

4.0 BACTERIA SOURCE IDENTIFICATION

4.1 LINKING WATERSHED TO WATER QUALITY

Since watersheds can encompass a large land mass, the activities of humans such as agriculture, industry and property development have an effect on the amount of pollutants and sediments that are delivered into waterbodies. Natural processes also play a role in impacting water quality through evaporation, precipitation, infiltration and the decomposition of organic matter. While knowledge of the function and potential of these processes is helpful to accessing current conditions, the purpose of watershed planning is to identify and mitigate the sources of pollutants produced by human activities. By evaluating the impact of pollutants on these natural processes, watershed planners can simulate the potential impact of bacteria within the watershed. Because a watershed represents a basin that drains into a common water body, investigation of climate, land use, human activity, and soil types of the entire watershed area factor in to the equation of water quality.

Watersheds are determined by the landscape and not political boundaries, watersheds often cross municipal and county boundaries. By using a watershed perspective, all potential sources of pollutants entering a waterway can be identified and evaluated and stakeholders in the watershed can be involved in the process.

4.2 AMBIENT WATER QUALITY MONITORING

The Texas Commission on Environmental Quality (TCEQ) evaluates the condition of the state's water bodies on a periodic basis under the Clean Water Act (CWA) Section 305(b). The results are contained within the Texas Water Quality Inventory and 303(d) List and are comprised of a complete listing of all water quality concerns in the state. The Texas Water Quality Inventory, 305(b) report, provides an overview of surface water quality throughout the state, including issues relating to public health, fitness for use by aquatic species and other wildlife, and specific pollutants and their possible sources. Waterbodies that do not meet established water quality standards are placed on the 303(d) List and are referred to as "impaired."

These water quality impairments are identified by comparing concentrations in the water to numerical criteria that represent the state's water quality standards or screening levels to determine if the waterbody supports its designated uses, such as suitability for aquatic life, for contact recreation, or for public water supply. This process determines if fish and aquatic insects have adequate oxygen, if people swimming in the water are exposed to pathogens that may cause illness and if the water is fit to be used as a source for public drinking water.

Water quality standards numerical criteria are used by TCEQ as the maximum or minimum instream concentrations that may result from permitted discharges and/or nonpoint sources and still meet designated uses. To resolve the issues of regional and geological diversity of the state, standards are developed for classified segments. Classified segments are defined segments of waterways that are unique from other segments. Lake Granbury is Segment 1205, while the Brazos River above Lake Granbury (below Possum Kingdom Lake) is Segment 1206. Appropriate water uses such as contact recreation, public water supply, and aquatic life are then applied to the segments. Specific water quality criteria have been developed for water

temperature, dissolved oxygen, pH, bacteria, chloride, sulfate and total dissolved solids for classified segments. Many streams that are not classified segments, such as Robinson Creek, Rucker Creek, Walnut Creek, etc., are assessed throughout the state and are considered unclassified segments. These unclassified segments do not have specific water quality standards developed for them. For assessment purposes, unclassified streams are assessed using the numeric criteria developed for the classified segment into which the stream flows.

In response to local concerns, the BRA began a large-scale monitoring initiative in the canals of Lake Granbury to assess the water quality of the coves. Beginning in May 2002, the Authority began collecting water quality samples on a monthly basis at more than 50 cove locations. Some of the locations showed no elevated concentrations of *E. coli* and were later discontinued. Some locations were added after a year of monitoring as new information was acquired on possible source locations. The data generated from this effort indicates that many of the canals on Lake Granbury are impacted by *E. coli* issues and indicates a concern for public health and contact recreation. The data also indicates that the water quality in the coves is more influenced by the surrounding land use rather than the main body of the lake.

The BRA's Lake Granbury canal monitoring program was the basis for the Ambient Water Quality Monitoring Plan adopted by the LGWPPSC. The LGWPPSC elected to add most of the BRA's canal monitoring locations for the Ambient Water Quality Monitoring Plan plus requested additional canal sites in the areas of Port Ridglea West, Mallard Point, Lambert Branch, Indian Harbor, Canyon Creek and Rough Creek (Figure 4). Additionally, the LGWPPSC requested monitoring on the major tributaries to Lake Granbury including: the Brazos River above Lake Granbury, Robinson Creek, Strouds Creek, Long Creek, Rucker Creek and Walnut Creek.

The sample collection and analysis under the Ambient Water Quality Monitoring Plan was implemented by the BRA's Field Operations Crew and Environmental Services Laboratory on September 1, 2006. A total of 47 sites are sampled monthly for water temperature, dissolved oxygen, pH, conductivity, salinity, chloride, sulfate, nitrate-nitrogen, orthophosphate phosphorus and *E. coli*.

Ambient water quality monitoring data in the canals reveals that the canal areas exhibit little or no circulation and mix slowly with the main body of the reservoir. This data collection effort has identified bacteria impairments in many of these canals and concerns for dissolved oxygen and elevated nutrient levels in a few of the canals. This seems to be a result of the stagnant conditions in the canals and lack of mixing with the main body of the lake. These concerns are not observed in the main body of Lake Granbury.

E. coli data from the ambient water quality monitoring program has been evaluated for compliance with both the State Water Quality Standard of 126 MPN/100mL and against the LGWPPSC's Goal of 53 MPN/100ml (Figure 5).

While all of the canal sites are in compliance with the State Water Quality Standard at this time, several are not in compliance with the LGWPPSC's Goal. Canals in Oak Trail Shores, Sky Harbor, Port Ridglea East, Indian Harbor and Blue Water Shores consistently fail to meet the

goal standard determined by the LGWPPSC.

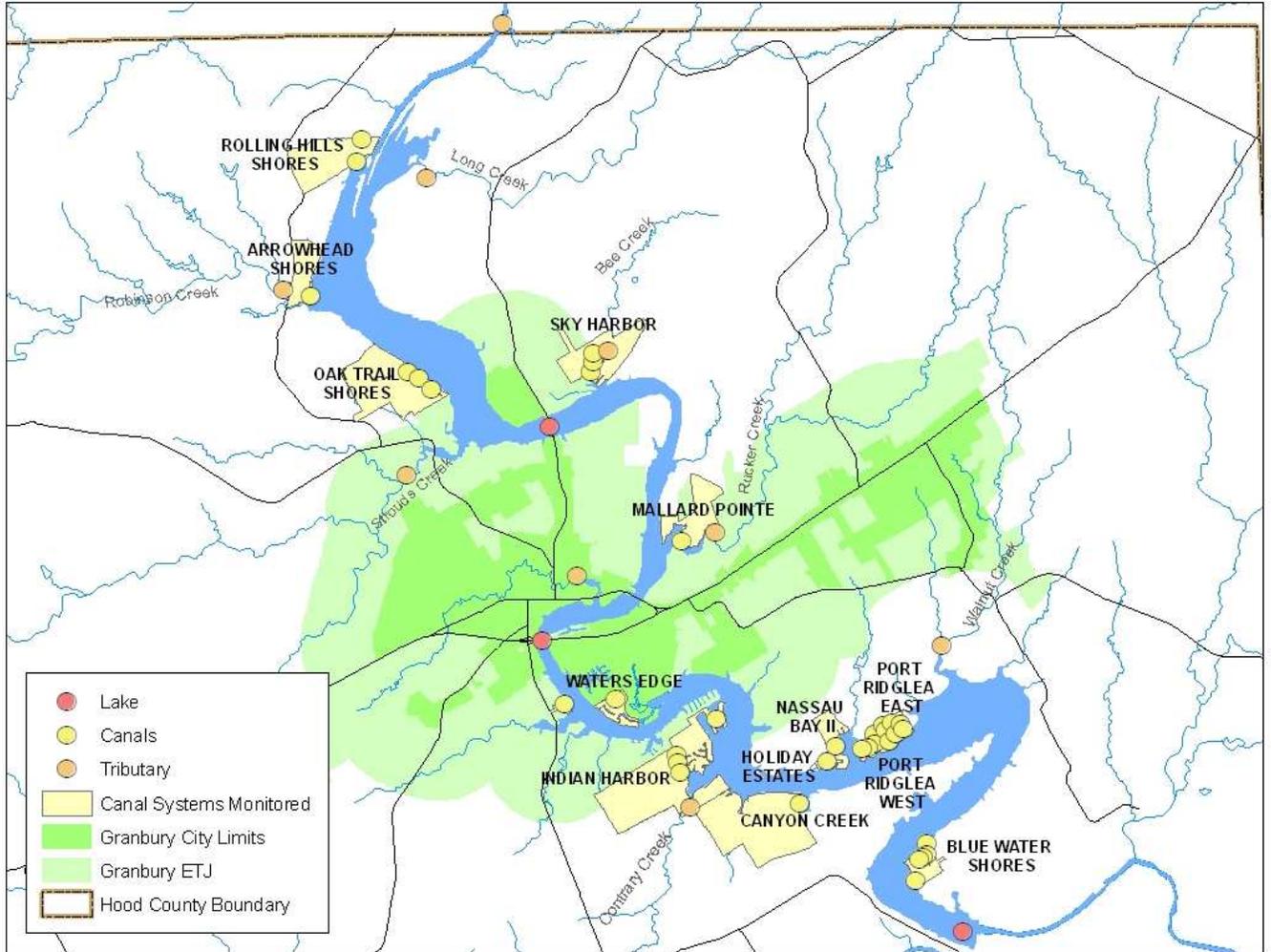


Figure 4. Ambient Water Quality Monitoring Plan Monitoring Sites and Canal Systems Assessed

