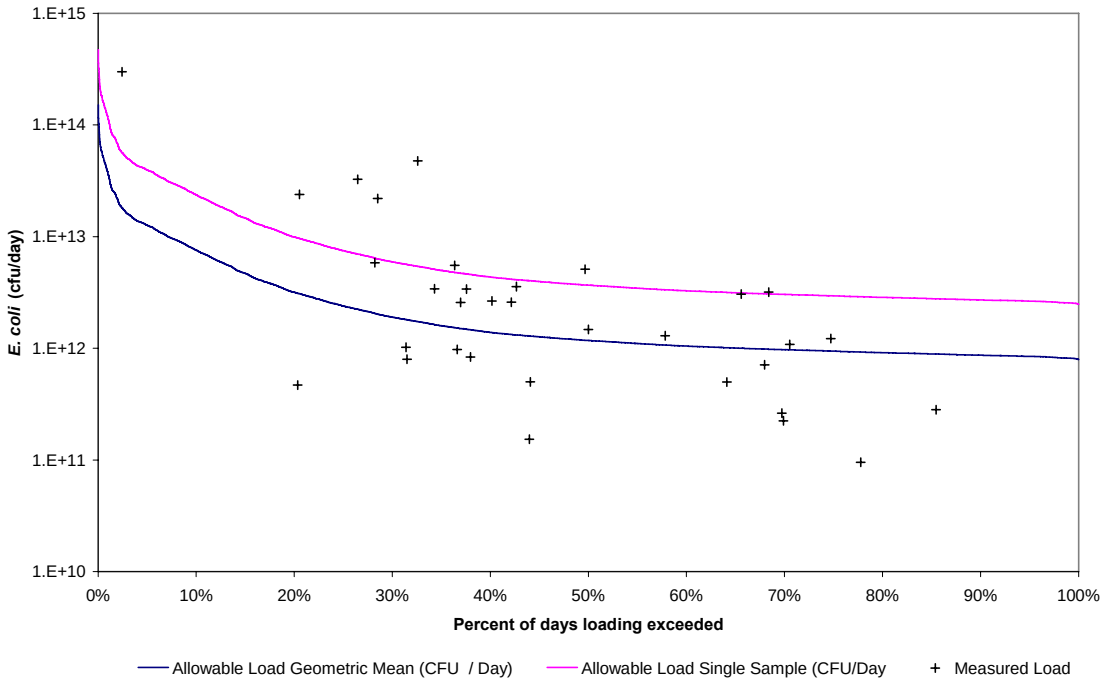

Figure 4-16 Bacteria load duration curve for station 11080, Segment 0841.

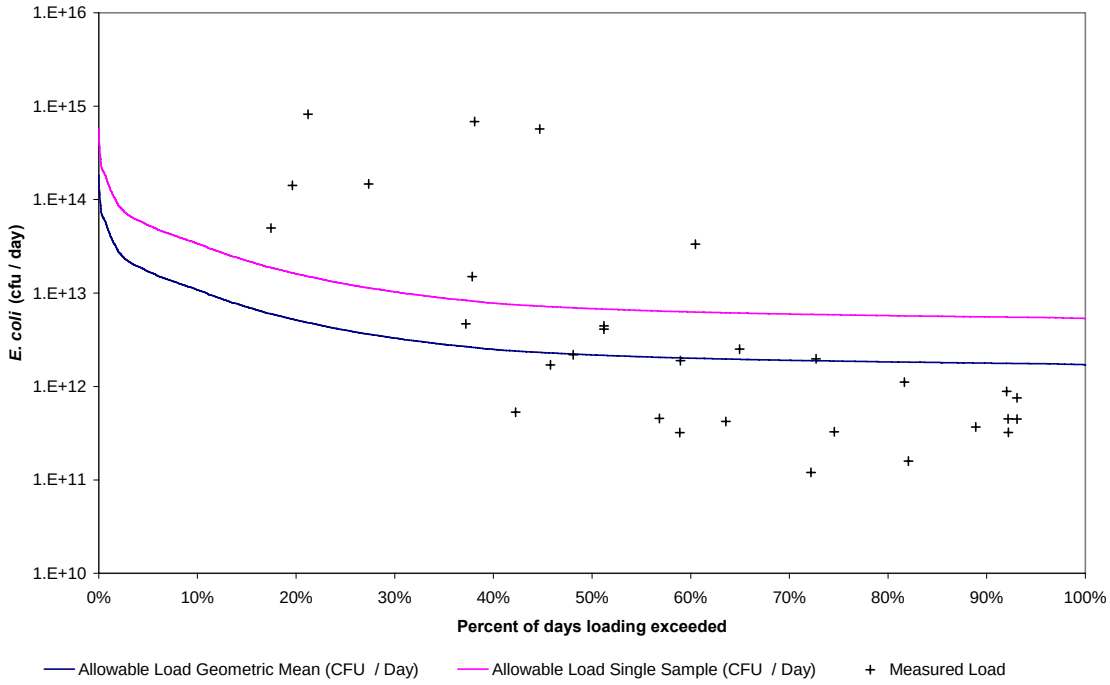

Figure 4-17 Bacteria load duration curve for station 11089, Segment 0841.

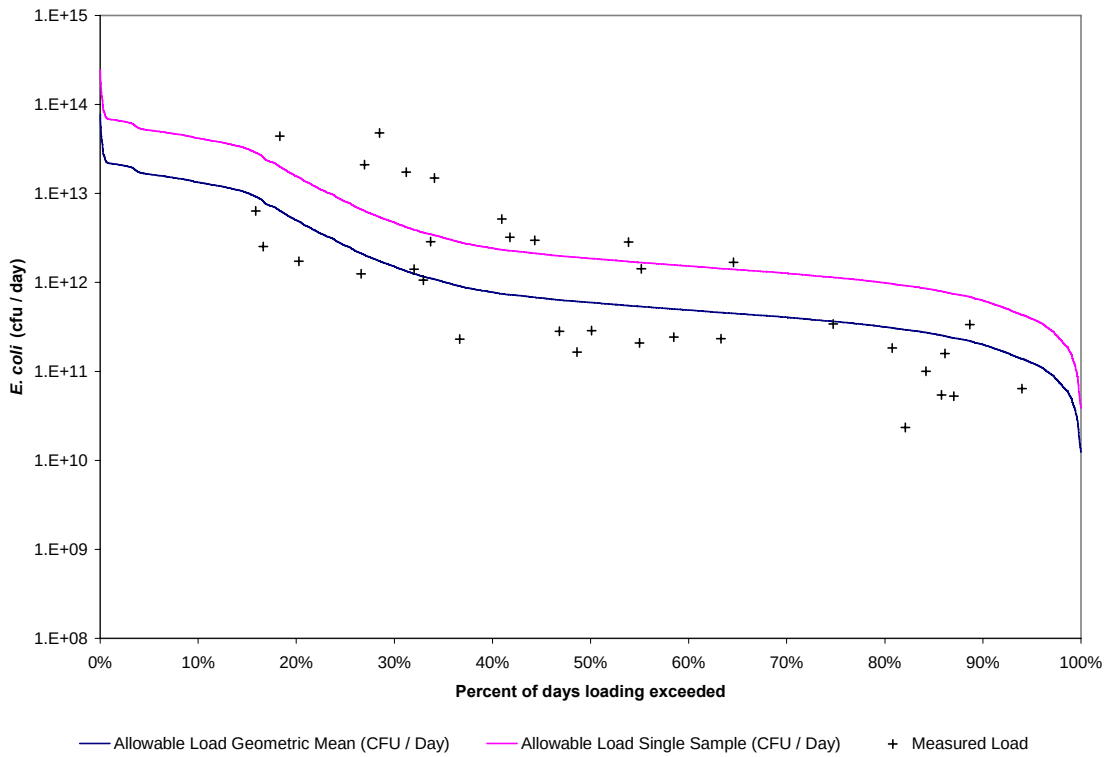

Figure 4-18 Bacteria load duration curve for station 17162, Segment 0822

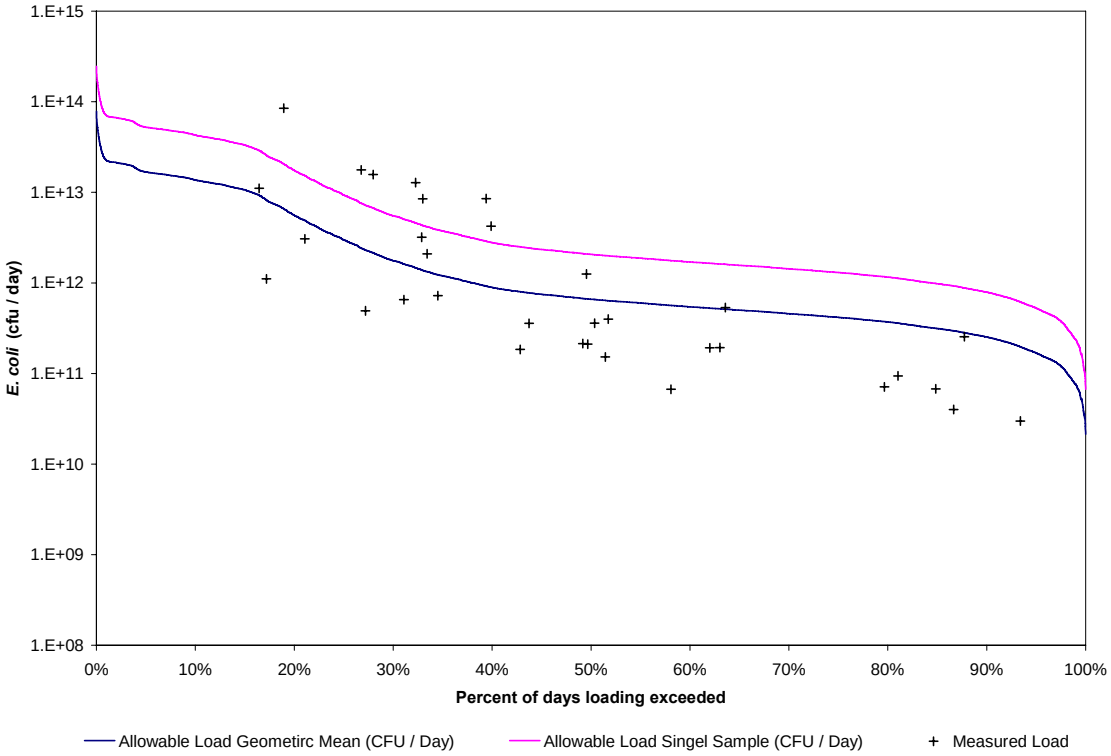

Figure 4-19 Bacteria load duration curve for station 17163, Segment 0822

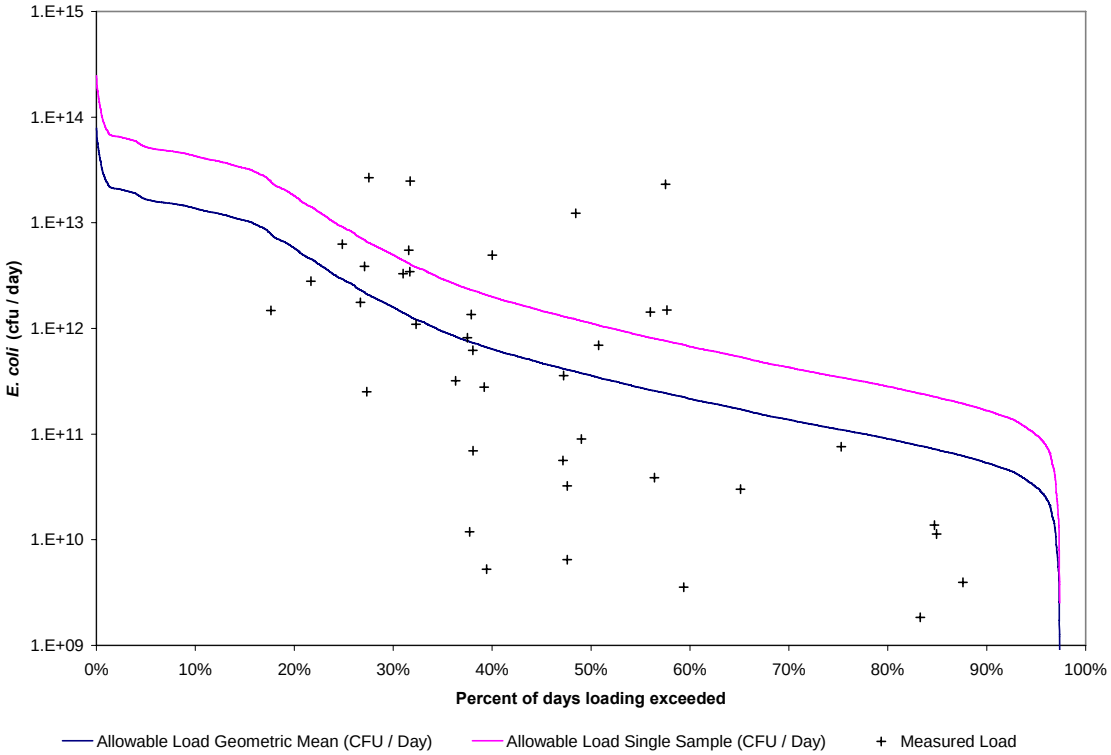

Figure 4-20 Bacteria load duration curve for station 18310, Segment 0822

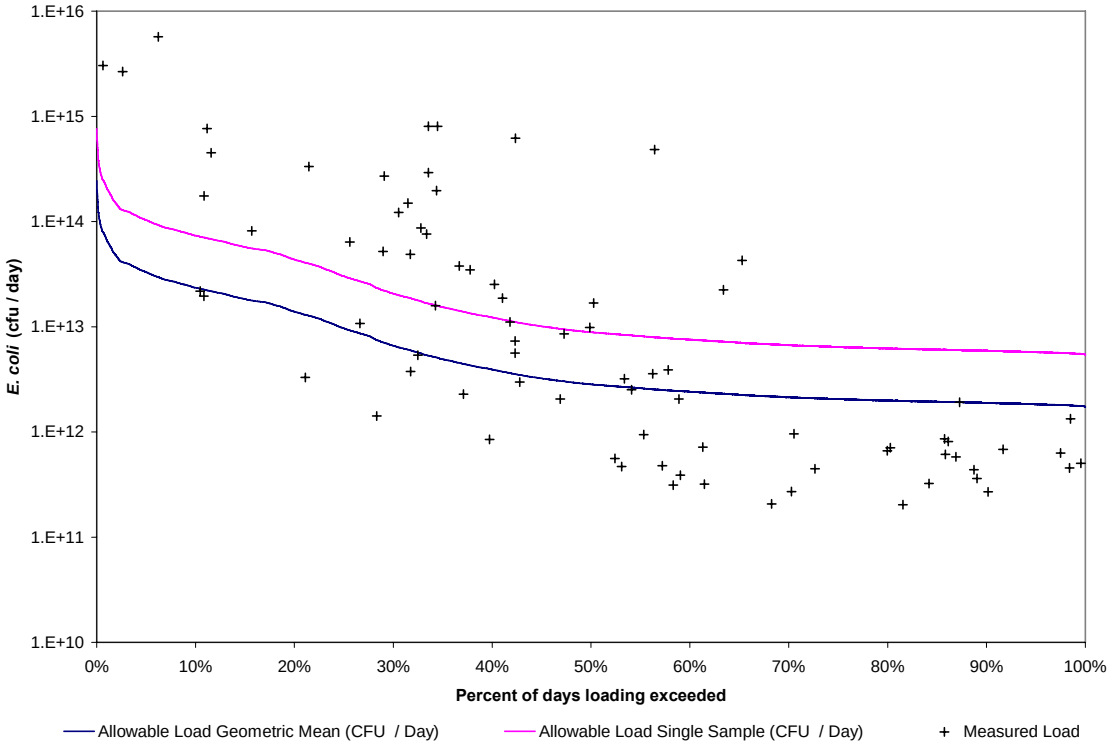

Figure 4-21 Bacteria load duration curve for station 10937, Segment 0805.