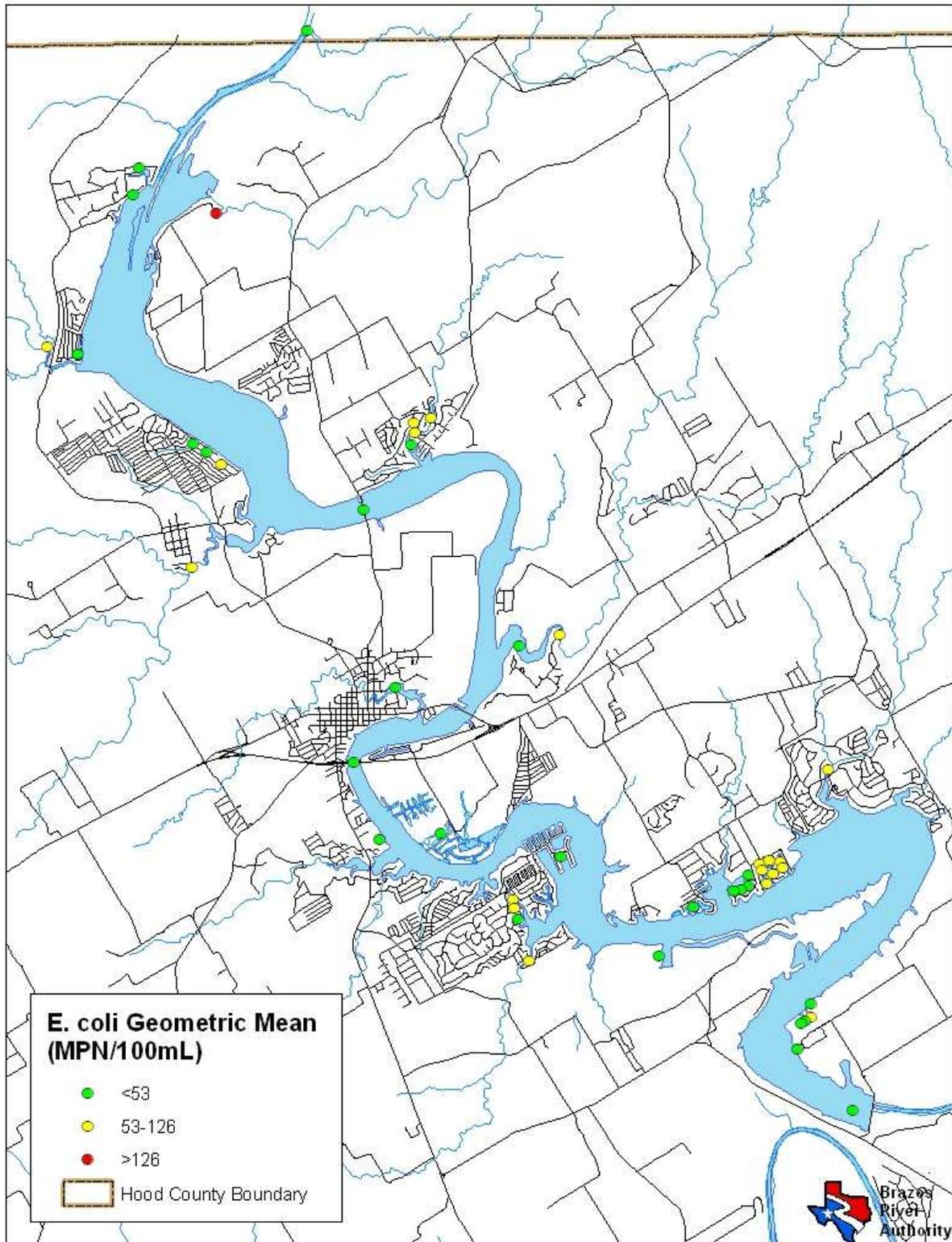


Figure 5. Lake Granbury *E. coli* Assessment Results through September 2009

4.3 LAND USE ASSESSMENT

Several items were evaluated for the land use analysis. A two-mile radius around Lake Granbury that includes portions of both Hood and Parker counties was selected by the Stakeholders for land use analysis (Figure 6). Basic land use analysis was conducted using one-foot aerial photography provided by the North Texas Council of Governments. The aerial photographs utilized for land use analysis were produced in 2007. When land use could not definitively be determined using aerial photography those parcels of land were identified by ground-truthing conducted by both Brazos River Authority Staff and the Stakeholder Group representative from the Granbury Association of Realtors. This land use assessment was also used as basis for additional, supplemental land use evaluation conducted as part of the SELECT watershed modeling bacteria source evaluation (see Section 4.7).

Land use using the aerial photographs was evaluated using the following categories:

- Multi-Family Residential;
- Single-Family Residential;
- Commercial/Services;
- Industrial;
- Utilities/Transportation;
- Recreational;
- Cropland and Pasture;
- Orchards;
- Other Agricultural;
- Rangeland; and
- Quarries and Gravel Pits.

Residential land uses range from Multi-Family Residential, which are represented by high-density, multiple-unit structures of urban cores, such as apartment buildings and condominiums. Single-Family Residential are represented by low-density housing, with no more than one residential structure per lot; however, in some developments lot sizes of single-family residences are small leading to a higher density of homes than would traditionally be observed in this category. Areas of sparse residential land use, such as farmsteads, were included in categories to which they are related.

Commercial/Services areas are those used predominantly for the sale of products and services. Components of the Commercial/Services category are urban central business districts, shopping centers, commercial strip developments, and resorts. The main buildings, secondary structures and areas supporting the basic use included office buildings, warehouses, driveways, sheds, parking lots, landscaped areas and waste disposal areas. Commercial/Services areas may include some noncommercial uses too small to be separated out such as churches and schools.

Industrial areas include a wide array of land uses from light manufacturing to heavy manufacturing plants to junkyards and salvage facilities. Identification of light industries, those focused on design, assembly, finishing, processing and packaging of products, were often determined based on the type of building, parking and shipping arrangements.

The land uses included in the Utilities/Transportation category include major highways and railways. The highways include rights-of-way, areas used for interchanges and service and terminal facilities. Rail facilities include stations, parking lots, roundhouses, repair and switching yards and related areas, as well as overland track and spur connections of sufficient width for delineation.

Airport facilities including the runways, intervening land, terminals, service buildings, navigation aids, fuel storage, parking lots and a limited buffer zone are also included in the Utilities/Transportation category. Communications and utilities areas such as those involved in processing, treatment and transportation of water, gas, oil and electricity and areas used for airwave communications are also included in this category.

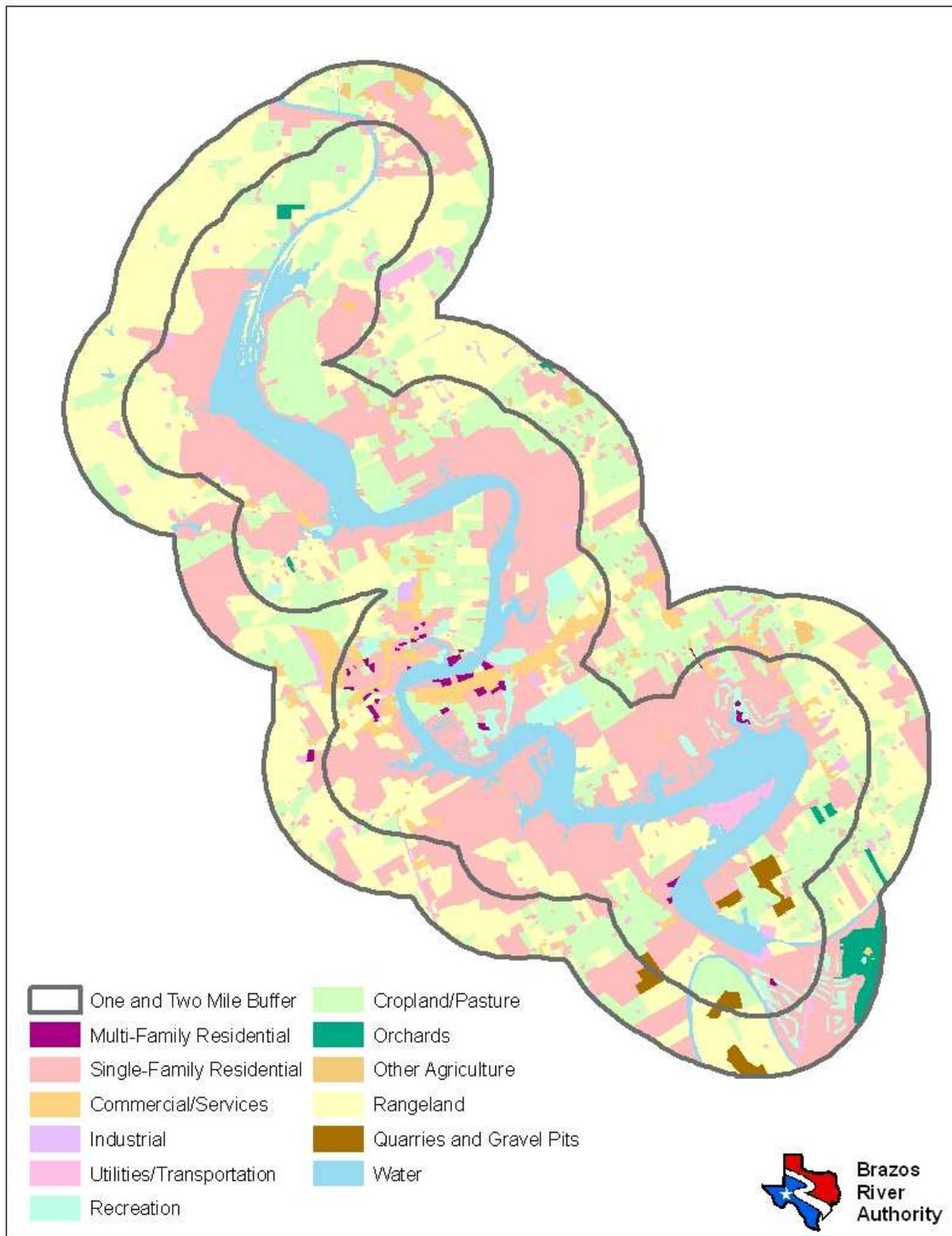


Figure 6. Land Use Within Two Miles of Lake Granbury 2007

The Recreational category typically consists of uses such as golf courses, driving ranges, zoos, urban parks, cemeteries and undeveloped land within an urban setting.

The several components of the Cropland and Pasture category include harvested cropland, cultivated summer fallow and idle cropland, land on which crop failure occurs, cropland used only for pasture in rotation with crops and pasture on land more or less permanently used for that purpose. From imagery alone, it generally is not possible to make a distinction between cropland and pasture; therefore, these uses were grouped into a single category for analysis purposes.

The Orchards category includes orchards, groves and vineyards that produce the various fruit and nut crops. Also, tree nurseries, which provide seedlings for plantation forestry, are included here.

The Other Agricultural category for the two-mile radius around Lake Granbury primarily includes holding areas for livestock such as corrals and breeding and training facilities on horse farms.

The Rangeland category was applied where the natural vegetation is predominantly grasses, grasslike plants, forbs or shrubs and where natural herbivory is an important influence. For this study, rangeland was not further subdivided into herbaceous range, shrub and brush rangeland and mixed rangeland.

Quarry and Gravel Pits were applied to extractive mining activities where vegetative cover and overburden are removed to expose such deposits as sand, gravel, limestone and sandstone. Current mining activity is not always distinguishable. Inactive, unreclaimed and active strip mines, quarries, borrow pits and gravel pits are included in this category.

The land use within a two-mile radius of Lake Granbury is almost equally divided between rangeland, crop and pasture land and single-family residences (Figure 7). Within a one-mile radius of Lake Granbury the dominant land use changes to single-family residences (Figure 8).

An analysis of the suitability of soils for use for septic absorption fields in the two-mile radius around Lake Granbury was also undertaken. The data for this analysis were provided by the United States Department of Agriculture's Natural Resource Conservation Service (USDA-NRC) Soil Survey Geographic Database (SSURGO). The SSURGO database ranks soil suitability by three categories:

1. Slight – soils are generally favorable for use for septic absorption fields;
2. Moderate – soil properties are unfavorable for use for septic absorption fields but limitations can be overcome by special planning and design; and
3. Severe – soil properties are so unfavorable for use for septic absorption fields and difficult to overcome that major soil reclamation, special designs, and intensive maintenance are required.

69 percent of the soils within in a two-mile radius of Lake Granbury are rated severe, 13 percent are rated moderate and 18 percent are rated slight (Figure 9).

Microwatershed determinations, made using United States Geological Survey (USGS) digital elevation models and hypsography data, revealed that while there are a few cove areas with

natural drainages where water quality may be impacted by watershed activities, most of the canal areas have small, isolated microwatersheds and are primarily impacted by activities in the immediate proximity to the cove. Land use analyses results for each individual microwatersheds surrounding the lake are included in Appendix B. Only a small group of microwatersheds were evaluated in this WPP focusing the modeling efforts on the areas of greatest concern/priority based on water quality monitoring data. The stakeholders felt the focus areas were good representative cases for the remainder of the lake.

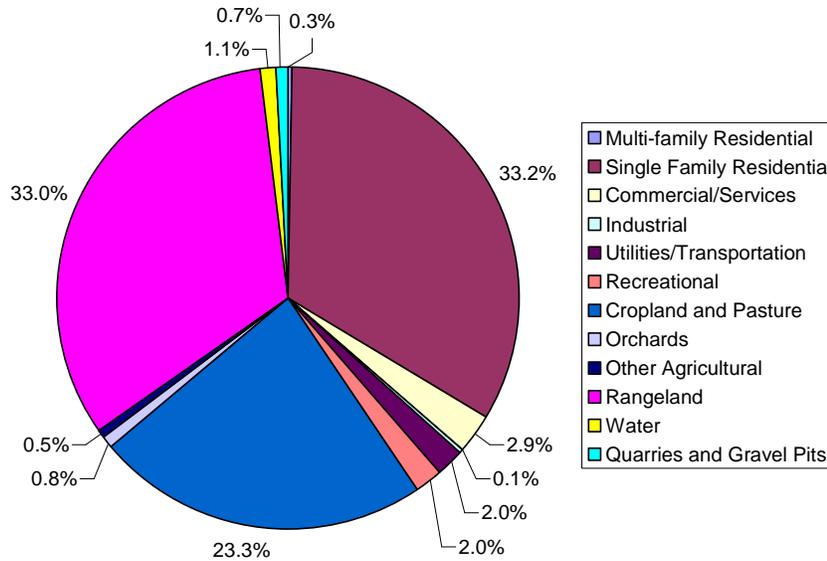


Figure 7. Land Use Between One and Two Mile Radius of Lake Granbury

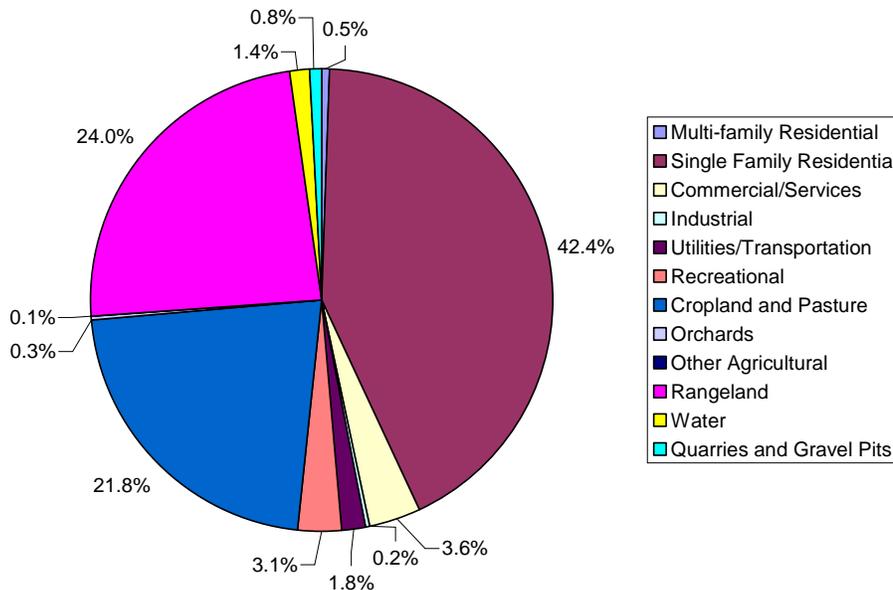


Figure 8. Land Use Between One Mile Radius and Lake Granbury

Subdivision development data and sewage disposal methodologies were determined using several sources including map data from the Hood County Appraisal District (HoodCAD), plating data filed at the Hood County courthouse, a survey of local utilities, input from the Hood County Health District (HCHD) and input from the Granbury Association of Realtors Stakeholder Group representative.

Age of development for subdivisions was also analyzed and it was determined that 74 percent of the subdivisions within two miles of Lake Granbury were developed prior to 1989 (Figure 10) when the Texas Legislature enacted the State’s On-site Sewage Disposal System Rules (Texas Health & Safety Code §§ 366.001-.0923). Before the adoption of Texas Health & Safety Code §§ 366.001-.0923, there were no significant regulations regarding system configuration and siting; septic system owners merely had to register their system. Further analysis also determined that 86 percent of the subdivisions within a two-mile radius of Lake Granbury rely on septic systems for waste disposal (Figure 11).

Animal populations were examined, at the county level, using data provided by the Lake Granbury Chamber of Commerce, the American Veterinary Medical Association and the USDA’s Agricultural Census. Humans account for 51 percent of the total mammal/avian population in Hood County (Table 7). Cattle are the second most dominant group with 32 percent of the total mammal/avian population. The USDA’s Agricultural Census data indicate that after a peak in 1997, the total livestock population in Hood County is declining (Figure 12).

Table 7. Hood County Population Counts

| Category | Population | Percent of Total Population |
|----------------------|-------------------|------------------------------------|
| Humans | 47,627 | 51% |
| Dogs | 3,489 | 4% |
| Cats | 3,491 | 4% |
| Cattle | 30,059 | 32% |
| Horses | 1,889 | 2% |
| Swine | 123 | <1% |
| Goats | 4,000 | 4% |
| Sheep/Lambs | 606 | <1% |
| Chickens | 1,386 | 1% |
| Domestic Ducks/Geese | 119 | <1% |
| Domestic Turkeys | 138 | <1% |
| Emus | 28 | <1% |

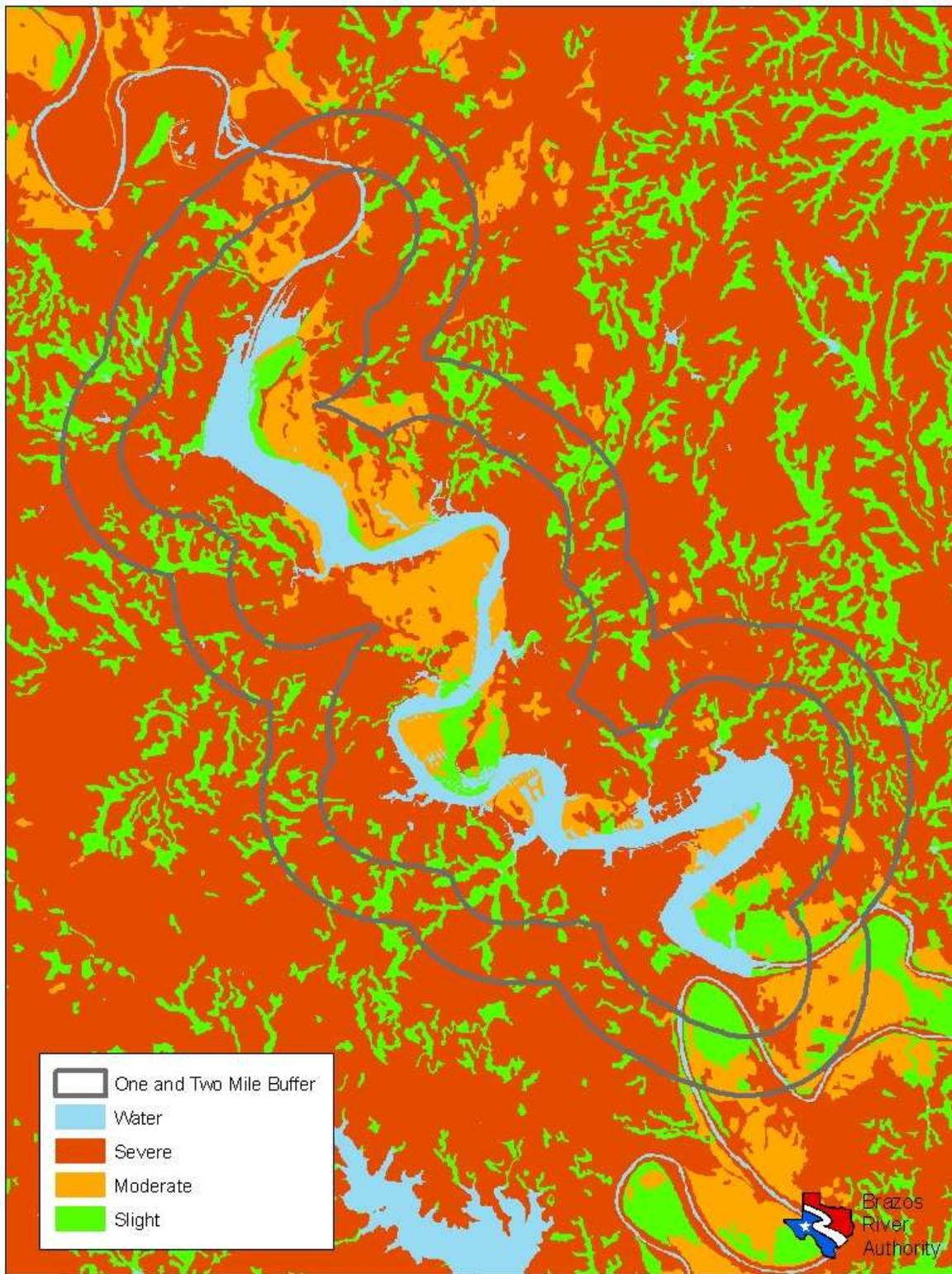


Figure 9. SSURGO Soil Suitability Rating for Septic Absorption Fields.

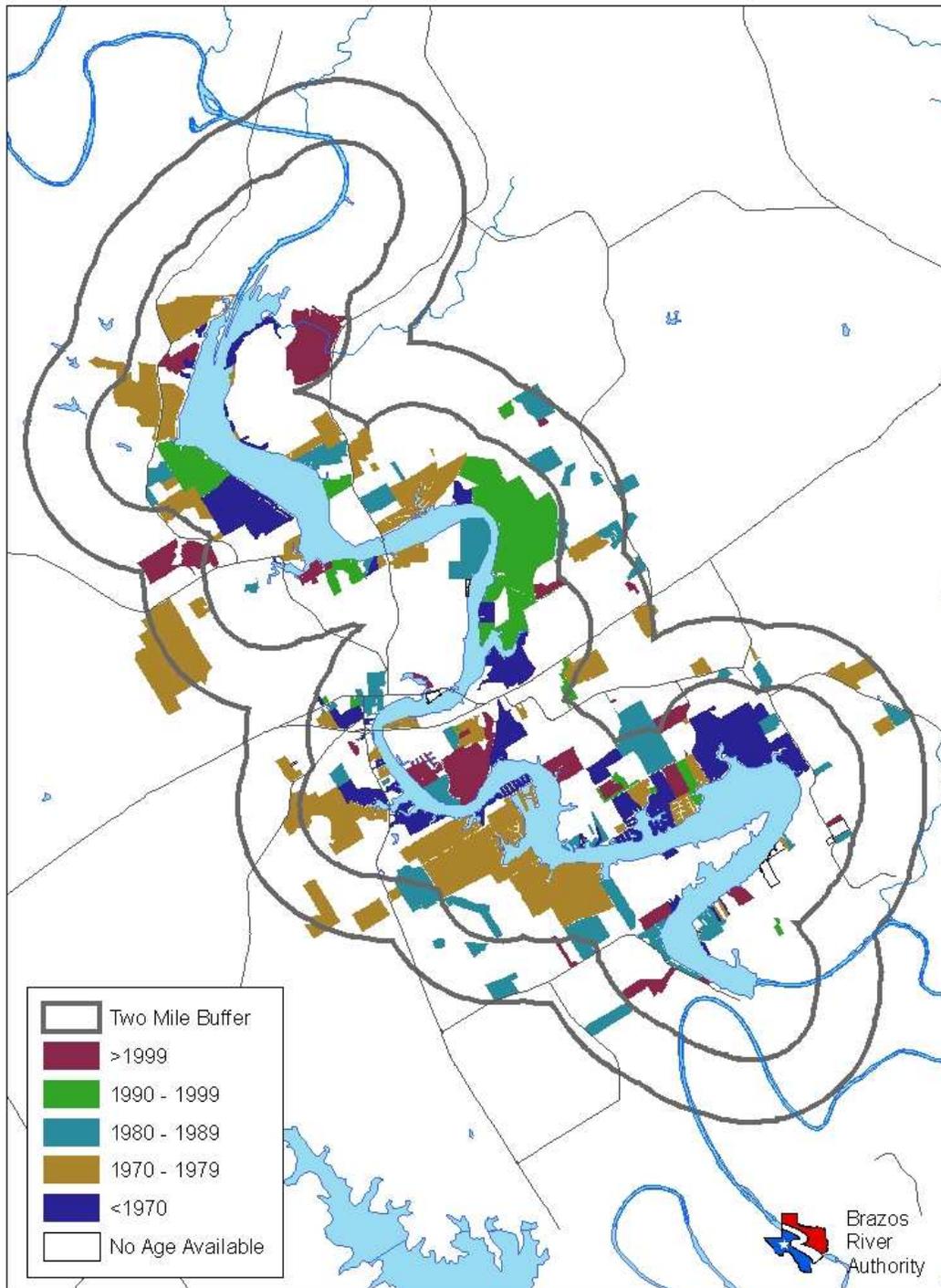


Figure 10. Age of Subdivisions within Two Miles of Lake Granbury.