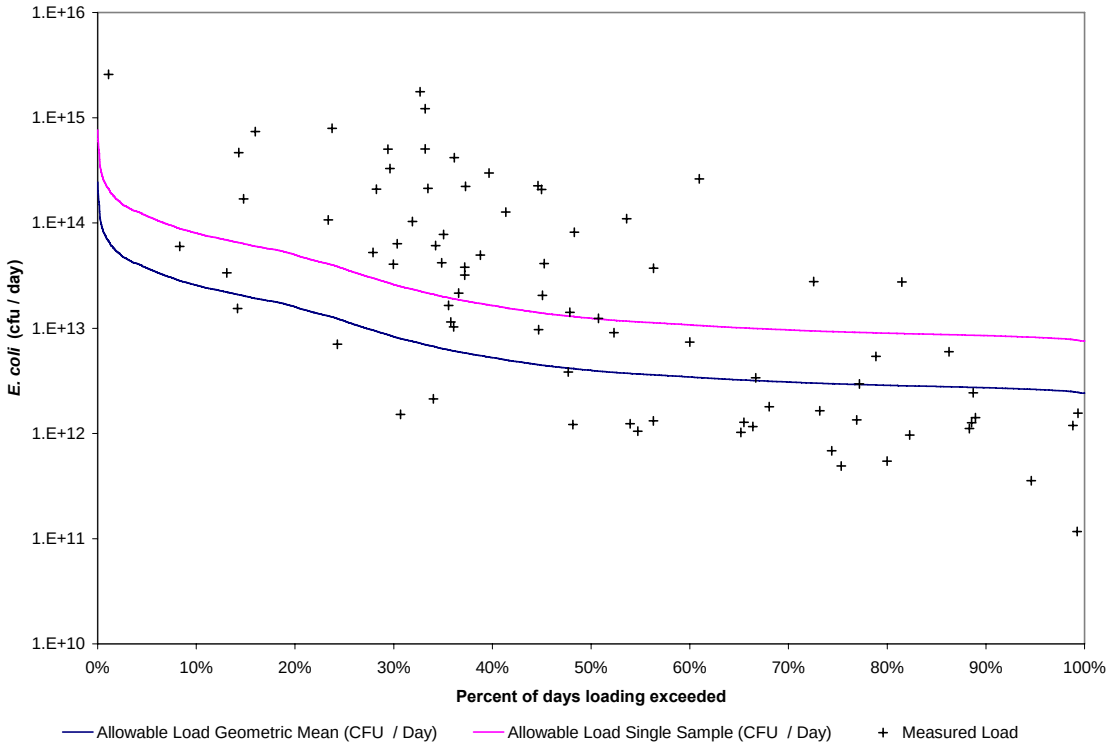

Figure 4-22 Bacteria load duration curve for station 10934, Segment 0805.

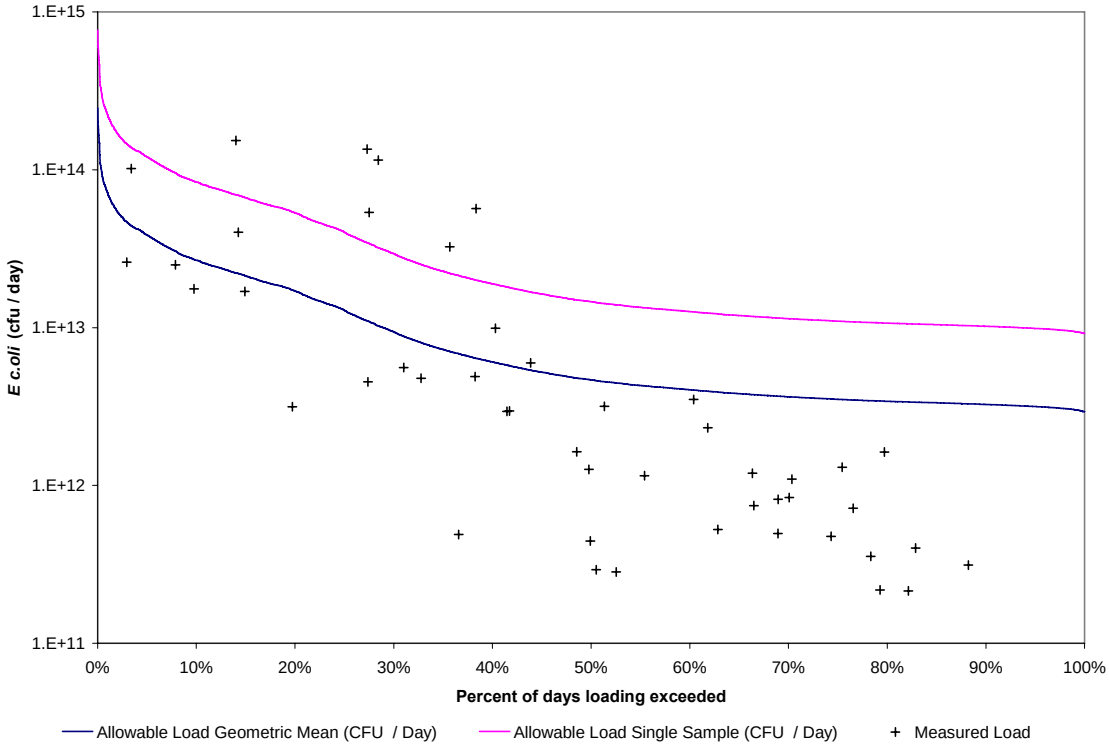

Figure 4-23 Bacteria load duration curve for station 10930, Segment 0805.

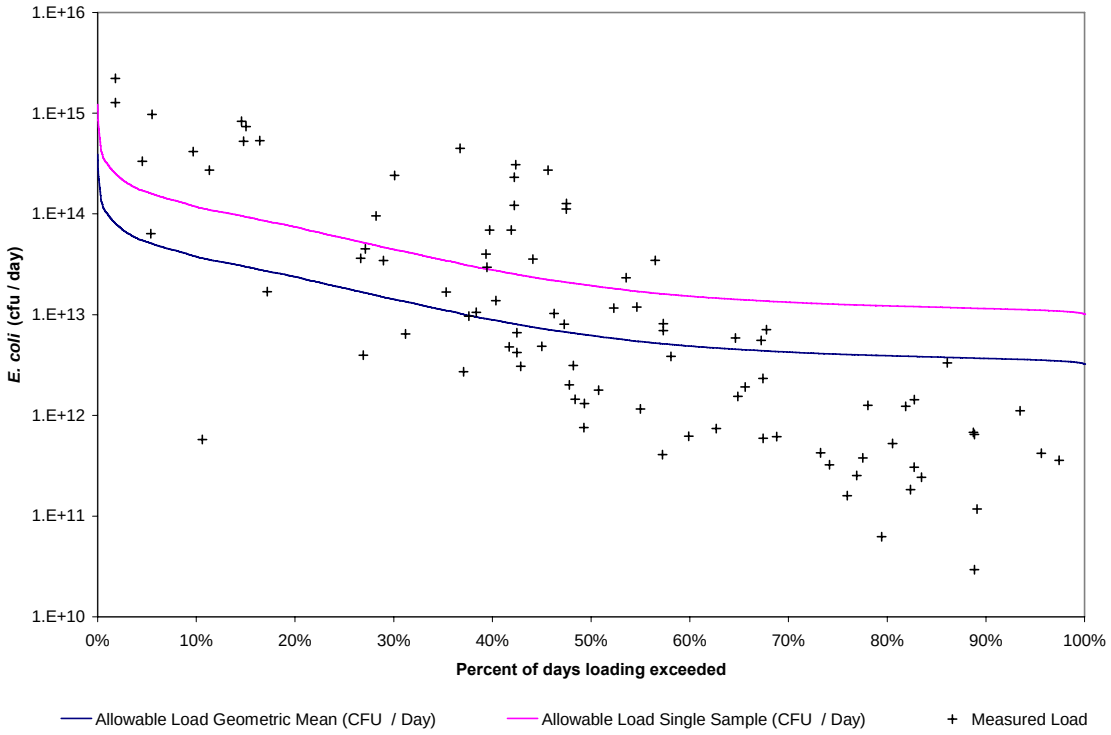

Figure 4-24 Bacteria load duration curve for station 10925, Segment 0805.

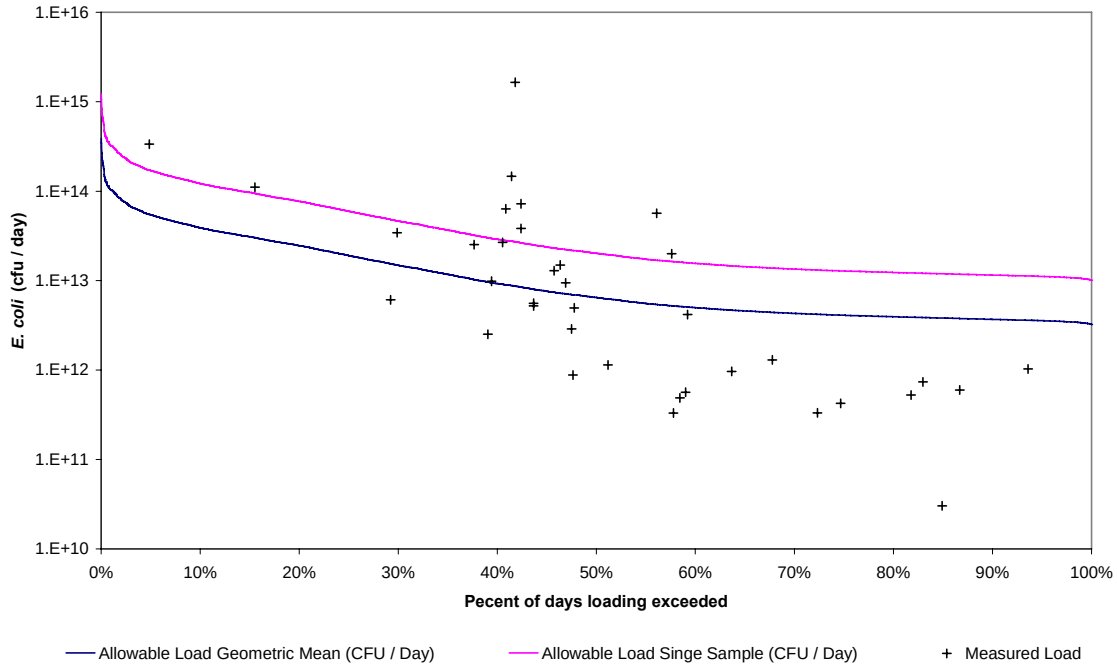

Figure 4-25 Bacteria load duration curve for station 10924, Segment 0805.

Section 5

TMDL ALLOCATION ANALYSIS

Within this report section is presented the development of the bacteria TMDL allocation. The allocation tool used for the West Fork Trinity River below Lake Worth (0806), Lower West Fork Trinity River (0841), Elm Fork Trinity River (0822), and Upper Trinity River (0805) 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, TMDL allocations, and other TMDL components are described herein.

The load duration curve method provided a flow-based approach to determine necessary reductions in bacteria loadings within these segments. 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.

An incremental contributing drainage area approach has been used to estimate flows in the TMDL development for each segment not supporting its contact recreation use. The incremental area is defined as the drainage area from the most downstream (or outlet) point of a segment up to the upstream terminus of the segment. Within this definition of the incremental drainage area, the incremental drainage area of other classified segments that enter the segment in question are not included, and, likewise, the area from upstream major reservoirs are excluded. This incremental area approach takes into account the continuity of downstream water flow through the Upper Trinity River Basin study area, the typically very low bacteria levels near the outlet (e.g., spillway, release gates, etc.) of a large reservoir, the requirement to develop specific TMDL allocations for each of the nonsupporting segments, and the downstream influences on bacteria loadings from upstream segments. It is also assumed within the implementation of this approach that upstream bacteria loadings are negligible from major reservoirs. Further within the actual implementation of this incremental approach, it is recognized that even though only specific reaches within each segment do not support the designated recreation use, that all sources within the watershed can contribute to the *E. coli* loading at a downstream point. Within the subsequent Implementation Plan, an adaptive approach will be used to bring the necessary spatial focus to improving water quality and restoring the contact recreation use.