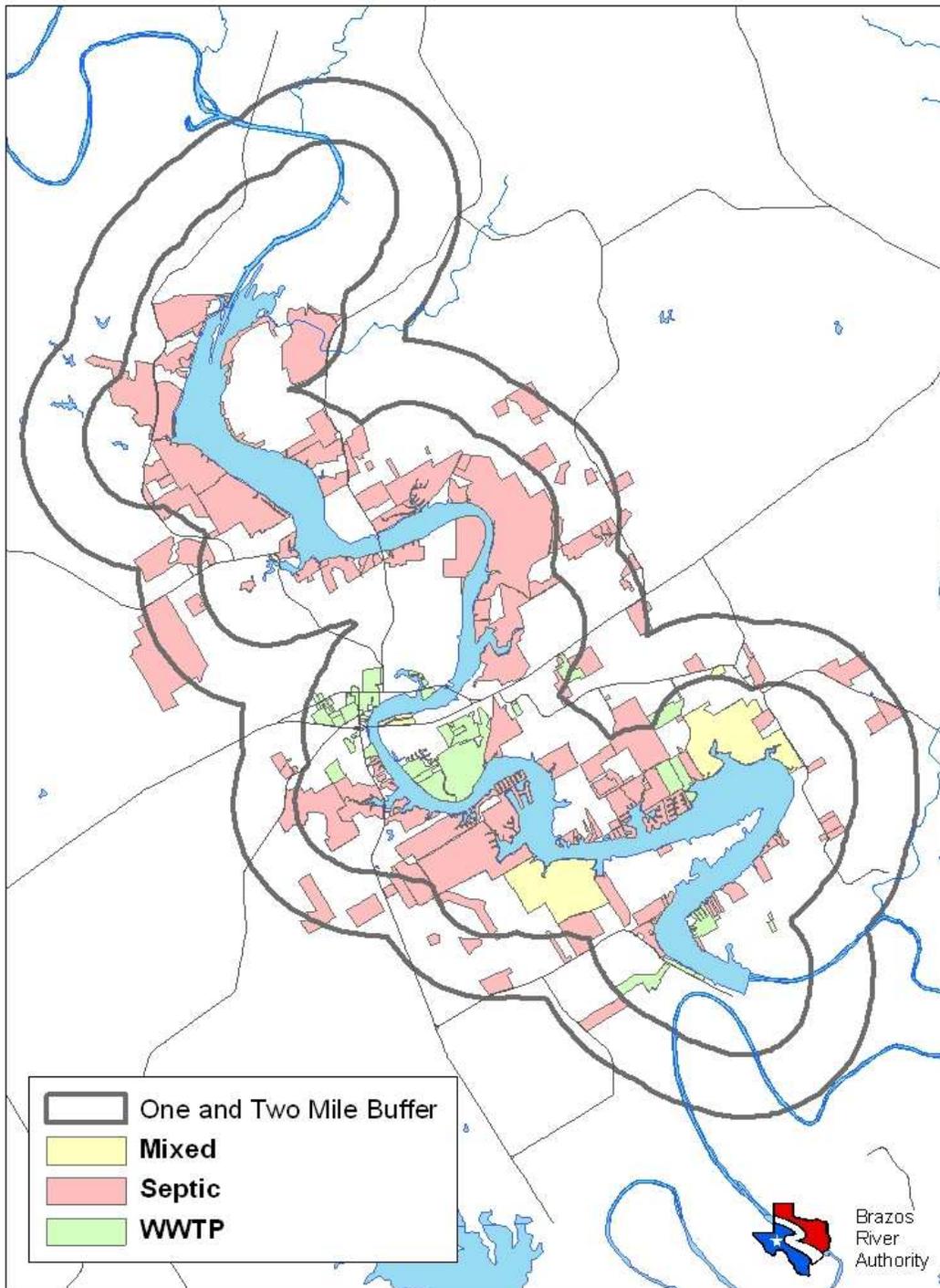


Figure 11. Sewage Disposal Methods within Two Miles of Lake Granbury.

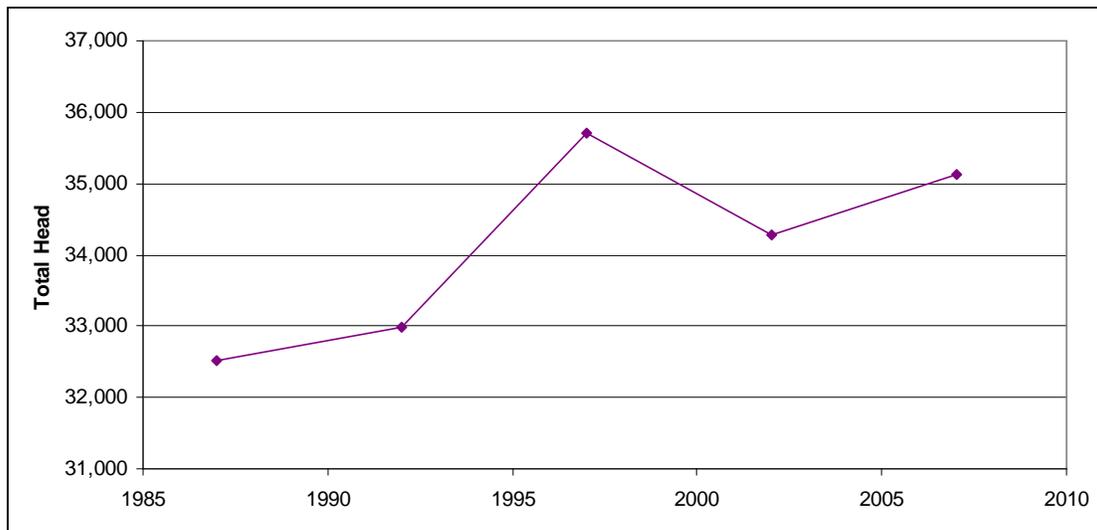


Figure 12. Total Head of Livestock in Hood County (NASS)

4.3.1 Land use assessment summary

Land use analysis seems to indicate that a chief source of bacterial contamination may be from human and pet sources. Thirty-three percent of the land use within two miles of Lake Granbury is single-family residential homes with most of those homes disposing of wastes via septic systems. Within one mile of the lake, land use by single-family residential properties increases to 42 percent. With nearly three-quarters of the residential properties developed prior to the development of the current stringent OSSF regulations and most of those early systems not meeting current standards, it seems to indicate that human sources may be impacting canals, especially in areas with little to no influence from the surrounding watershed. Additionally, the livestock population in Hood County is stabilizing, while the human population and urban/suburban land use are on the rise. With a rise in human population comes an increase in the pet population. Improper pet waste management may also be impacting the canals.

All areas demonstrating water quality concerns are dominated by single-family residential land use, OSSF for waste management and soils that are not desirable for OSSF applications without significant manipulation. This further supports the implication that sources found on residential properties may be significantly impacting the canals of concern.

While the land use analysis points toward human and pet sources; additional source identification activities have been undertaken to confirm these findings. Both water quality modeling and bacterial source tracking results, along with these land use results, were evaluated to make the final source determination. Supplemental watershed and land use characterization is presented in subsequent sections relating to watershed modeling source identification.

4.4 PRELIMINARY ASSESSMENT OF FECAL POLLUTION SOURCES IMPACTING LAKE GRANBURY AS DETERMINED BY BACTERIAL SOURCE TRACKING

On March 26, 2006, a presentation by the Texas Farm Bureau staff regarding the use of bacterial source tracking (BST) technology in Lake Waco and Lake Belton, Texas was presented to the Stakeholders. Following the presentation, Stakeholders expressed interest in the developing technology and requested that a BST assessment be developed for Lake Granbury. The Authority worked with Dr. George DiGiovanni of Texas AgriLife Research at El Paso, who performed the work on Lake Waco and Lake Belton, to develop a draft 10-site sampling approach. The stakeholders selected the 10 sites and indicated that 5 of these sites were preferred. This 10-site sampling approach was presented to the stakeholders on February 13, 2007. Stakeholders approved the plan and directed the Authority to pursue a contract with Texas AgriLife Research. Unfortunately, due to budget constraints, all 10 sites were not financially feasible and the BST study was finalized using the stakeholders 5 most preferred sites.

The five sites on Lake Granbury selected for bacterial source tracking (BST) included Lake Granbury at Highway 377 (11861); Sky Harbor (18015); Waters Edge (18018); Indian Harbor (20215); and Port Ridglea East (18038). BST involved monthly targeted grab sampling from the sampling sites for a period of six months. BRA collected 100 ml water grab samples from the selected sites for both *E. coli* detection using USEPA Method 1603 with modified mTEC medium (USEPA 2005) and *Bacteroidales* analysis. Method 1603 modified mTEC plates with *E. coli* colonies were sent to AgriLife Research for isolation and analysis of *E. coli*. Water samples for *Bacteroidales* analysis were filtered, placed in lysis buffer and frozen, then sent on dry ice to AgriLife Research for analysis.

Additionally, fifty-nine known source samples from wildlife, domestic septage/sewage, pets, and livestock from the Lake Granbury area were collected and shipped to AgriLife Research. These samples were used to evaluate the distribution of *Bacteroidales* host-specific markers in the Lake Granbury watershed. In addition, *E. coli* isolated from the samples were included in the *E. coli* identification library.

Assessment and identification of fecal pollution sources using *E. coli* utilized the BST library developed by the El Paso AgriLife Research Environmental Microbiology Laboratory (Texas *E. coli* source library) which contains over 2,000 *E. coli* isolates from over 1,500 different domestic sewage and animal fecal samples. The library contains diverse *E. coli* isolates which were selected after screening over 4,500 isolates by genetic fingerprinting to exclude identical isolates from the same sample and include isolates with unique genetic fingerprints. In addition, the library-independent *Bacteroidales* PCR method was used to assess fecal pollution sources.

The BST methods used included DNA fingerprinting of *E. coli* bacteria isolated from water samples using ERIC-PCR and RiboPrinting, and the PCR detection of *Bacteroidales* fecal bacteria present in water samples.

4.4.1 ERIC-PCR and RiboPrinting of *E. coli*

In the BST project for Lake Waco and Belton Lake, *E. coli* isolates were analyzed using four BST techniques: RiboPrinting (RP), ERIC-PCR, pulsed field gel electrophoresis (PFGE) and Kirby-Bauer antibiotic resistance analysis (KB-ARA) (Casarez, Pillai et al. 2007). BST analyses were performed using the individual techniques, as well as composite data sets. The four-method composite library generated the most desirable BST results in regards to accuracy and ability to identify water isolates. However, as few as two methods in combination were found to be useful based on congruence measurements, library internal accuracy (i.e. rates of correct classification, RCCs), and comparison of water isolate identifications. In particular, the combinations of ERIC-PCR and RiboPrinting (ERIC-RP), or ERIC-PCR and Kirby-Bauer antibiotic resistance analysis (ERIC-ARA) appeared promising. These two-method composite data sets were found to have 90.7% and 87.2% congruence, respectively, to the four-method composite data set. More importantly, based on the identification of water isolates, they identified the same leading sources of fecal pollution as the four-method composite library. The combination of ERIC-PCR and ERIC-RP was recommended by Dr. DiGiovanni and selected by the stakeholders for analysis of water samples for this study.

E. coli isolates from water samples and source samples were DNA fingerprinted using a repetitive sequence polymerase chain reaction (rep-PCR) method known as enterobacterial repetitive intergenic consensus sequence PCR (ERIC-PCR) (Versalovic, Schneider et al. 1994). For source samples, ERIC-PCR was used to identify unique *E. coli* isolates from each sample to maximize the diversity of isolates added to the local library and eliminate further analysis of identical isolates (clones). At least one *E. coli* isolate from each fecal, wastewater, etc. sample will be included in the local library, even if it is identical to a previously isolated *E. coli*.

Following ERIC-PCR analysis, *E. coli* water isolates and selected source isolates were RiboPrinted using the automated DuPont Qualicon RiboPrinter and the restriction enzyme Hind III (“RiboPrinting”). All bacterial isolate sample processing is automated using standardized reagents and a robotic workstation, providing a high level of reproducibility.