In practice the incremental drainage area approach was defined as follows beginning at the most upstream segment and moving downstream:

- West Fork Trinity River below Lake Worth (0806): The incremental area of this segment was defined by the drainage area included from the outlet of the segment (a point immediately upstream of the West Fork and Village Creek confluence) to Lake Worth Dam excluding the incremental drainage area of the Clear Fork Trinity River below Benbrook Lake (Segment 0829). Hence, this incremental area was defined to include the drainage area of Segment 0806 and not include the drainage area of Segment 0829 (Figure 2-1).

- Lower West Fork Trinity River (Segment 0841): The incremental area of this segment was defined by the drainage area included from the segment outlet (a point immediately upstream of the confluence with the Elm Fork) to the outlet of upstream Segment 0806 (Figure 2-1).
- Elm Fork Trinity River below Lewisville Lake (Segment 0822): The incremental area of this segment was the drainage area from the outlet of the segment at the confluence with the West Fork to Lewisville Lake Dam excluding the incremental drainage area of Denton Creek (Segment 0825). Hence, this incremental area was defined to include the drainage area of Segment 0822 and not include the drainage area of Segment 0825 (Figure 2-1).
- Upper Trinity River (Segment 0805): The incremental area of this segment was defined as the drainage area from the segment downstream outlet, which is a point immediately upstream of the confluence of the Cedar Creek Lake discharge canal, to the confluence of the West Fork and Elm Fork and to Lake Ray Hubbard Dam less the incremental drainage area of the East Fork Trinity River (Segment 0819). Hence, this incremental area was defined to include the drainage area of Segment 0805 and not include the drainage area of Segment 0819 (Figure 2-1).

5.1 Endpoint Identification

The West Fork Trinity River below Lake Worth, Lower West Fork Trinity River, Elm Fork Trinity River below Lewisville Lake, and Upper Trinity River have a designated use for contact recreation, which is protected by numeric criteria for the indicator bacteria of *E. coli*. Indicator bacteria are not generally pathogenic and are indicative of potential viral, bacterial, and protozoan contamination originating from the feces of warm-blooded animal. *E. coli* criteria to protect freshwater contact recreation consist of single sample and geometric mean concentrations not to be exceeded of 394 org/100 ml and 126 org/100ml (TNRCC, 2000). Further, for a water body to be considered as supporting contact recreation use the single sample criterion of 394 org/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).

5.2 Assessment Results from Routine Monitoring *E. coli* Data

As previously presented in this report, routine monitoring *E. coli* data were available for 17 monitoring stations within Segments 0806, 0841, 0822, and 0805. Of the 17 stations 9 failed to meet the contact recreation use—stations 17863 and 16120 in Segment 0806, stations 11080, 17669, and 11081 in Segment 0841, station 17162 in Segment 0822, and stations 10937, 10934, and 10925 in Segment 0805. The *E. coli* data for all nine stations failed to meet the geometric mean criterion, while the data from stations 16120, 11081, 17162, 10937, 10934, and 10925 also failed to meet the percent single sample exceedance criteria based on the binomial method (see Section 2.2.2 — Analysis of Bacteria Data).

5.3 Seasonality

Seasonal variations or seasonality occur when there is a cyclic pattern in streamflow and, more importantly, in water quality constituents, which for this study was *E. coli.* If seasonality was pronounced (i.e., statistically significant) then the TMDL process should take this factor into account. Seasonality in the historical *E. coli* concentrations was evaluated for the impaired reaches of each segment. The *E. coli* data from all stations in impaired reaches of each segment were combined into a single data set, which was statistically evaluated using a correlogram of monthly data as described by Reckhow et al. (1993). For all four segments *E. coli* concentrations did not show any statistically significant seasonal variation. While not statistically significant (α=0.05), a slight seasonal pattern was apparent for Segment 0822, which may be an artifact of the relatively small data set that was available for that segment. The variability in the geometric mean of *E. coli* concentrations for each month per segment is illustrated in Figure 5-1. Because no significant seasonal patterns were apparent in the data, the TMDLs do not include a seasonal component.

5.4 Linkage Analysis

Establishing a relationship between instream water quality and the source of loadings is an important component in developing TMDLs. This relationship allows for the evaluation of management options that will achieve the desired endpoint. The relationship may be established through a variety of techniques.

In the development of these TMDLs, load relationships and possible sources were defined through load duration curves combined with historical *E. coli* data and the associated daily average flow for the flow duration curves (see Figures 4-10 — 4-25). In general the load duration curves and historical data plots indicated greater *E. coli* concentrations and a greater number of exceedances with increasing flow, which was an indication that rainfall-runoff was an important factor in the contribution of bacteria from the urban and rural landscape within the Trinity River Basin study area. Bacterial source tracking was also used to better define sources of bacteria and the results from those studies will be used to inform the implementation process. The BST study design and results were provided in Section 3 — Bacterial Source Tracking.

5.5 Margin of Safety

The margin of safety (MOS) for pollutant load allocations is required to provide a greater level of certainty that prescribed allowable loadings will result in attainment of water quality targets. There are two methods in which a MOS may be utilized when calculating a TMDL:

- implicitly incorporating the MOS using conservative model assumptions to develop allocations; or
- explicitly assigning a portion of the total TMDLs as the MOS and using the remainder for allocations

This TMDL contains an implicit MOS by not accounting for decay and/or die off of *E. coli* and the assumption that WWTFs discharge continuously contains *E. coli* loadings at the

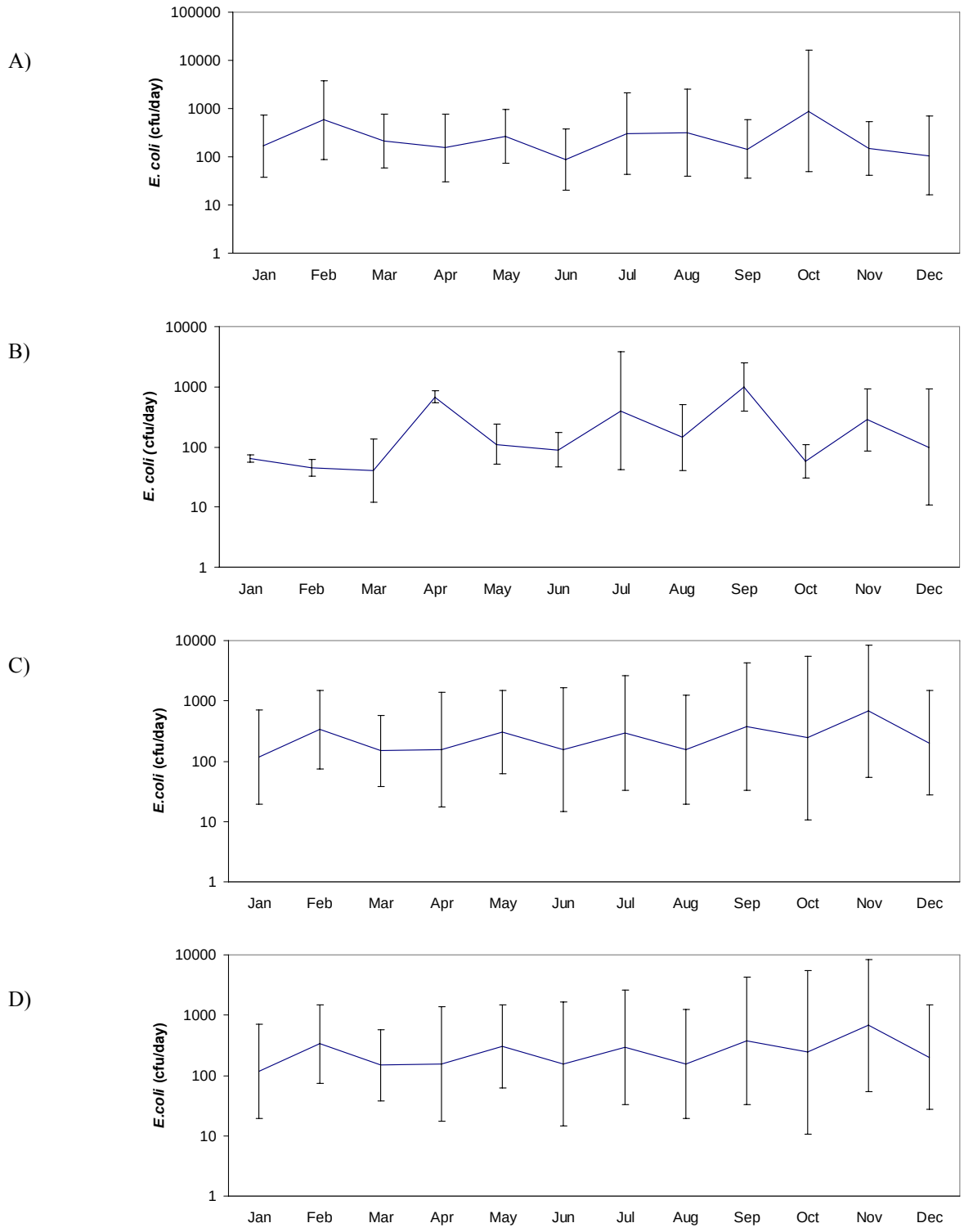

Figure 5-1 Geometric mean of *E. coli* concentrations from impaired stations for each month A) Segment 0806, B) Segment 0841, C) Segment 0822, and D) Segment 0805. Error bars indicate the upper and lower bounds of the standard deviation.

maximum allowable loading. In addition to these conservative assumptions the water quality standard also provides an implicit MOS because the *E. coli* criterion correlates with a low illness rate of less than 1.0 percent.

5.6 Flow Regimes for Load Duration Curves

A useful refinement of the load duration curve approach in load reduction and TMDL allocation analysis is to divide the curve into flow-regime regions and to develop load reductions and allocations for each flow regime. This approach will assist in guiding implementation efforts to develop solutions to conditions when exceedances are occurring. A commonly used set of regimes that is provided in Cleland (2003) is based on the following five intervals along the x-axis of the flow duration and load duration curves: (1) 0 – 10 % (high flows); (2) 10 – 40 % (upper mid-range conditions; (3) 40 – 60 % (mid-range flows); (4) 60 – 90 % (lower mid-range conditions); and (5) 90 – 100 % (low flows). Evaluation of the load duration curves including the historical data (Figure 4-10 — 4-25) indicated at several stations a paucity of data at the outer extreme intervals (high flows and low flows) and that the mid-range flows often provided a transition from higher occurrences of exceedances in *E. coli* concentrations in the interval of 0 – 40 % to fewer occurrences in the interval of 60 – 100 %. Based on these characteristics of the load duration curves, the five intervals were reduced to four intervals: 0 – 10 % (referred to as High Flows); 10–40% (referred to as Upper Mid-Range Flow), 40 – 60 % (referred to as Mid-Range Flows); and 60 – 100 % (referred to as Lower Mid-Range/Low Flows). The High Flows regime typically represents periods in which flows are dominated by runoff from large rainfall-runoff events that results in situations where successful containment of pollutants from nonpoint sources would be very difficult. The Upper Mid-Range Flows regime also represents periods in which flow are dominated by runoff from rainfall-runoff events; however, these events will be smaller than those encountered during High Flow situations and thus efforts to contain pollutants from nonpoint sources are more likely achieved. The Mid-Range Flows regime typically represents periods in which flows are dominated by runoff from smaller storm events and high base flow. The Lower Mid-Range/Low Flows regime typically represents periods that are dominated by conditions ranging from small runoff events to dry conditions in which flow is dominated by either natural base flow and/or effluent discharges.

5.7 Load Reduction Analysis

A single percent load reduction required to meet the allowable loading for each of the four flow regimes was determined for each segment using the historical *E. coli* data from within impaired reaches. For simplicity of computation and presentation, the load reduction calculations were based on concentrations rather than loadings (concentration multiplied by flow), since the flow would be identical in both the existing and allowable loadings computations and, thus, the flow would effectively cancel out of the calculations. For the calculation of the required percent reduction, the computations considered the greater of the reduction to meet the geometric mean criterion and the reduction to meet the single sample criterion, since both criteria need to be met to support the recreation use. The following steps were used to determine the required percent load reduction for each segment and each flow regime:

1. Develop load duration curves for all sampling stations within each segment's impaired reaches or reaches (Figures 5-2 through 5-16). Stations 18459, 17368, 10938, and 16120 were used in Segment 0806 (Figures 5-2 through 5-5). Stations 17669, 11081, 11080, and 11089 within the impaired reach for Segment 0841 were used (Figures 5-6 through 5-9). Station 17162 was used as it was the only station within the impaired reach of Segment 0822 (Figure 5-10). Finally, stations 10937, 10934, and 10925 within the impaired reaches of Segment 0805 were used (Figures 5-13 through 5-16).
2. For each station and flow regime, determine the 75th percentile and geometric mean concentrations of the historical data within each of the four flow regimes, which represent the appropriate concentrations for comparison to the single sample criterion (394 org/100 ml) and the geometric mean criterion (126 org/100 ml) respectively (Table 5-1).
3. For each station and flow regime, determine the percent reduction required to achieve the single sample criterion by calculating the difference in the existing 75th percentile concentration and the 394 org/100 ml criterion and dividing that difference by the 75th percentile concentration. Similarly, the required reduction for attaining the geometric mean criterion was determined by calculating the difference in the existing geometric mean concentration and the 126 org/100 ml criterion and dividing that difference by the geometric mean concentration.
4. The overall required reduction per flow regime for each segment was then calculated by averaging the highest reduction required for either the geometric mean criterion or the single sample criterion across stations within the segment (Tables 5-1 and 5-2).

Table 5-1 Geometric mean (Geomean) and 75th percentile values of historical *E. coli* data for sampling stations within impaired reaches. (Highlighted values represent values requiring the greatest reduction to meet water quality criterion.)

Station[a]	Segment/ Assessment Unit	High Flows (0-10 %)		Upper Mid-Range Flows (10-40 %)		Mid-Range Flows (40-60 %)		Lower Mid-Range/Low Flows (60-100 %)	
		Geomean (org/100 ml)	75th Percentile (org/100 ml)	Geomean (org/100 ml)	75th Percentile (org/100 ml)	Geomean (org/100 ml)	75th Percentile (org/100 ml)	Geomean (org/100 ml)	75th Percentile (org/100 ml)
18459	0806_01	NA[b]	NA[b]	425	2,775	109	280	74.9	169
17368	0806_01	1,662	2,419	87.7	206	19.6	76.8	15.3	25.4
10938	0806_01	1,311	4,840	241	1,732	36.4	108	13.5	32.3
16120	0806_01	1,255	2,419	528	2,419	216	491	26.9	39.3
17669	0841_01	4,355	4,838	1,046	3,408	162	370	82.6	102
11081	0841_01	1,928	4,838	1,306	4,837	142	308	99.3	163
11080	0841_01	2,090	2,090	268	847	145	269	79.8	158
11089	0841_01	NA[b]	NA[b]	2,970	13,320	151	240	48.3	73.5
17162	0822_02	NA[b]	NA[b]	257	1,300	170	555	64.7	99.0
10937	0805_04	9,850	16,180	756	3,106	200	411	46.4	53.0
10934	0805_03	3,716	22,270	1,139	4,838	559	3,025	90.4	133
10925	0805_02	1,184	2,311	346	2,165	198	776	20.7	45.0

[a] See Table 4-7 for individual station descriptions

[b] Bacteria data was not collected during high flow conditions for this station.