Analysis of composite ERIC-RP DNA fingerprints was performed using Applied Maths BioNumerics software. Genetic fingerprints of *E. coli* from ambient water samples were compared to fingerprints of known source *E. coli* isolates in the Texas library and the likely host of origin (e.g. cattle, wildlife, human) identified. To identify the potential sources of the unknown water isolates, their ERIC-RP composite patterns were compared to the library using a best match approach and an 80% similarity cutoff. If a water isolate was not at least 80% similar to a library isolate, it was considered unidentified. Although fingerprint profiles are considered a match to a single entry, identification is to the host source class, and not to the individual animal represented by the best match. Host sources were divided into five groups, 1) domestic sewage (human); 2) pet; 3) livestock (including cattle and other non-avian livestock); 4) avian (includes wild and domestic) and; 5) wildlife (non-avian, and including deer and feral hog).

4.4.2 *Bacteroidales* PCR and quantitative PCR (qPCR)

Library-independent source tracking methods have been developed as alternatives to the library-dependent methods, and may prove to be a more rapid and cost-effective approach for assessment of fecal pollution in source water. The *Bacteroidales* PCR method is a culture-independent molecular method which targets genetic markers of *Bacteroides* and *Prevotella* spp. fecal bacteria that are specific to humans, ruminants (including cattle and deer) and pigs (including feral hogs) (Bernhard and Field 2000; Dick, Bernhard et al. 2005). There is also a general *Bacteroidales* marker (GenBac) that can be used as a general indicator of fecal pollution. The method has high specificity and moderate sensitivity (Field, Chern et al. 2003). For this method, 100 ml water grab samples were concentrated by filtration, DNA extracted from the concentrate and purified, and aliquots of the purified DNA analyzed by PCR. Results are expressed as either the qualitative presence/absence of the host-specific genetic markers, or semi-quantitative marker abundance as determined by quantitative PCR.

In theory, the GenBac marker detects the majority of the *Bacteroidales* in the samples, including those detected with the host-specific markers. GenBac standard curves were developed using 10^0 , 10^{-1} , 10^{-2} , and 10^{-3} dilutions of each water sample DNA (36 standard curves). Since the actual copy number of GenBac target sequences in each sample was unknown, arbitrary values of 10,000; 1,000; 100 and 10 were assigned to the dilutions, respectively. All GenBac standard curves had R^2 values of ≥ 0.9 . The Hog, Human and Ruminant host-specific markers were quantified using the GenBac standard curve for each water sample. This attempted to make the marker quantitation data for different water samples comparable by accounting for sample-to-sample variation in *Bacteroidales* DNA concentration and any effects of PCR inhibitors on quantitation. This approach makes it possible to compare the relative abundance of each marker between stations or at the same station over time. However, it is not appropriate to compare the abundance of one marker to another (e.g. Hog vs. Human), since that would require DNA extraction controls and marker-specific quantitation standards which were not employed in the current study.

4.4.3 Bacteria Source Tracking Results

4.4.3.1 Texas *E. coli* identification library, including Lake Granbury source isolates (local library)

A total of 80 *E. coli* isolates obtained from 59 different fecal specimens collected in the Lake Granbury area (i.e. local library) were included in the Combined Texas Restricted Cross-Validated library. The Restricted Cross-Validated library was derived from the larger Combined Texas Library (almost 2,000 isolates from over 1,500 fecal samples), and consists of 150 *E. coli* isolates selected specifically for their geographic stability (presence in more than one Texas watershed) and host specificity. Description of the identification library used for this study and evaluation of its identification accuracy is included in (Table 8). Rates of correct classification (RCC; identification accuracy) ranged from 67% to 92% for a five-way split of pollution sources, and were much higher than random based on library composition.

Table 8. *E. coli* identification library composition and source identification rates of correct classification (RCC)

| Source Class | Lake Granbury Local Library | | Combined Texas Restricted Cross Validated Library and Lake Granbury Local Library | | | |
|---|-----------------------------|------------|---|---------------|--------------|-----------|
| | # fecal samples | # isolates | # fecal samples | # isolates | % Random RCC | % RCC |
| Sewage/Septage | 17 | 21 | 96 | 101 | 44 | 92 |
| Pets | 2 | 3 | 7 | 8 | 4 | 67 |
| Livestock (includes cattle + other non-avian) | 5 (1+4) | 6 (1+5) | 37 (24+13) | 39 (25+14) | 17 | 81 |
| Avian (includes wild and domestic) | 6 | 11 | 27 | 32 | 14 | 70 |
| Wildlife (non-avian) | 29 | 39 | 40 | 50 | 22 | 79 |
| Total | 59 | 80 | 207 | 230 | 100 | |

Although this identification library is composed of *E. coli* isolates derived from a large number of fecal samples and isolates from other studies, it does only have a small number of isolates from the Lake Granbury area. In particular, there are only a small number of isolates from Lake Granbury pet and domestic sewage/septage sources, and this could affect accurate identification of those sources of fecal pollution.

4.4.3.2 Identification of *E. coli* isolates from water at each sampling site

Approximately 50 *E. coli* isolates from each of the five sampling sites were analyzed by ERIC-RP composite DNA fingerprinting. Identification of these isolates by site is described in Figure 13 through Figure 17 below. In contrast to previous studies able to identify almost 70% of water isolates using the restricted library, only 57% of the Lake Granbury water isolates were identifiable. Identification of additional Lake Granbury water isolates would only be possible through expansion of the library with additional *E. coli* from Granbury fecal sources.

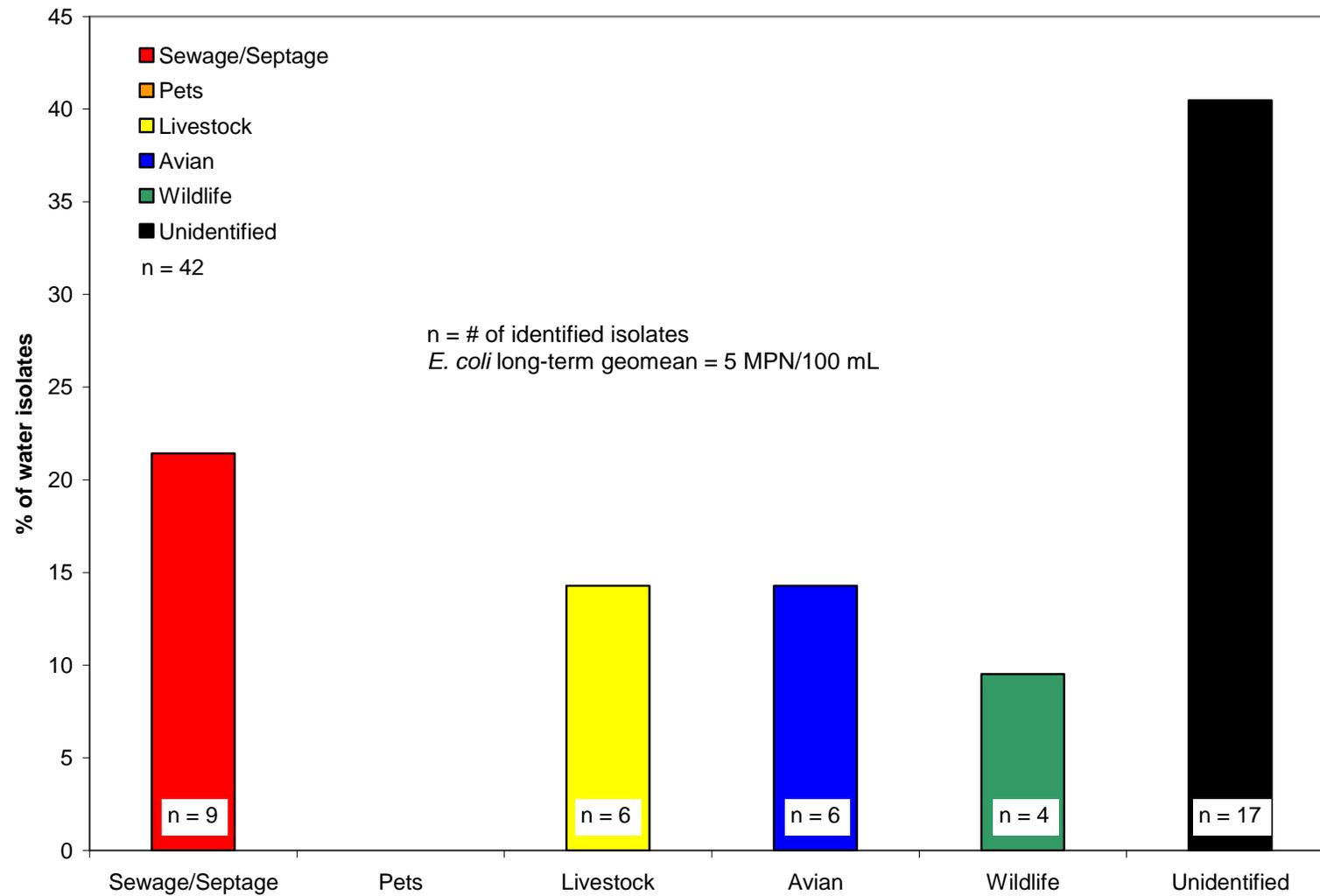


Figure 13. *E. coli* source identification for the Lake Granbury at Highway 377 (11861) site. The *E. coli* long-term geometric mean at this site is low (5 MPN/100 ml).

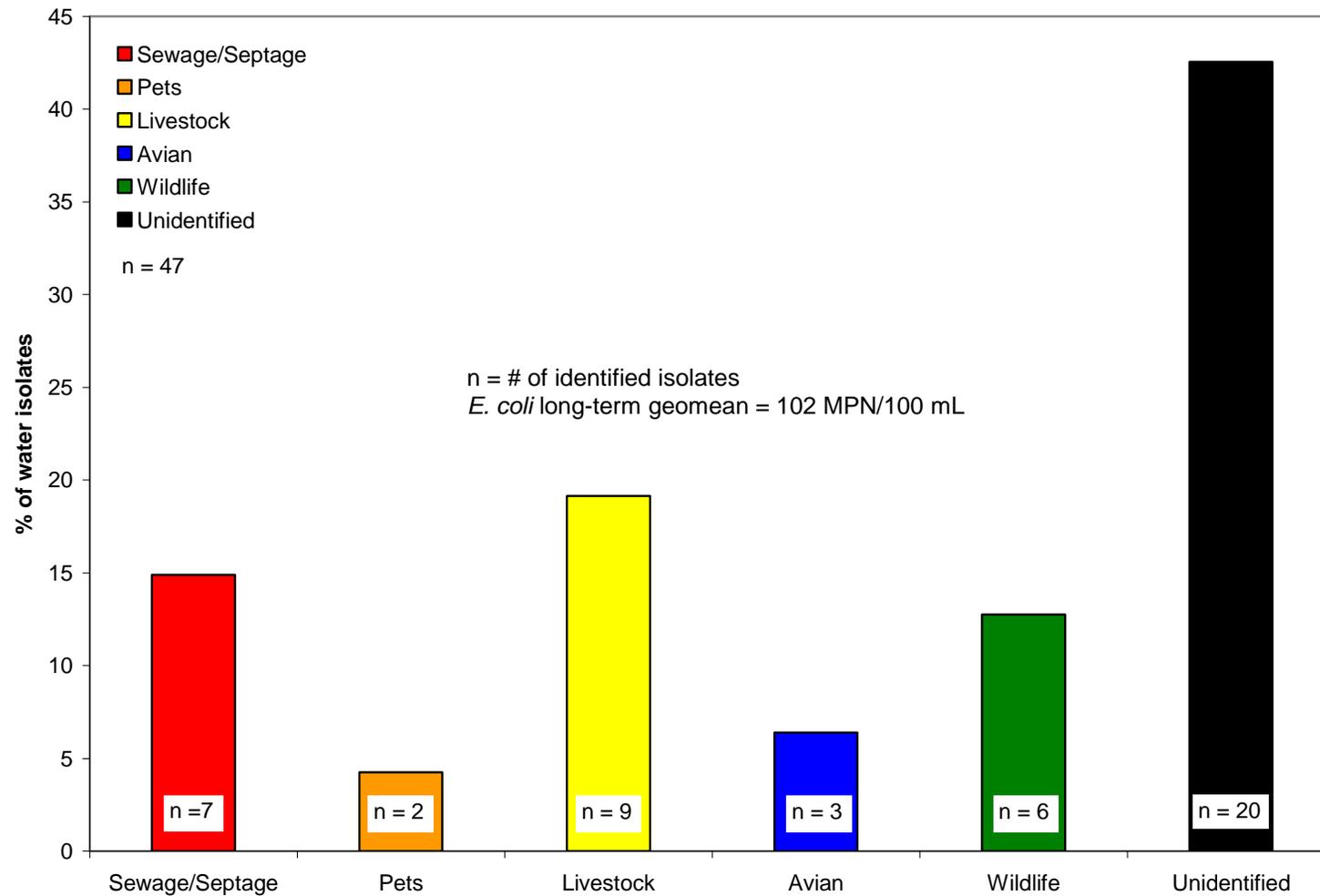


Figure 14. *E. coli* source identification for the Sky Harbor (18015) site. The *E. coli* long-term geometric mean at this site is moderately high (102 MPN/100 ml).

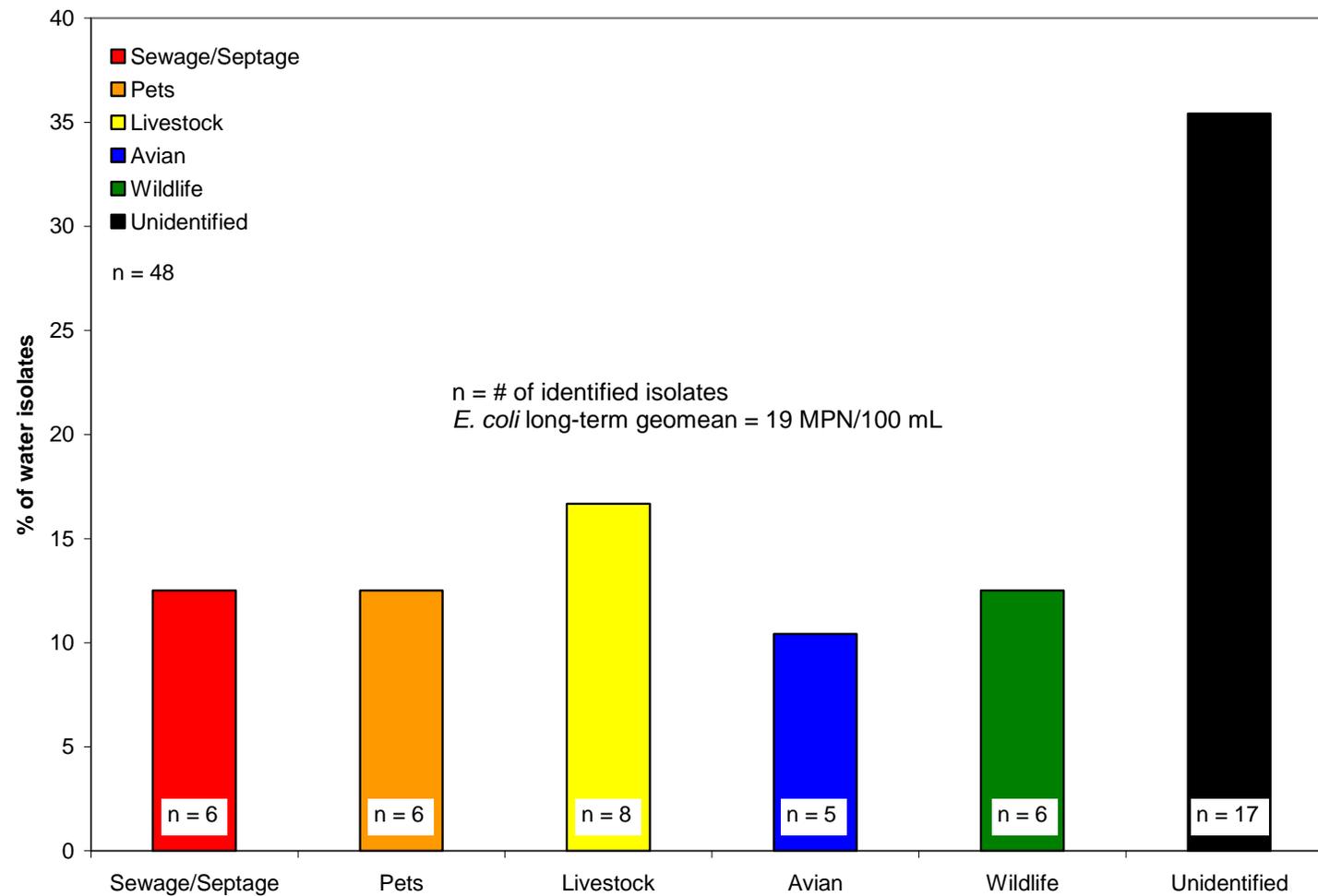


Figure 15. *E. coli* source identification for the Waters Edge (18018) site. The *E. coli* long-term geometric mean at this site is low (19 MPN/100 ml).

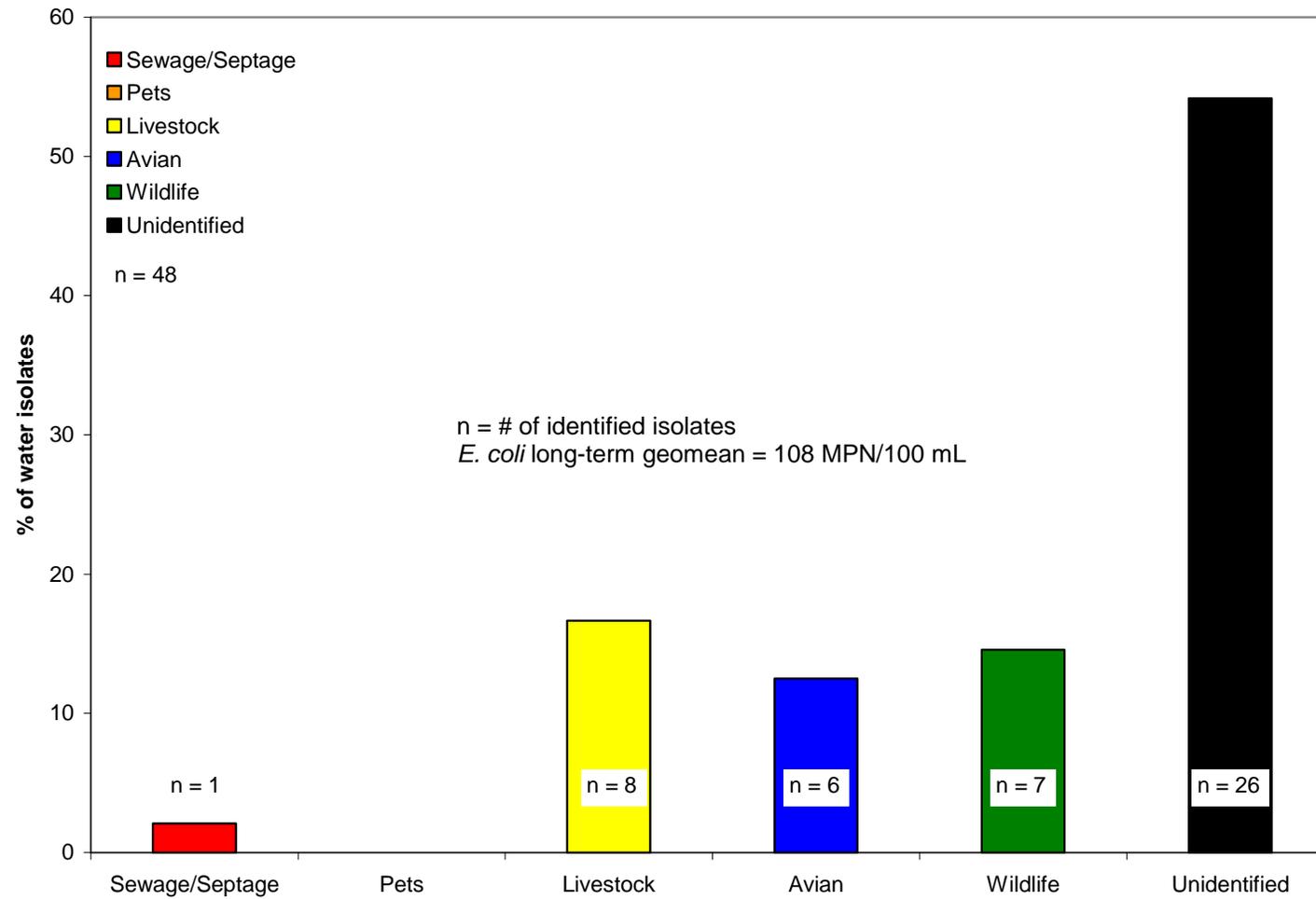


Figure 16. *E. coli* source identification for the Indian Harbor (20215) site. The *E. coli* long-term geometric mean at this site is moderately high (108 MPN/100 ml).

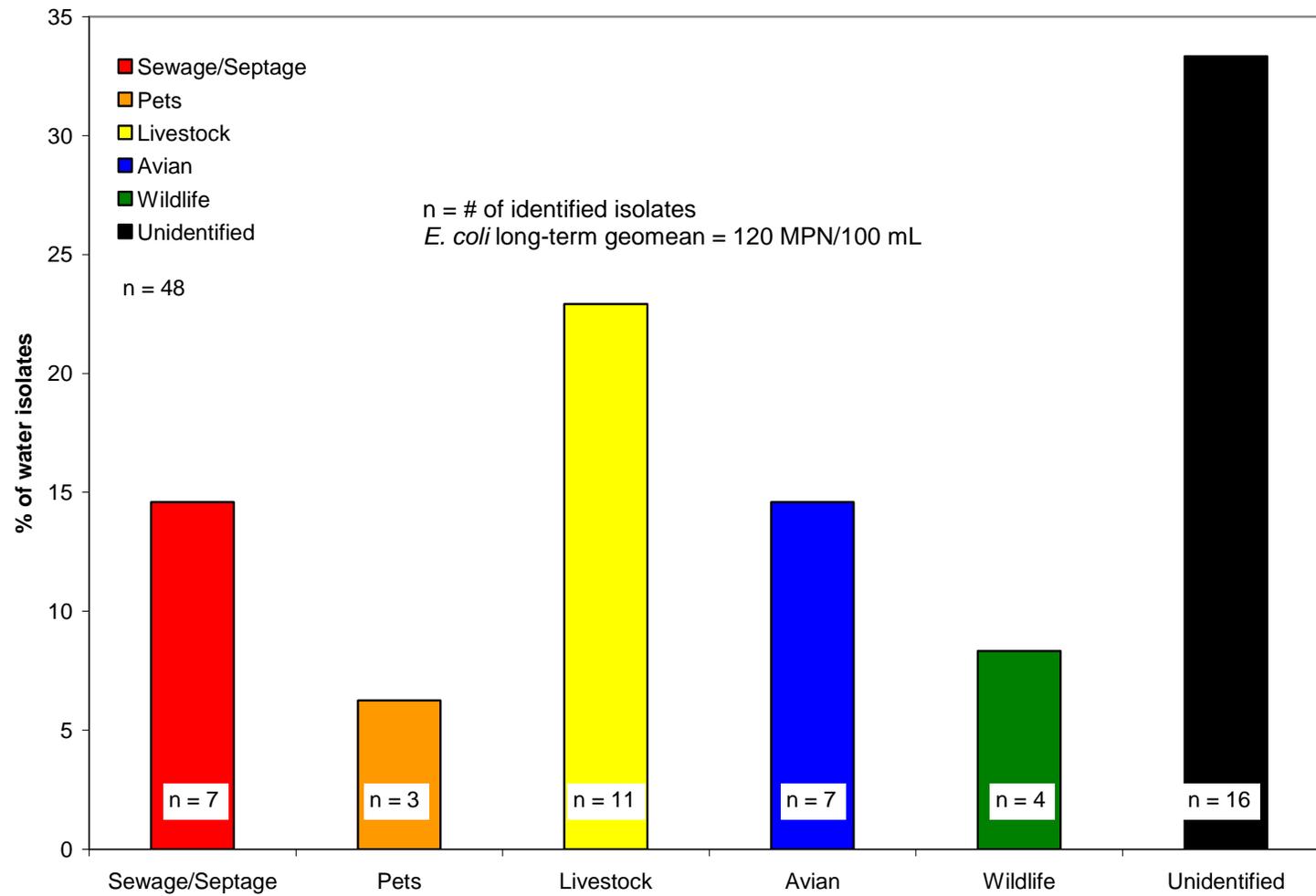


Figure 17. *E. coli* source identification for the Port Ridglea East (18038) site. The *E. coli* long-term geometric mean at this site is high (120 MPN/100 ml).