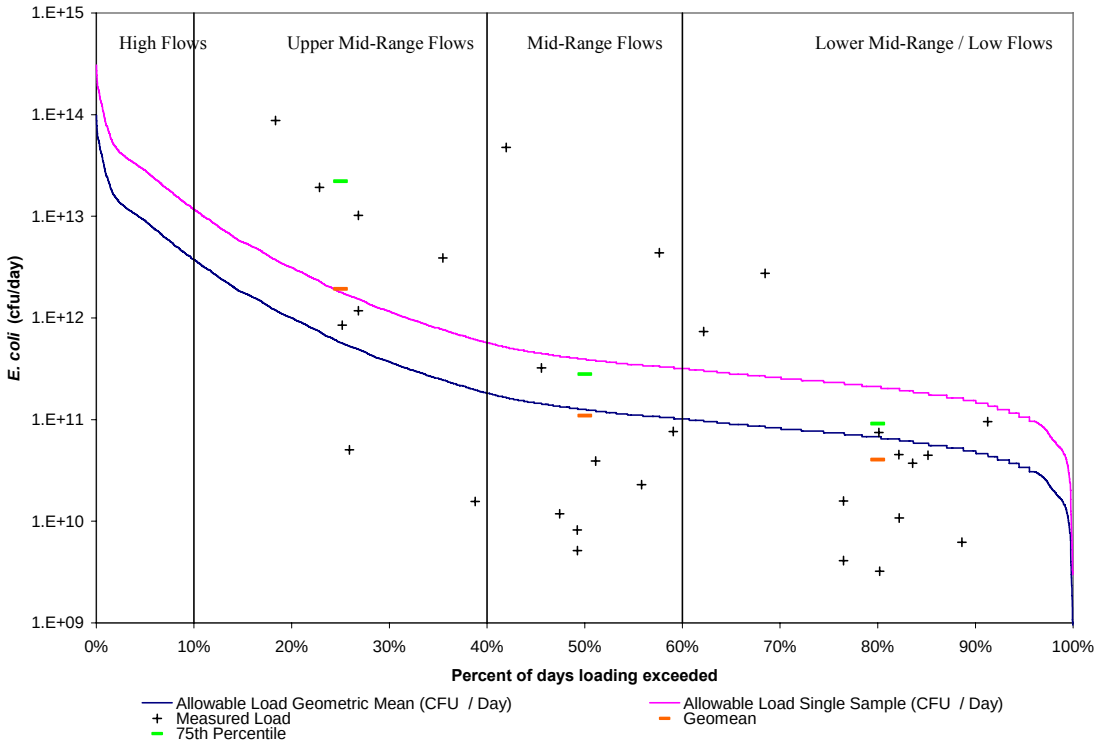

Figure 5-2 Bacteria load duration curve for station 18459, Segment 0806

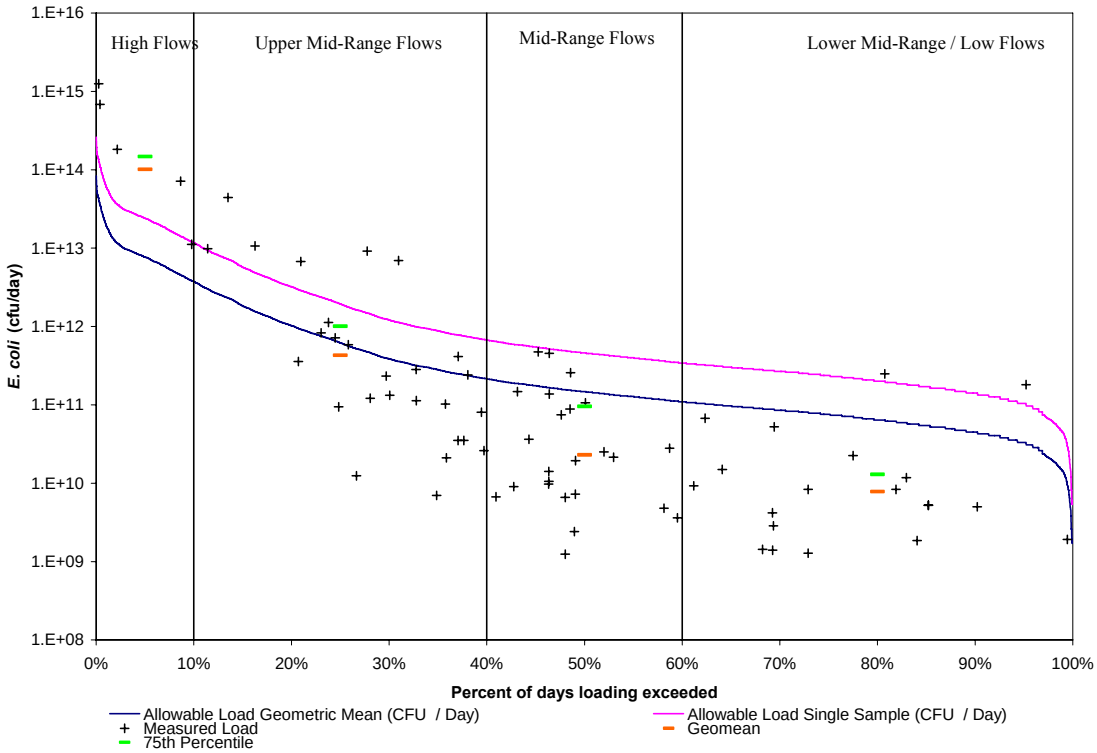

Figure 5-3 Bacteria load duration curve station 17368, Segment 0806

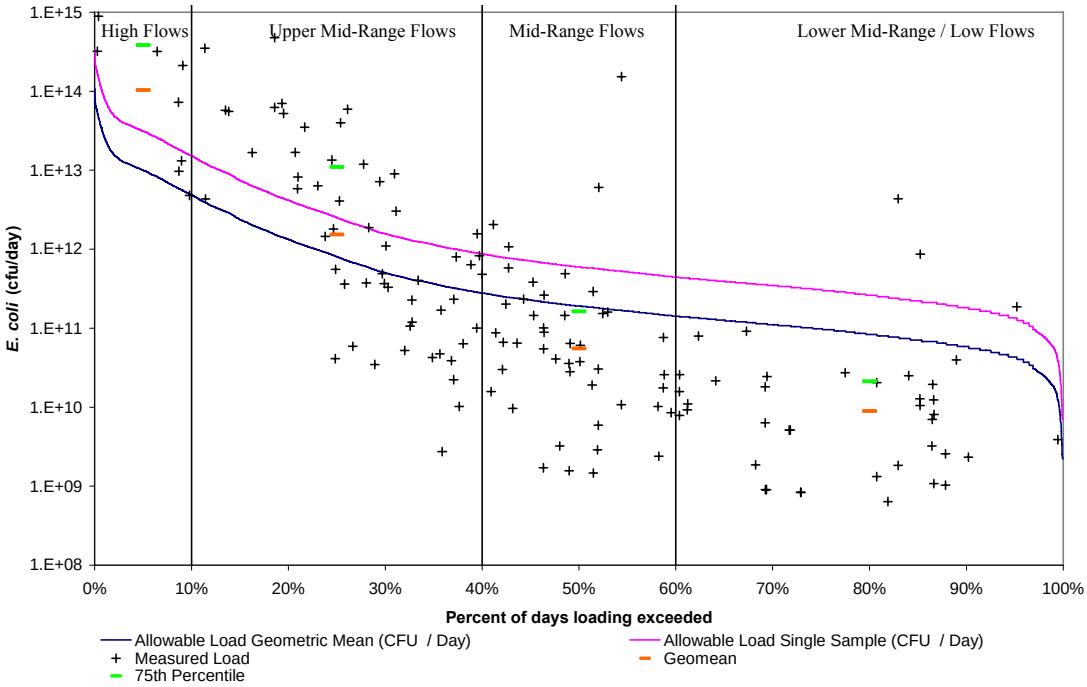

Figure 5-4 Bacteria load duration curve for station 10938, Segment 0806

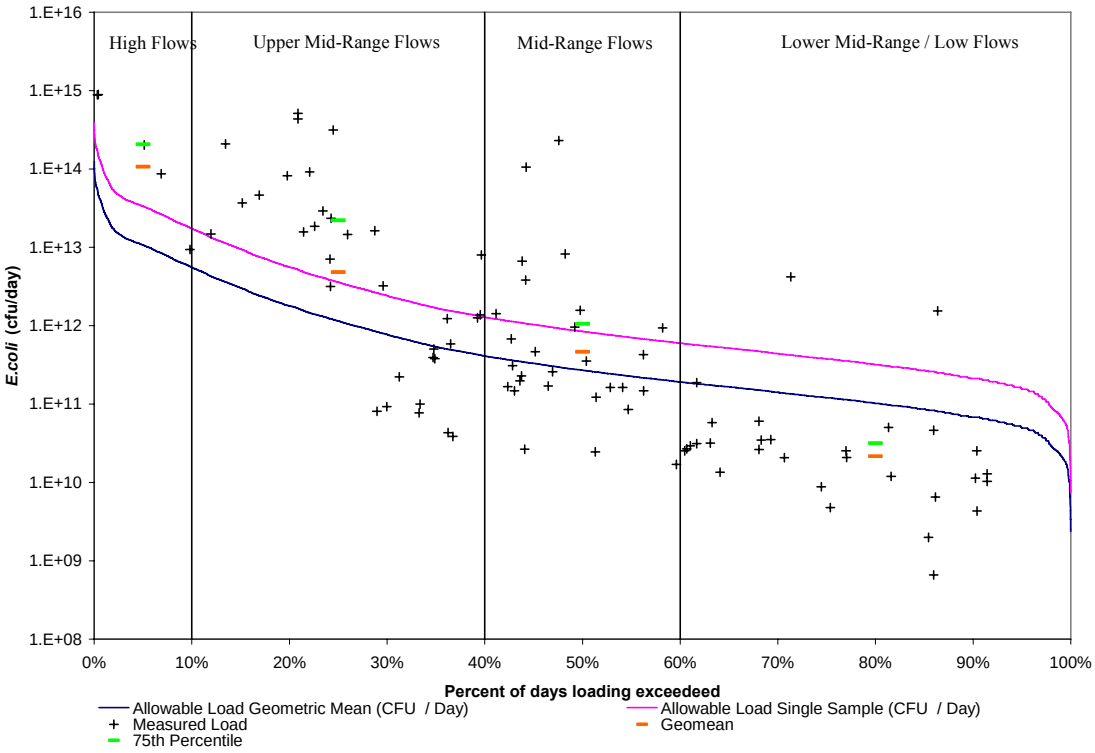

Figure 5-5 Bacteria load duration curve for station 16120, Segment 0806

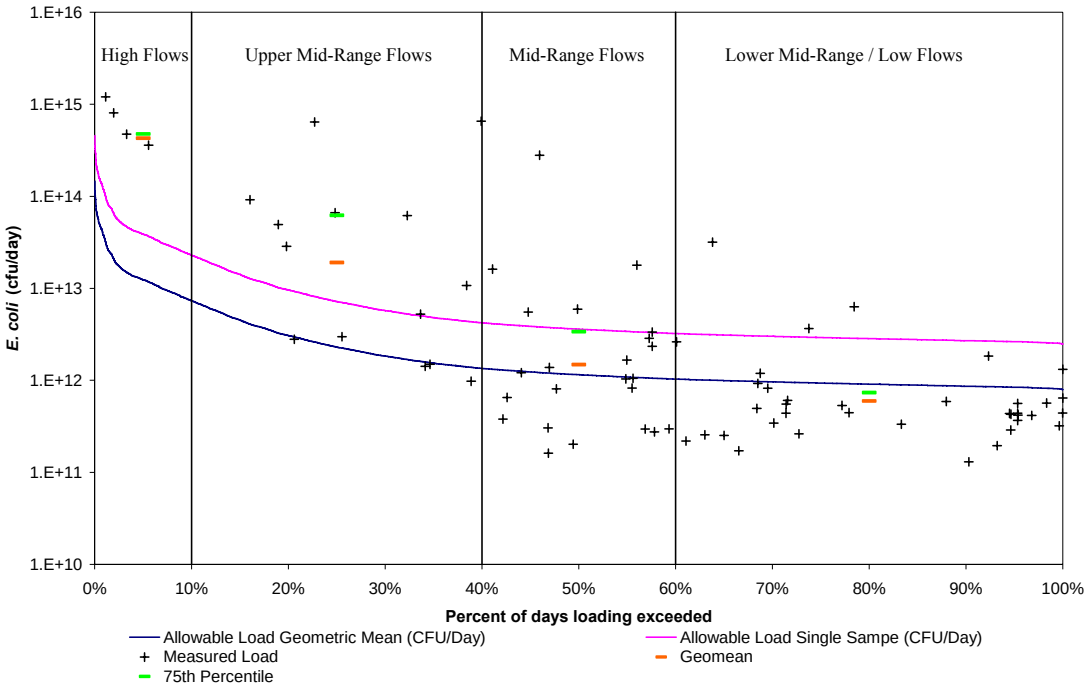

Figure 5-6 Bacteria load duration curve for station 17669, Segment 0841

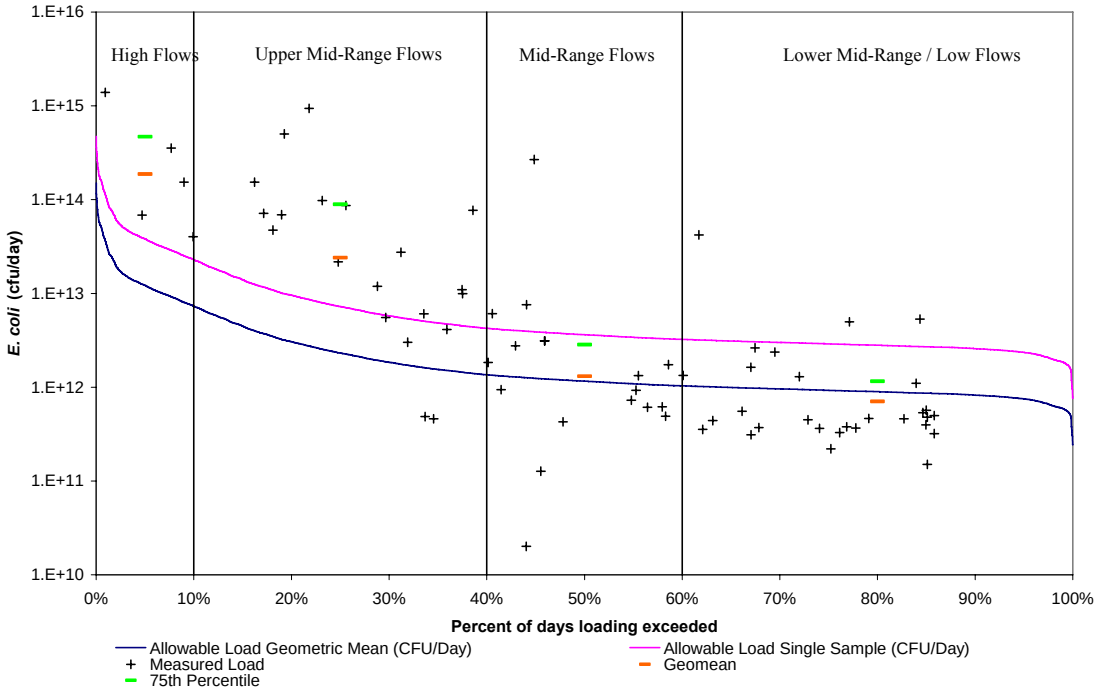

Figure 5-7 Bacteria load duration curve for station 11081, Segment 0841

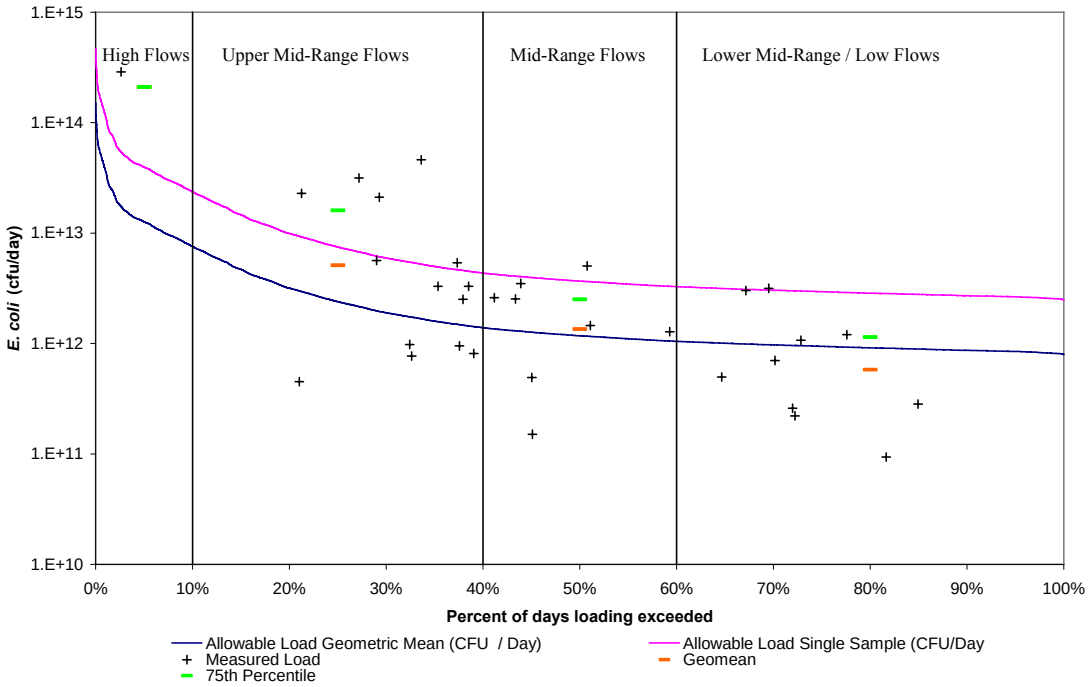

Figure 5-8 Bacteria load duration curve for station 11080, Segment 0841

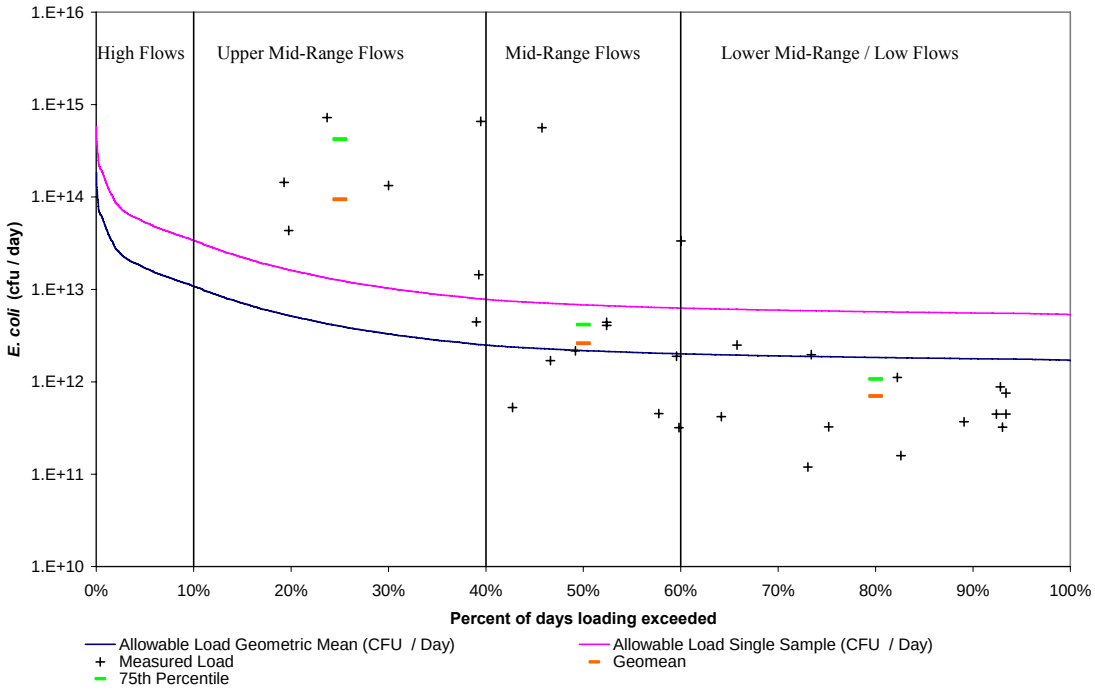

Figure 5-9 Bacteria load duration curve for station 11089, Segment 0841

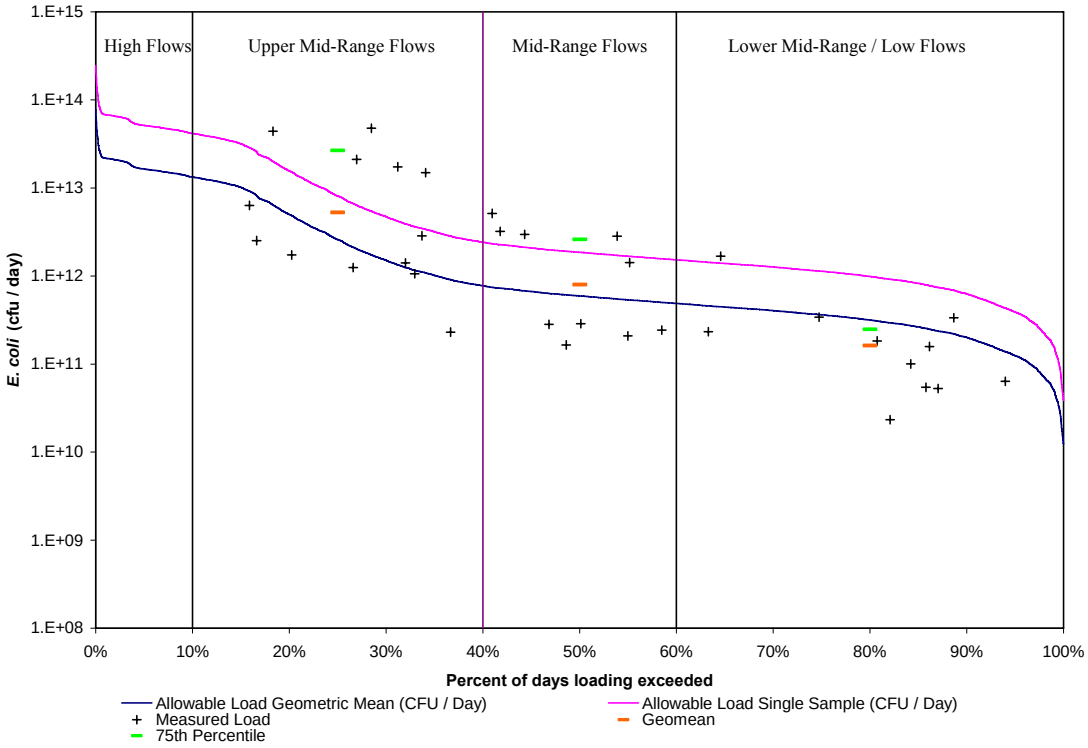

Figure 5-10 Bacteria load duration curve for station 17162, Segment 0822

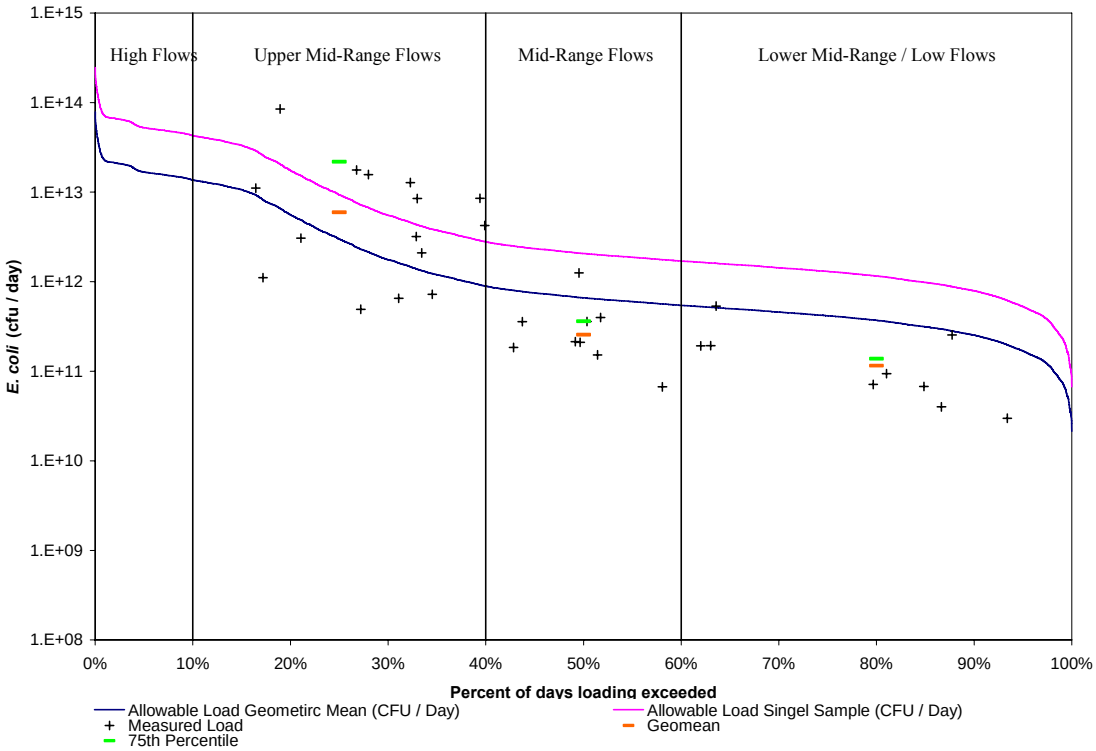

Figure 5-11 Bacteria load duration curve for station 17163, Segment 0822

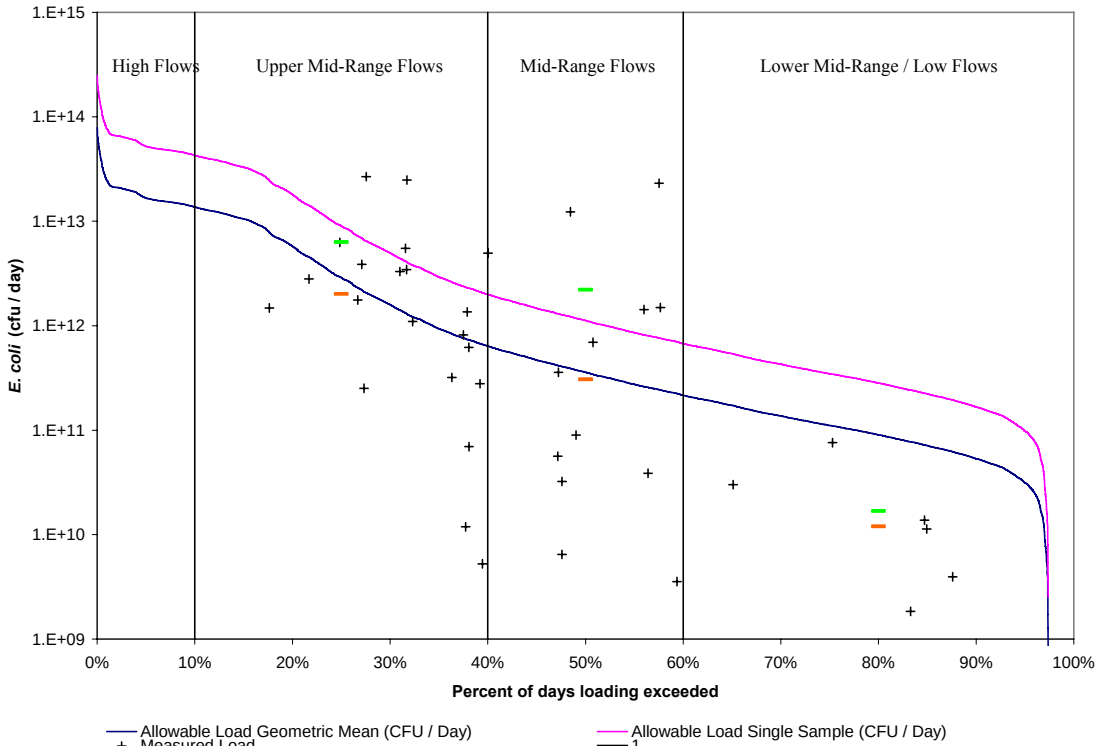

Figure 5-12 Bacteria load duration curve for station 18310, Segment 0822

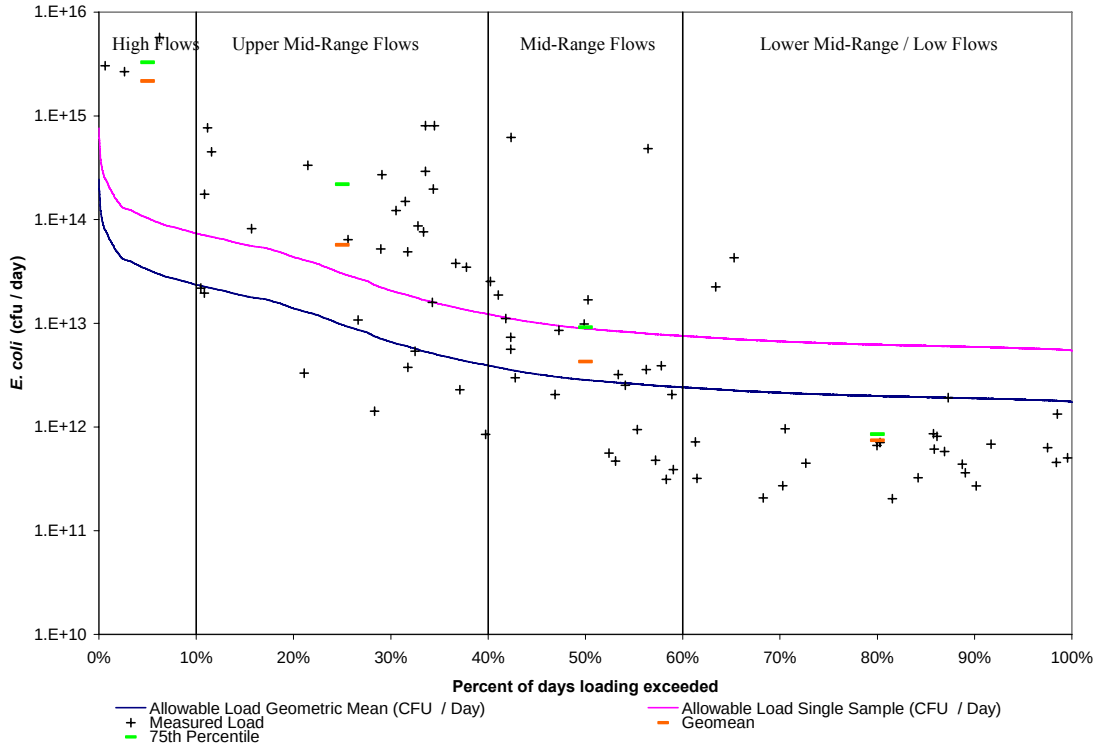

Figure 5-13 Bacteria load duration curve for station 10937, Segment 0805

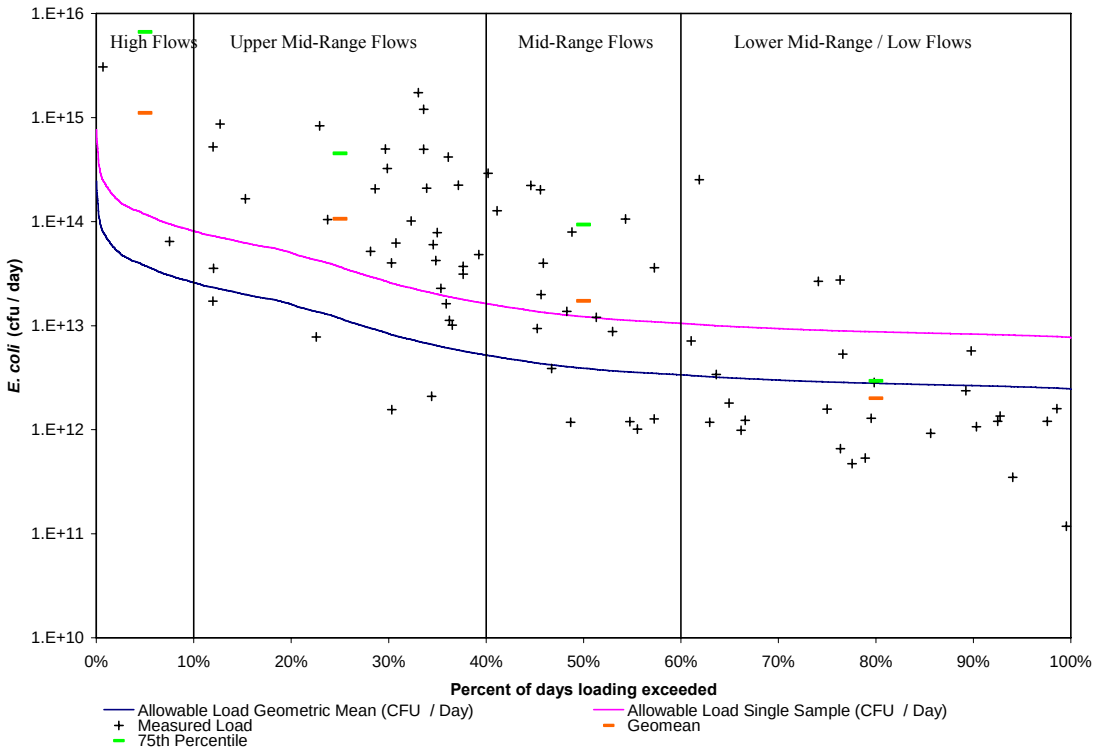

Figure 5-14 Bacteria load duration curve for station 10934, Segment 0805

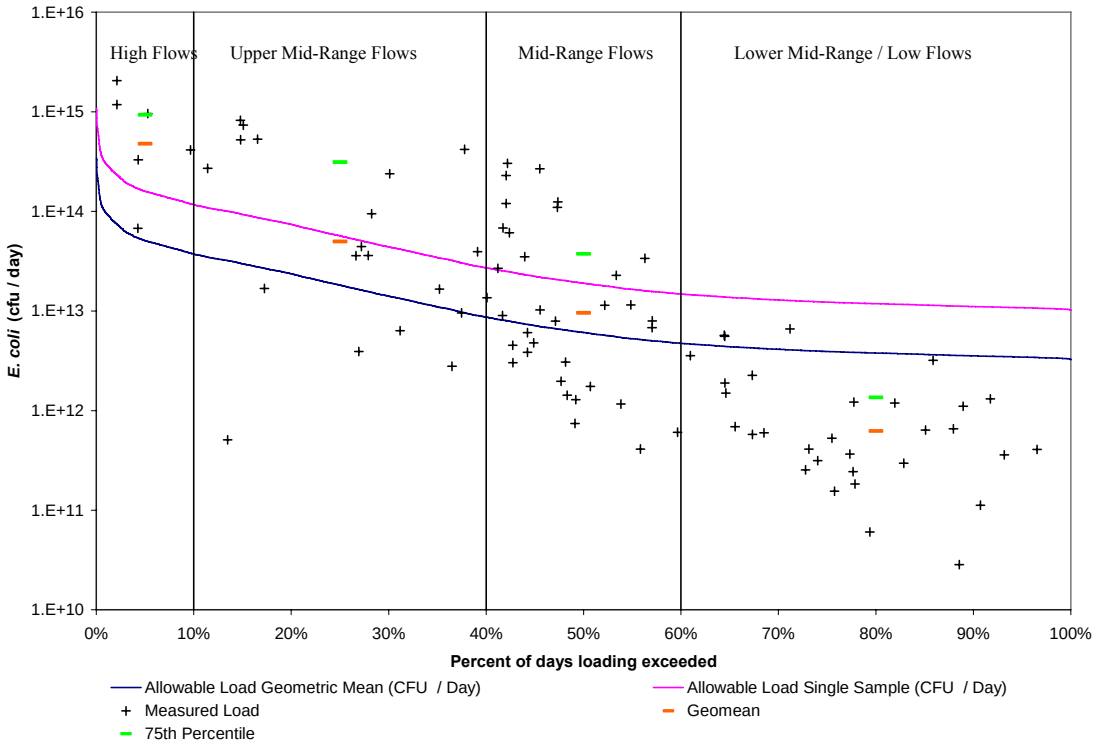

Figure 5-15 Bacteria load duration curve for station 10925, Segment 0805

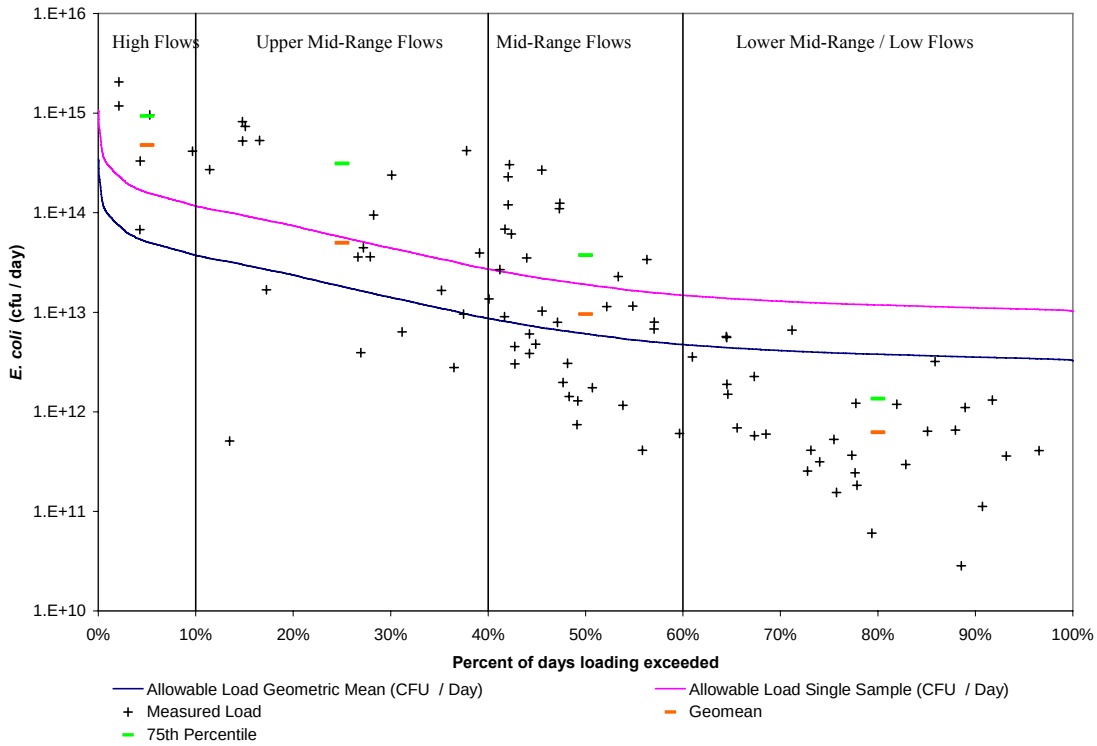

Figure 5-16 Bacteria load duration curve for station 10924, Segment 0805

Table 5-2 Percent reductions to meet geometric mean and single sample criteria

Station[a]	Segment/ Assessment Unit	High Flows (0-10 %)	Upper Mid-Range Flows (10-40 %)	Mid-Range Flows (40-60 %)	Lower Mid-Range/Low Flows (60-100 %)
		Greatest Required Percent Reduction[b]			
18459	0806_01	NA[c]	86	0	0
17368	0806_01	92	0	0	0
10938	0806_01	92	77	0	0
16120	0806_01	90	84	42	0
Average Required Percent Reduction – 0806		91	62	11	0
17669	0841_01	97	88	22	0
11081	0841_01	93	92	11	0
11080	0841_01	94	53	13	0
11089	0841_01	NA[c]	97	17	0
Average Required Percent Reduction – 0841		95	83	16	0
17162	0822_02	NA[c]	70	29	0
Average Required Percent Reduction – 0822		NA[c]	70	29	0
10937	0805_04	99	87	37	0
10934	0805_03	98	92	87	0
10925	0805_02	89	83	48	0
Average Required Percent Reduction – 0805		95	87	57	0

[a] See Table 4-7 for individual station descriptions.

[b] Greatest required percent reduction calculated based on highlighted values from Table 5-1.

[c] Bacteria data was not collected during high flow conditions for this station.