4.4.3.3 *Bacteroidales* marker distribution in Lake Granbury known source fecal samples

A total of 94 known source fecal samples from the Lake Granbury area were analyzed for the presence of *Bacteroidales* PCR host markers (Table 9). This allowed us to determine the local distribution of the markers in both target and non-target human and animal host groups.

Table 9. Bacteroidales marker occurrence for Lake Granbury known fecal samples

| Marker occurrence | | | | | |
|-----------------------------------|--------------|--------|------|-------|----------|
| Host class | # Samples | GenBac | Hog | Human | Ruminant |
| Lamb | 1 | 1/1 | 0/1 | 0/1 | 1/1 |
| Llama | 3 | 3/3 | 0/3 | 0/3 | 3/3 |
| Goat | 2 | 2/2 | 0/2 | 0/2 | 2/2 |
| Deer | 2 | 2/2 | 0/2 | 1/2 | 2/2 |
| Cow | 4 | 4/4 | 0/4 | 0/4 | 4/4 |
| Compost | 5 | 0/5 | 0/5 | 0/5 | 0/5 |
| Horse (includes mini-horse) | 4 | 4/4 | 0/4 | 0/4 | 0/4 |
| Domestic Pig | 6 | 6/6 | 6/6 | 0/6 | 5/6 |
| Feral Hog | 7 | 7/7 | 7/7 | 0/7 | 6/7 |
| Septic | 6 | 6/6 | 0/6 | 3/6 | 0/6 |
| Domestic Sewage | 10 | 10/10 | 8/10 | 10/10 | 0/10 |
| Pets (Dogs and Cats) | 10 | 9/10 | 0/10 | 0/10 | 0/10 |
| Rabbit (includes jack rabbit) | 7 | 7/7 | 0/7 | 5/7 | 0/7 |
| Coyote | 8 | 5/8 | 0/8 | 3/8 | 0/8 |
| Raccoon | 11 | 5/11 | 0/11 | 1/11 | 0/11 |
| Armadillo | 1 | 0/1 | 0/1 | 0/1 | 0/1 |
| Possum | 1 | 1/1 | 0/1 | 0/1 | 0/1 |
| Ducks (includes domestic duck) | 3 | 2/3 | 0/3 | 0/3 | 0/3 |
| Domestic Goose | 1 | 1/1 | 0/1 | 0/1 | 0/1 |
| Chicken | 1 | 0/1 | 0/1 | 0/1 | 0/1 |
| Buzzard | 1 | 0/1 | 0/1 | 0/1 | 0/1 |

In most cases, the occurrence of the *Bacteroidales* host source markers were as anticipated. The exceptions were for the Ruminant and Human markers. Other research teams have recently reported that the Ruminant marker may be detected in other non-ruminant animal populations. In particular, the Ruminant marker is often present in feces from domestic pigs and feral hogs. Therefore, water samples positive for the Ruminant marker may indicate fecal pollution not only by ruminant animal sources, but also feral hogs. The Hog marker appears quite specific, with the exception that domestic wastewater samples often give a weak signal. However, the Human marker signal from wastewater samples is much more intense, and therefore sites impacted by domestic sewage (and not hogs) would be positive for the Human marker, but not likely provide a false-positive for the Hog marker. The Human marker may also occasionally be detected in the feces from some animal groups, such as coyotes and raccoons. Of the tested fecal samples from Lake Granbury, 3 of 8 coyote and 1 of 11 raccoon samples tested positive for the Human marker. We also had 5 of 7 rabbit samples test positive for the Human marker, but 4 of these were pet rabbits in close contact with humans.

4.4.3.4 Detection of *Bacteroidales* host markers in water samples from each sampling site

A total of 36 grab water samples were collected for *Bacteroidales* PCR analysis. Six sets of samples were collected from each sampling site, and duplicate samples were collected from the Sky Harbor (18015) site. *Bacteroidales* results are presented in two different formats, either percentage of positive samples (Table 10), or relative abundance of markers (Figure 18 through Figure 20). It is important to note that while specific marker abundance can be compared between sites, it is not appropriate to compare the abundance of one marker to another (e.g. Hog vs. Human), since that would require DNA extraction controls and marker-specific quantitation standards which were not employed in the current study.

Table 10. *Bacteroidales* marker occurrence for Lake Granbury known fecal samples, by site

| Site | Name | # samples | % GenBac | % Hog | % Human | % Ruminant* |
|-------|----------------------------|-----------|----------|-------|---------|-------------|
| 11861 | Main Lake | 6 | 100 | 33 | 50 | 83 |
| 18015 | Sky Harbor | 6 | 100 | 67 | 50 | 50 |
| 18015 | Sky Harbor Field Duplicate | 6 | 100 | 83 | 67 | 50 |
| 18018 | Waters Edge | 6 | 100 | 50 | 33 | 50 |
| 20215 | Indian Harbor | 6 | 100 | 50 | 50 | 100 |
| 18038 | Port Ridglea E. | 6 | 100 | 67 | 0 | 100 |

*Ruminant marker may detect cattle, deer, goats, sheep, llamas and other non-ruminant feral hogs

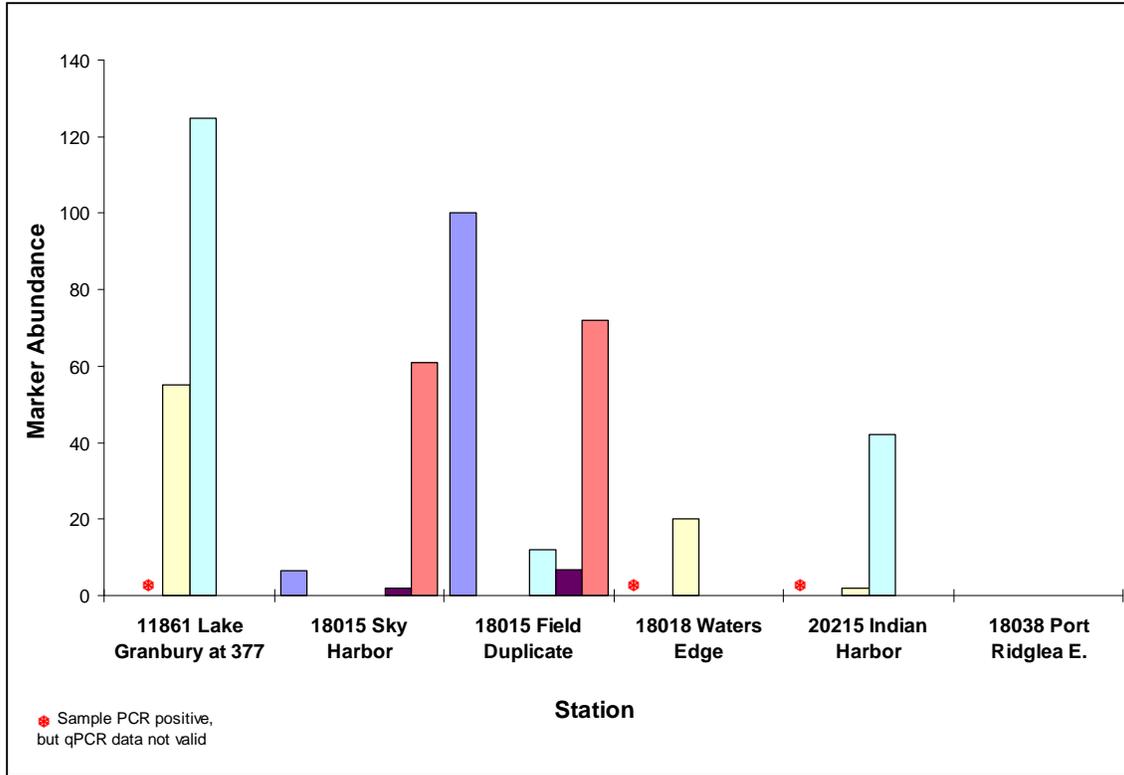


Figure 18. Bacteroidales Human marker abundance by site for the six sets of samples.

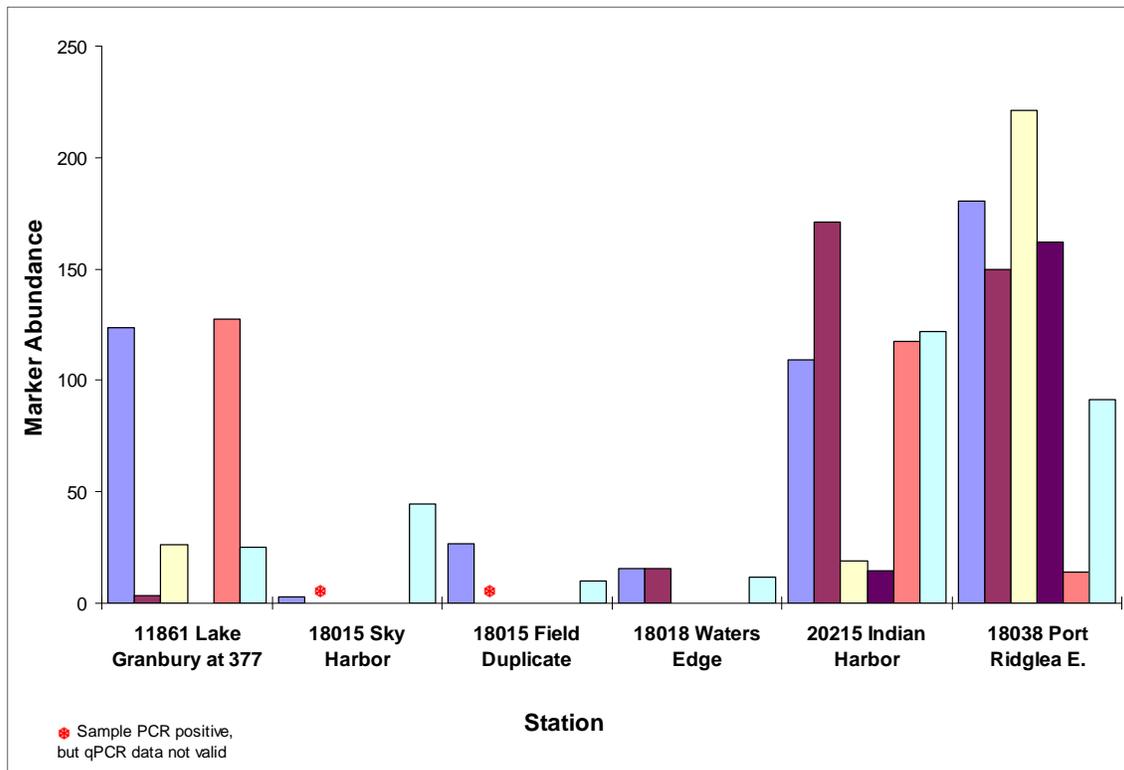


Figure 19. Bacteroidales Ruminant marker abundance by site for the six sets of samples.