Therefore the estimated load reduction required to meet both the single sample criterion and the geometric mean criterion are as follows:

- Segment 0806: calculated load reduction to meet both criteria is an average of 91% with a range of 90 to 92% during High Flow conditions, an average of 62% with a range of 0 to 86% during Upper Mid-Range Flow conditions, an average of 11% with a range of 0 to 42% during Mid-Range Flow conditions, and no reduction required during Lower Mid-Range/Low Flow conditions.
- Segment 0841: calculated load reduction to meet both criteria is an average of 95% with a range of 93 to 97% during High Flow conditions, an average of 83% with a range of 53 to 97% during Upper Mid-Range Flow conditions, an average of 16% with a range of 11 to 22% during Mid-Range Flow conditions, and no reduction required during lower Mid-Range/Low Flow conditions.
- Segment 0822: calculated load reduction to meet both criteria is 70% during Upper Mid-Range Flow conditions, 29% during Mid-Range Flow conditions, and no reduction required during Lower Mid-Range/Low Flow conditions. It should be noted that no samples were collected within segment 0822 during high flow conditions thus a required load reduction during High Flow conditions could not be calculated. Also only a single monitoring station was located in the impaired assessment unit so that a range is not reported for the percent load reductions.
- Segment 0805: calculated load reduction to meet both criteria is an average of 95% with a range of 89 to 99% during High Flow conditions, an average of 87% with a range of 83 to 92% during Upper Mid-Range Flow conditions, an average of 57% with a range of 37 to 87% under Mid-Range Flow conditions, and no reduction required during lower Mid-Range/Low Flow conditions.

5.8 Pollutant Load Allocations

5.8.1 TMDL Definition

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 this study the TMDL was calculated per flow regime based on the geometric mean criterion of 126 org/100 ml, and the median flow value within each regime for the most downstream station within each segment, except for Segment 0822. It is noted that while the TMDL allocation is determined in terms of the geometric mean criterion, the load reduction computations (Section 5.7) used the greater of the percent reduction to meet the single sample criterion or the geometric criterion. Therefore the load reduction analysis ensures that both criteria will be met.

The large amount of municipal water withdrawal between the impaired reach and the lowest station presented an added complication in Segment 0822. The most downstream station above the municipal water intakes (station 17163) was used in the computation of pollutant load allocations for Segment 0822. However, the allowable pollutant loading for the most downstream station, which is 18310, was also calculated for Segment 0822, since the allowable

loading at station 18310 best represented the loading entering Segment 0805 from Segment 0822.

A further complication for these TMDLs was the development of pollutant load allocations for upstream and tributary segments, which needed to be accounted for in downstream segments. To account for the upstream allocations, an incremental drainage area approach (see discussion beginning on last paragraph of page 5-1) was used in the TMDL calculations. For purposes of bacteria load allocation, the TMDL load allocation is defined by the following equation:

$$TMDL = \Sigma\ WLA + \Sigma\ LA + MOS$$

where the variables are defined as follows:

1) WLA is the waste load allocation for point (TPDES-regulated) sources, which for purposes of this TMDL includes discharges from WWTFs and Phase I and II MS4 permitted areas. The two types of WLA loadings will be designated as those from WWTFs, which will be referred to as WLA_{WWTF}, and those from MS4 permitted discharges, which will be referred to as WLA_{MS4}. The discharge used in estimating the loading for WWTFs was based on the final full permitted discharge of each WWTF, while the MS4s loading was based on the median flow value for each flow regime. The full permitted discharge is used for WWTFs, since this amount is considered the maximum allowable discharge. The median flow is defined as the representative flow within each flow regime.

2) The LA includes the load allocation assigned to nonpoint sources that are not under TPDES regulation, and the total allocated load assigned to both point and nonpoint sources that enter from upstream and/or tributary segments. The two types of LA loadings will be designated as those from nonpoint sources within the segment, which will be referred to as LA_{NPS}, and those from upstream and/or tributary segments, which will be referred to as LA_{UT}. The LA_{NPS} for nonpoint sources was calculated based on the median flow value for each flow regime and the geometric mean criterion. Nonpoint sources include non-regulated stormwater runoff and direct deposition from warm-blooded animals. The LA_{UT} is based on the loadings calculated at the most downstream station within a segment or in the case of nonimpaired segments (i.e., Segments 0829, 0825, and 0819) the point immediately upstream of the confluence with the impaired segment. The purpose of the LA_{UT} component is to take into account the total allocated loadings entering from any upstream or tributary segments.

3) The MOS for this TMDL is implicitly applied using conservative model assumptions described in Section 5.5. Because of the high bacteria removal efficiencies of major reservoirs, negligible loadings are assumed to occur from these reservoirs in the TMDL allocation computations. While assuming negligible loadings from reservoirs is not a conservative assumption, the conservative assumption of ignoring instream die off and settling of *E. coli* is considered to more than offset this nonconservative assumption.

5.8.2 Existing and Maximum Allowable Daily Loadings

Existing daily loading and maximum allowable daily loading were determined for each segment using historical *E. coli* data and the load duration curves. The loadings were determined for the median flow within each of the four flow regimes used as a refinement of the load duration curves.

The existing daily loading for each segment, which includes upstream and tributary loadings from classified stream segments, was calculated for each flow regime using the median flow and geometric mean of the *E. coli* concentration within each flow regime for each station within a segment. For each flow regime, the existing loading was considered as the largest value calculated for any station within the segment. The calculation of the existing loading was performed by multiplying the median flow in units of cubic meters per second (cms) by the geometric mean concentration in org/100 ml and further multiplied by a conversion factor of 8.64 E+08 to convert to units of organism per day. For Segment 0806 the existing loading for High, Upper Mid-Range, and Mid-Range flows was calculated using data from station 16120, while the existing loading for Lower Mid-Range/Low Flow conditions utilized data from station 18459. The existing loading for High Flow conditions were calculated for Segment 0841 using data from station 17669, while Upper Mid-Range and Mid-Range Flow conditions were calculated using data from station 11089, and Lower Mid-Range/Low Flow existing loadings were calculated using data from station 11081. For Segment 0822 existing loadings for Upper Mid-Range Flow conditions was calculated using data from station 17163, while the existing loading for Mid-Range and Lower Mid-Range/Low Flow conditions utilized data from station 17162. For Segment 0805 existing loadings for High Flow conditions were calculated using data from station 10937, while the existing loading for Upper Mid-Range, Mid-Range, and Lower Mid-Range/Low Flow conditions utilized data from station 10934. The existing daily loading for each segment is provided in Table 5-3.

The maximum allowable daily loading for the four flow regimes was determined using the load duration curve for the most downstream station in each segment, except in Segment 0822. Because of the large amount of water withdrawals that occurred before the most downstream station in Segment 0822, station 17163, which is the most downstream station above the municipal intakes, was used in the computation of maximum allowable daily loading. The maximum allowable daily loading was also computed at station 18310, which is the most downstream station, in order to provide the estimated allowable loading entering Segment 0805 from Segment 0822. The calculation of maximum allowable daily loading was performed by multiplying the median flow in units of cms by the geometric mean criterion 126 org/100 ml and further multiplied by the conversion factor of 8.64 E+08. The maximum allowable daily loading for each segment that includes the loads from upstream segments is provided in Table 5-3.

Table 5-3 Existing and maximum allowable daily loadings for nonsupporting segments

	Flow Regime (%)			
	0 – 10	**10 – 40**	**40 - 60**	**60 – 100**
Segment 0806				
Sampling Station [a]	16120	16120	16120	18459
Median Flow (cms)	98.3	10.6	2.48	0.93
Existing Loading (billion org/day)	106,500	4817	464	40
Max. Allowable Loading (billion org/day)	10,697	1150	271	102
Segment 0841				
Sampling Station [a]	17669	11089	11089	11081
Median Flow (cms)	156	36.8	20.0	16.8
Existing Loading (billion org/day)	427,800	94,460	2614	705
Max. Allowable Loading (billion org/day)	16,973	4008	2175	1831
Segment 0822				
Sampling Station [a]	NA[c]	17163	17162	17162
Median Flow (cms)	154	27.4	6.06	3.40
Existing Loading (billion org/day)	NA[c]	5939	801	162
Max. Allowable Loading (billion org/day)[b]	16,770	2987	660	371
Segment 0805				
Sampling Station [a]	10937	10934	10934	10934
Median Flow (cms)	477	173	57.7	34.9
Existing Loading (billion org/day)	2,587,000	106,400	17,300	2000
Max. Allowable Loading (billion org/day)	51,910	18,882	6286	3801

[a] Sampling station row represent sampling station used in estimating the existing loading.

[b] The downstream maximum allowable loading from Segment 0822 that enters Segment 0805 was based on streamflow conditions at station 18310 as follows:

0 – 10 %	16,647 billion org/day
10 – 40 %	2,895 billion org/day
40 – 60 %	359 billion org/day
60 – 100 %	90 billion org/day

[c] Bacteria data was not collected during high flow conditions for segment 0822.

As presented in Section 4.2.3 three segments that have been assessed as supporting the contact recreation use (nonimpaired) lie within the study area. These segments are Clear Fork Trinity River below Benbrook Lake (Segment 0829), Denton Creek (Segment 0825), and East Fork Trinity River (Segment 0819). Allowable loadings for each of these nonimpaired segments were calculated based on the median flow within each flow regime at a point immediately upstream of the confluence with the impaired segment (Table 5-4). Loadings arising from these nonimpaired segments are a part of the LA term in the TMDL equation (see Section 5.8.1).

Table 5-4 Maximum allowable loadings from supporting segments

	Flow Regimes %			
	0 – 10	**10 - 40**	**40 - 60**	**60 - 100**
Segment 0829				
Median Flow (cms)	29.1	2.40	0.81	0.36
Max. Allowable Loading (billion org/day)	3169	261	88	39
Segment 0825				
Median Flow (cms)	44.0	5.96	1.45	0.72
Max. Allowable Loading (billion org/day)	4784	648	158	79
Segment 0819				
Median Flow (cms)	120	35.7	4.51	2.71
Max. Allowable Loading (billion org/day)	13,083	3881	491	295

5.8.3 TMDL Allocations for Segment 0806

The allowable loading of *E. coli* that Segment 0806 can receive on an average daily basis was determined using the geometric mean criterion load duration curve of the most downstream station in the segment, which is station 16120. The allowable loading arising from the Clear Fork of the Trinity River (Segment 0829) was determined using the geometric mean criterion load duration curve based on the calculated flows for the Clear Fork Trinity River as described in Section 4.2.3. This allowable loading from the Clear Fork Trinity River was then included in the allowable loading for Segment 0806. Currently there are no permitted WWTFs within Segment 0806; however, portions of Segment 0806 are within the Urbanized Area defined in the 2000 Census, which constitutes regulation of storm water runoff by either an individual Phase I MS4 permit or the Phase II MS4 general permit. Therefore WLA calculations for Segment 0806 were solely based on the area under which stormwater runoff is regulated by the MS4 general permit. The drainage area of Segment 0806 includes 121,628 acres of which 100,385 acres are within the Urbanized Area. The total allowable loading from permitted and nonpermitted stormwater runoff was calculated by subtracting the LA_{UT} for Segment 0829 from the TMDL for Segment 0806 (TMDL – LA_{UT}). The allowable load allocation for the Urbanized Area (WLA_{MS4}) within each flow regime was determined by multiplying (TMDL – LA_{UT}) for each flow regime by the area ratio of the Urbanized Area to the Total Drainage area of Segment 0806 (100,385/121,628=0.825). In a similar manner, the LA that represents loadings not regulated by permits was computed using the ratio of its area to the total drainage area ((121,628-100,385) / 121,628 = 0.175) multiplied by (TMDL – LA_{UT}) for each flow regime. The resulting waste load allocations for WLA_{MS4} and LA are summarized by flow regime in Table 5-5.

Table 5-5 TMDL allocation summary for Segment 0806

Flow Regime	WLA_{WWTF}	WLA_{MS4}	LA	LA_{UT}	TMDL
(all units in billion org per day)					
High (0-10 %)	0	6,213	1,315	3,169	10,697
Upper Mid-Range (10-40 %)	0	734	155	261	1,150
Mid-Range (40-60 %)	0	151	32	88	271
Lower Mid-Range/Low (60-100 %)	0	52	11	39	102

5.8.4 TMDL Allocations for Segment 0841

The allowable loading of *E. coli* that Segment 0841 can receive on an average daily basis was determined using the geometric mean criterion load duration curve of station 11089. Seven wastewater treatment facilities with a combined permitted discharge of 328.2 MGD operate within Segment 0841 (Table 5-6). The recent (actual) discharge for each facility is also presented in Table 5-6; however, it is required that the TMDL allocation be based on the permitted discharge for each facility, not the recent discharges. The maximum allowable *E. coli* concentration for each of these facilities is the geometric mean criterion (126 org/100 ml). The combined discharge and geometric mean criterion were multiplied together and further multiplied by the conversion factor of 8.64 E+08 providing the WLA_{WWTF} of 1,568 billion org / day. Because the combined permitted discharge and associated allowed loadings of all WWTFs is continuous (i.e., would apply equally to all days of each year regardless of streamflow), the same calculated WLA_{WWTF} is allocated to each flow regime.

Table 5-6 Permitted and actual recent discharge of WWTFs in Segment 0841.

WWTF	Permitted Discharge (MGD)	Actual Discharge (MGD)
TRA Central Regional	162.0	106.9
City of Fort Worth Village Creek	166.0	110.8
Alta Vista Mobile Home Park	0.0080	0.0042
Golden Triangle Estates	0.0900	0.0290
Regency Conversions	0.0050	0.0027
Pine Tree Mobile Home Park	0.0420	0.0300
Pine Tree Estates #2	0.0420	0.0251
Total WWTF	328.2	217.8

The allowable load allocation from permitted and nonpermitted stormwater runoff was calculated by subtracting the WLA_{WWTF} of Segment 0841and the previously allocated TMDL from upstream Segment 0806 (station 16120) from the TMDL for Segment 0841 for each flow regime (TMDL – WLA_{WWTF} – LA_{UT}). The drainage area of Segment 0841 includes 164,740 acres of which 155,637 acres are within the Urbanized Area. The allowable load allocation (WLA_{MS4}) for the Urbanized area within each flow regime was determined by multiplying (TMDL – WLA_{WWTF} – LA_{UT}) for each flow regime by the area ratio of the Urbanized Area to the total drainage area of Segment 0841 (155,637/164,740=0.945). In a similar manner, LA was estimated using the ratio of its area to the total drainage area ((164,740-155,637) / 164,740 = 0.055) multiplied by (TMDL – WLA_{WWTF} – LA_{UT}) for each flow regime. The TMDL allocation is summarized in Table 5-7.

Table 5-7 TMDL allocation summary for Segment 0841

Flow Regime	WLA_{WWTF}	WLA_{MS4}	LA	LA_{UT}	TMDL
(all units in billion org per day)					
High (0-10 %)	1,568	4,448	260	10,697	16,973
Upper Mid-Range (10-40 %)	1,568	1,219	71	1,150	4,008
Mid-Range (40-60 %)	1,568	317	19	271	2,175
Lower Mid-Range/Low (60-100 %)	1,568	152	9	102	1,831

5.8.5 TMDL Allocations for Segment 0822

The maximum allowable daily loading of *E. coli* that Segment 0822 can receive on an average daily basis was determined using the geometric mean criterion load duration curve of station 17163 (Table 5-3). A separate allowable loading of *E. coli* to be used as a more accurate representation of the flow and associated loading entering into Segment 0805 was calculated for Segment 0822 based on the geometric mean criterion load duration curve of downstream station 18310 (see footnote on Table 5-3). The withdrawal of water by the City of Dallas and Park Cities drinking water intakes between station 17163 and station 18310 necessitated the separate allowable loading determination at the downstream station. This separate allowable loading was used in the TMDL calculations for downstream Segment 0805 to represent the loading that enters from Segment 0822. The loading arising from Denton Creek (Segment 0825) was determined using the geometric mean criterion load duration curve based on the calculated flows for the Denton Creek as described in Section 4.2.3. This allowable loading from the Denton Creek was then removed from the allowable loading for both stations 17163 and 18310.

One WWTF with a full-permitted discharge of 18.0 MGD operates within Segment 0822 (Table 5-8). The maximum allowable *E. coli* concentration for this facility is the geometric mean criterion (126 org/100 ml). The discharge and geometric mean criterion were multiplied together and further multiplied by the conversion factor of 8.64 E+08 providing the WLA_{WWTF} of 86 billion org / day.

Table 5-8 Permitted and actual recent discharge of WWTF in Segment 0822

WWTF	Permitted Discharge (MGD)	Actual (MGD)
City of Lewisville	18.0	8.186

The total allowable daily load allocation from permitted and nonpermitted stormwater runoff was calculated by subtracting the WLA_{WWTF} and LA_{UT} which is the estimated loading from Denton Creek (Segment 0825) from the TMDL for Segment 0822 for each flow regime. The drainage area of Segment 0822 includes 126,664 acres of which 91,900 acres are within the 2000 Census Urbanized Area. The WLA_{MS4} within each flow regime was determined by multiplying (TMDL – WLA_{WWTF} – LA_{UT}) for each flow regime by the area ratio of the Urbanized Area to the total drainage area of Segment 0822 ((91,900/126,664) = 0.726). In a similar manner, LA was estimated using the ratio of its area to the total drainage area ((126,664-91,900/126,664) = 0.274) multiplied by (TMDL – WLA_{WWTF} – LA_{UT}) for each flow regime. The TMDL allocations are summarized in Table 5-9.

Table 5-9 TMDL load allocation summary for Segment 0822

Flow Regime	WLA_{WWTF}	WLA_{MS4}	LA	LA_{UT}	TMDL
(all units in billion org per day)					
High (0-10 %)	86	8,634	3,266	4,784	16,770
Upper Mid-Range (10-40 %)	86	1,635	618	648	2,987
Mid-Range (40-60 %)	86	302	114	158	660
Lower Mid-Range/Low (60-100 %)	86	149	57	79	371

5.8.6 TMDL Allocations for Segment 0805

The maximum allowable daily loading of *E. coli* that Segment 0805 can receive on an average daily basis was determined using the geometric mean load duration curve of station 10924, which is the most downstream station in the segment (Table 5-3). The loading arising from the East Fork Trinity River was determined using the geometric mean load duration curve based on flows calculated for the East Fork Trinity River as described in Section 4.2.3. Seven wastewater treatment facilities with a combined permitted discharge of 290.3 MGD operate within Segment 0805 (Table 5-10). The maximum allowable *E. coli* concentration for each of these facilities is the geometric mean criterion (126 org/100 ml). The combined discharge and geometric mean criterion were multiplied together and further multiplied by the conversion factor of 8.64 E+08 providing the WLA_{WWTF} of 1,387 billion org / day.

Table 5-10 Permitted and actual recent discharge of WWTFs in Segment 0805

WWTF	Permitted Discharge (MGD)	Actual (MGD)
City of Dallas Central Regional	150	141.8
City of Dallas Southside	110	66.63
TRA Ten Mile Creek	24	15.17
TRA Red Oak Creek	6	2.368
City of Palmer	0.226	0.2372
Scurry-Rosser ISD	0.04	0.0009
D Bar B Mobile Home Park	0.024	0.004
Total WWTF	290.3	226.2

The total allowable load allocation from permitted and nonpermitted stormwater runoff was calculated by subtracting the WLA_{WWTF}, and LA_{UT} for upstream Segments 0841 (station 11089), 0822 (station 18310), and 0819 (East Fork Trinity of the Trinity River) from the TMDL for Segment 0805 (TMDL – WLA_{WWTF} – LA_{UT}). The drainage area of Segment 0805 includes 668,862 acres of which 180,351 acres are within the 2000 Census Urbanized Area. This urbanized area is concentrated mostly in the upper portion of Segment 0805, while the majority of the land-use contained in the lower portion is comprised of a more rural use (Figure 2-3 and Table 2-3). The allowable load allocation for the Urbanized Area within each flow regime was determined by multiplying (TMDL – WLA_{WWTF} – LA_{UT}) for each flow regime by the area ratio of the Urbanized Area to the Total Drainage area of Segment 0805 (180,351/668,862=0.270). In a similar manner, LA was estimated using the ratio of its area to the total drainage area ((668,862-180,351) / 668,862 = 0.730) multiplied by (TMDL – WLA_{WWTF} – LA_{UT}) for each flow regime. The resulting TMDL allocations are summarized in Table 5-11.

Table 5-11 TMDL allocation summary for Segment 0805

Flow Regime	WLA_{WWTF}	WLA_{MS4}	LA	LA_{UT}	TMDL
(all units in billion org per day)					
High (0-10 %)	1,387	1,030 *	2,790 *	46,703	51,910
Upper Mid-Range (10-40 %)	1,387	1,810 *	4,901 *	10,784	18,882
Mid-Range (40-60 %)	1,387	505	1,369	3,025	6,286
Lower Mid-Range/Low (60-100 %)	1,387	53	145	2,216	3,801

* WLA_{MS4} and LA loadings are less under the High Flow condition than the Upper Mid-Range Condition indicating that under High Flow less streamflow originates from directly within Segment 0805 than under the Upper Mid-Range Condition.

5.9 Future Growth

Because increased urbanization is anticipated in the Upper Trinity River Basin, additional increases in permitted discharges for treating domestic wastes are anticipated in the future. Compliance with these TMDLs is based on keeping bacteria concentrations below the limits in the criteria. Future growth for existing or new permitted discharges is not limited by these TMDLs as long as they do not cause bacteria to exceed existing criteria. In accordance with these bacteria TMDLs, any new permitted discharges and any additional increases in permitted daily flow for existing facilities will be held to the same bacteria limits used in this allocation process. The disinfection requirements on existing facilities are expected to meet the ambient stream criteria for bacteria in the Upper Trinity River Basin, and this expectation is supported by the fact that no reductions were required in any segments under streamflow conditions defined as low flow. At worst, additional discharges should result in a neutral impact on basin segments by increasing the assimilative capacity of the streams through increased streamflow while adding bacteria at concentrations meeting protective criteria. Options available to TCEQ to ensure the WWTF discharges are incompliance include inspections and monitoring of effluent, routine monitoring by WWTFs (at a frequency and duration to be determined during the implementation phase of the project, if deemed necessary), routine examination of self-reporting data for chlorine residuals, or other methods.

The anticipated increased urbanization in watershed will also change land uses in addition to increasing permitted discharges. Urban lands will increase and agricultural and rural lands will decrease. Relative contributions to bacteria loadings by different sources would also change, though it is not possible to reasonably estimate whether bacteria loadings to Segments 0806, 0841, 0822, and 0805 will increase or decrease. Bacteria control practices may need to be adjusted in the future to respond to these changing conditions.

The assimilative capacity of these segments will increase as the flow increases with any future increases in discharges, thus increases in flow will allow for increased loadings. The LDCs will guide the determination of the assimilative capacity of the segments including future growth.

5.10 TMDL Summary

The load duration curve method was used to develop TMDL allocations for Segments 0806, 0841, 0822, and 0805. Existing daily bacteria loads were estimated for each segment by flow regime using available water quality data, while the total allowable bacteria loading was estimated based on the geometric mean criterion of 126 org/100 ml and median streamflows within each of the four flow regimes. An implicit margin of safety was selected for this TMDL through the use of conservative model assumptions and should provide for a greater level of certainty that the prescribed allowable loadings will result in compliance with the contact recreation use criteria.

The average percent reduction in *E. coli* required to comply with the contact recreation use standards considered both the single sample and geometric mean criteria and was calculated for flow regime based on the largest estimated existing loading from any station within each

segment. Required reductions for all segments were greater for High Flow conditions when compared to Upper Mid-Range and Mid-Range Flow conditions, and no segment required reductions in existing loadings during Lower Mid-Range/Low Flow conditions.

Four separate TMDLs for each segment were calculated representing each flow regime (Table 5-12). It should be noted that if percent reductions were calculated based on existing and allowable loadings in Table 5-12 those percent reductions would be different than those found in the table. The reason for this discrepancy is as follows. The percent reductions described in Section 5.7 (Table 5-2) were based on the greatest average reduction required for either the single sample or the geometric mean criteria of all impaired stations within a segment resulting in a reduction that would allow attainment of the contact recreation use along the entire impaired reach, whereas in Table 5-12 the allowable loadings are based only on the geometric mean criterion and the existing loading of the most downstream station within a segment regardless of impairment status with the exception of Segment 0822.

Table 5-12. TMDL allocation summary by segment and flow regime

Condition	Flow Regime			
	High (0-10 %)	**Upper Mid-Range (10-40 %)**	**Mid-Range (40-60 %)**	**Lower Mid-Range/Low (60-100 %)**
Segment 0806				
Median Flow (cms)	98.3	10.6	2.48	0.93
Existing Loading (billion org/day)	106,500	4,817	464	40
Total Maximum Daily Load (billion org/day)	10,697	1,150	271	102
Waste Load Allocation (billion org/day)	6,213	734	151	52
WLA_{WWTF} (billion org/day)	0	0	0	0
WLA_{MS4} (billion org/day)	6,213	734	151	52
Load Allocation (billion org/day)	4,484	416	120	50
LA_{UT} (billion org/day)	3,169	261	88	39
LA_{NPS} (billion org/day)	1,315	155	32	11
Margin of Safety (billion org/day)	Implicit	Implicit	Implicit	Implicit
Required Percent Reduction	91%	62%	11%	0%
Segment 0841				
Median Flow (cms)	156	36.8	20.0	16.8
Existing Loading (billion org/day)	427,800	94,460	2,614	705
Total Maximum Daily Load (billion org/day)	16,973	4,008	2,175	1,831
Waste Load Allocation (billion org/day)	6,016	2,787	1,885	1,720
WLA_{WWTF} (billion org/day)	1,568	1,568	1,568	1,568
WLA_{MS4} (billion org/day)	4,448	1,219	317	152
Load Allocation (billion org/day)	10,957	1,221	290	111
LA_{UT} (billion org/day)	10,697	1,150	271	102
LA_{NPS} (billion org/day)	260	71	19	9
Margin of Safety (billion org/day)	Implicit	Implicit	Implicit	Implicit
Required Percent Reduction	95%	83%	16%	0%

Condition	Flow Regime			
	High (0-10 %)	**Upper Mid-Range (10-40 %)**	**Mid-Range (40-60 %)**	**Lower Mid-Range/Low (60-100 %)**
Segment 0822				
Median Flow (cms)	154	27.4	6.06	3.40
Existing Loading (billion org/day)	NA*	5,939	801	162
Total Maximum Daily Load (billion org/day)	16,770	2,987	660	371
Waste Load Allocation (billion org/day)	8,720	1,721	388	235
WLA_{WWTF} (billion org/day)	86	86	86	86
WLA_{MS4} (billion org/day)	8,634	1,635	302	149
Load Allocation (billion org/day)	8,050	1,266	272	136
LA_{UT} (billion org/day)	4,784	648	158	79
LA_{NPS} (billion org/day)	3,266	618	114	57
Margin of Safety (billion org/day)	Implicit	Implicit	Implicit	Implicit
Required Percent Reduction	NA*	70%	29%	0%
Segment 0805				
Median Flow (cms)	477	173	57.7	34.9
Existing Loading (billion org/day)	2,587,000	106,400	17,300	2,000
Total Maximum Daily Load (billion org/day)	51,910	18,882	6,286	3,801
Waste Load Allocation (billion org/day)	2,417	3,197	1,892	1,440
WLA_{WWTF} (billion org/day)	1,387	1,387	1,387	1,387
WLA_{MS4} (billion org/day)	1,030	1,810	505	53
Load Allocation (billion org/day)	49,493	15,685	4,394	2,361
LA_{UT} (billion org/day)	46,703	10,784	3,025	2,216
LA_{NPS} (billion org/day)	2,790	4,901	1,369	145
Margin of Safety (billion org/day)	Implicit	Implicit	Implicit	Implicit
Required Percent Reduction	95%	87%	57%	0%

* Bacteria data was not collected during high flow conditions for segment 0822.

Section 6

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