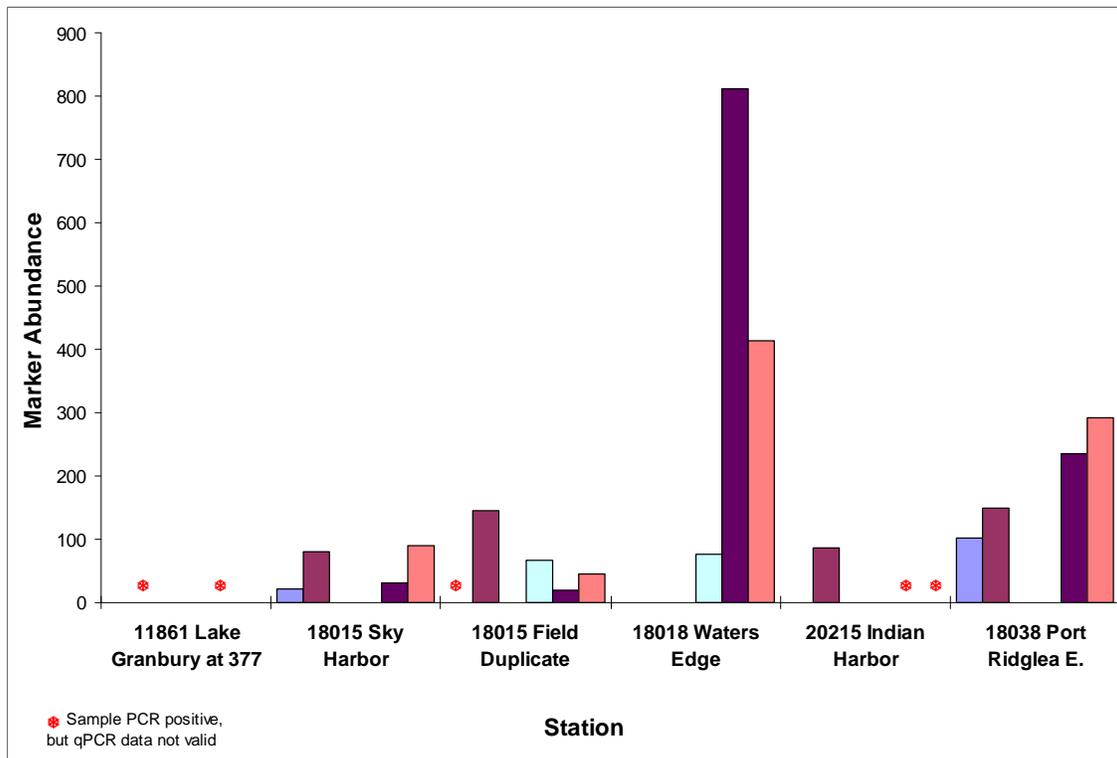


Figure 20. Bacteroidales Hog marker abundance by site for the six sets of samples.

4.4.3.5 *Bacteroidales* results for additional Waters Edge and Port Ridglea East water samples

E. coli and *Bacteroidales* BST results suggested that the sites were impacted primarily by animal-derived (wildlife) fecal pollution. These findings were surprising, particularly for the Port Ridglea East site that was assumed to be highly impacted by human fecal pollution from leaking septic systems. Unexpectedly, Waters Edge also had two samples with high Hog marker occurrence.

As a follow-up, more intensive sampling was performed at the Port Ridglea East and Waters Edge sites in December, 2008. Two sets of samples were collected approximately two weeks apart from five locations within Waters Edge and ten locations within Port Ridglea East for *Bacteroidales* analysis (Table 11). Additional fecal samples were also collected in an attempt to identify possible animal populations (other than deer and feral hogs), which may have contributed to the unanticipated Ruminant and Hog marker results at those sites. One possible source discussed at the December, 2008 stakeholder meeting was compost used for lawn fertilizer, as this may represent a possible source of Ruminant and Hog marker. *Bacteroidales* PCR results for fecal samples and compost samples are presented in Table 9.

Table 11. Bacteroidales marker and *E. coli* occurrence for additional Waters Edge and Port Ridglea East water samples*

| Location | Site # | # Samples | GenBac | Hog | Human | Ruminant | <i>E. coli</i> (MPN/100 mL) on 12-08-08 | <i>E. coli</i> (MPN/100 mL) on 12-12-08 |
|-------------------|------------|-----------|--------|-----|-------|----------|---|---|
| Waters Edge | 18017 | 2 | +/+ | -/- | -/- | -/+ | 17 | 27 |
| Waters Edge | 18018 | 2 | +/+ | -/- | +/- | +/+ | 24 | 16 |
| Waters Edge | 18019 | 2 | +/+ | -/- | +/- | -/- | 7 | 14 |
| Waters Edge | 18020 | 2 | +/+ | -/- | -/- | -/+ | 8 | 2 |
| Port Ridglea East | 18031 | 2 | +/+ | -/- | -/- | +/- | 550 | 120 |
| Port Ridglea East | 18032 | 2 | +/+ | -/- | -/- | +/+ | 410 | 96 |
| Port Ridglea East | 18033 | 2 | +/+ | -/- | -/- | +/- | 61 | 93 |
| Port Ridglea East | 18034 | 2 | +/+ | +/- | -/- | +/+ | 330 | 78 |
| Port Ridglea East | 18035 | 2 | +/+ | +/+ | -/- | +/+ | 2400 | 1300 |
| Port Ridglea East | 18036 | 2 | +/+ | +/+ | -/- | +/- | 370 | 77 |
| Port Ridglea East | 18037 | 2 | +/+ | -/- | -/- | +/+ | 310 | 86 |
| Port Ridglea East | 18038 | 2 | +/+ | -/- | -/- | +/+ | 86 | 45 |
| Port Ridglea East | 18039 | 2 | +/+ | -/- | -/- | +/+ | 150 | 73 |
| Port Ridglea East | 18040 | 2 | +/+ | -/- | -/- | +/+ | 24 | 62 |
| Port Ridglea East | 18040 FD** | 2 | +/+ | -/- | -/- | -/+ | 30 | 62 |

* Samples collected on 12-08-08 and 12-12-08

** FD, Field Duplicate

Compost samples tested negative for all *Bacteroidales* markers, so this does not appear to be a potential source, and no other wildlife sources of the Ruminant marker were identified. Follow-up Waters Edge samples tested negative for the Hog marker. Therefore, the fecal pollution source responsible for the previous Hog marker occurrence remains unidentified, and the low levels of fecal pollution observed at Waters Edge appear to be due to various nonpoint sources. In contrast, water samples from Port Ridglea East again revealed the presence of animal fecal pollution and the absence of human source pollution, despite some of the samples having very high *E. coli* levels. It should also be noted that the water samples were collected under base flow water conditions (no rainfall events for several weeks prior to sampling), so runoff was not a factor. Sample collectors noted numerous ducks in the Port Ridglea East coves during collection of the follow-up samples. In addition, Port Ridglea East water samples were also tested for two additional markers of human fecal pollution using PCR: *Methanobrevibacter smithii* and human polyomavirus. Only the Port Ridglea East 18040 and 18040FD (field duplicate) samples from the second set of follow-up samples tested positive for the human polyomavirus.

4.4.4 BST Source Identification Summary

Large disparities existed between the BST results and the results of Land Use Analysis, Watershed Modeling and local stakeholder knowledge of the watershed. These disparities caused uncertainty among all stakeholders related to the accuracy and usefulness of BST in its current form as a tool to identify sources. The Lake Granbury Watershed Protection Plan Steering Committee (LGWPPSC) indicated that they feel, after reviewing the BST results, that BST technology is not currently developed well enough for them to base management decisions using this data. The LGWPPSC chose not to rely heavily on the BST results. When directing the project team to pursue management measures for specific sources, the LGWPPSC made their decisions for these areas based on local watershed knowledge, Land Use Analysis, Watershed Modeling and Water Quality Modeling.

4.5 MODELING ASSESSMENT OF FECAL POLLUTION SOURCES IMPACTING LAKE GRANBURY

Land Use Analysis and Watershed Modeling of the Lake Granbury watershed reveal a shift toward increased urbanization and the resulting issues. This region was farmed and ranched extensively during the early part of the 20th Century. After completion of Lake Granbury in 1969 and as agricultural usage in the watershed gradually transitioned through the 1970s and 1980s to the modern urban environment, new water quality issues in Lake Granbury began to arise. While the old concerns for agricultural impact still exist (e.g. increased erosion, sedimentation, animal waste) in the watershed, those potential sources are more removed from the vicinity of Lake Granbury than they were several decades ago. Stormwater runoff from residential properties, greater totals of impervious cover, reduced vegetation buffers between developed property and the lake, increased effluent from wastewater treatment plants, and an increased concentration of aging septic systems are all products of the rapidly increasing development of the Lake Granbury watershed and are the greatest threat to the long-term health of the lake.

Watershed and lake water quality modeling tools to consider these factors were developed as part of this WPP project. The SELECT watershed modeling approach (Teague 2007; Teague 2009; Riebschleager 2008) was used to evaluate how potential sources of bacteria differed for sub-watershed areas surrounding the lake, considering differences in land use patterns. Lake modeling tools were also developed to evaluate how bacteria concentration in lake and cove waters responds to differences in inflow, precipitation and cove geometry. The modeling parameters, approaches and tools for both watershed and lake environments were developed by the Espey Consultants, Inc., (EC) project team in collaboration with project team expert advisors Dr. Srinivasan and Dr. Karthikeyan (both of Texas A&M University with expertise in watersheds and bacteria modeling) and Dr. Ward and Dr. Armstrong (both of University of Texas with expertise in water body water quality modeling). The modeling approaches were also vetted through TCEQ staff modeling professionals assembled by the TCEQ management team. Additional discussion and advisement on modeling purposes, inputs and outputs was provided by the stakeholders to the project team.

Watershed modeling focused on the sources and magnitude of fecal bacteria on the ground surface that could potentially be transported during rainfall runoff events to nearby waterbodies and ultimately Lake Granbury. To characterize the production and distribution of waste and associated pathogens, the SELECT approach was utilized for the Lake Granbury watershed. This approach addresses the major sources of fecal bacteria production (and associated pathogens), as estimated through land use analysis, literature review, and experimental data. Wildlife such as migratory birds and rodents are a “background” source of bacteria that are often present but not easily quantified and thus are not included in the model. Additionally, a characteristic animal such as beef cattle can be used for load estimation but could be serve as a surrogate for analysis of other similar species of livestock. Similarly, dogs are used as a surrogate for domestic pets. Stakeholder input is important in identifying sources of bacteria in site-specific areas.

The lake/cove water quality modeling of the canals along Lake Granbury (“lake/cove models”) focused on scenario analyses to evaluate the type of loading occurring by comparison with actual observation data. This evaluation depends upon theoretical rather than actual loads from either

direct (point) or diffuse (nonpoint) sources and thus does not identify animal specific sources or magnitudes. This approach does however characterize the movement of pollutants through the specific canal waterbodies based on site specific properties such as dispersion coefficients and channel geometries.

Together with the land use analysis, the watershed models and lake/cove models were used as part of a multi-pronged approach to identify most likely sources of bacteria for each area. Since the watershed and cove models consider different inputs and characteristics, a direct comparison or a direct linkage between the two models is not possible. However, the suite of models developed throughout the WPP area enabled evaluation of a range of potential sources and mechanisms affecting bacteria levels in the lake (Table 12).

Table 12. Sources evaluated by lake/cove and watershed modeling approaches

| Sources evaluated | |
|---|--|
| Lake/Cove Model | Watershed Model |
| <i>Point sources</i> | |
| 1. Direct discharge into canals by malfunctioning OWTF (human) a) continuous discharge b) intermittent discharge* 2. Main-lake as a bacteria source to canals* | 4. WWTP (human) |
| <i>Distributed non-point sources within the watershed</i> | |
| 3. Non-species-specific watershed non-point source (urban runoff related to rainfall events) | 5. OWTF (human) 6. Dog 7. Cattle 8. Deer 9. Feral Hogs |

*in selected subdivisions

4.6 DATA TO SUPPORT MODELING EFFORTS

Playing an active role in this WPP process, the stakeholder group provided input on use of parameters important to the development of watershed and lake models to ensure they are representative of watershed areas affecting water quality of Lake Granbury. Assumptions and decision points used in the watershed and lake models were presented, and the stakeholders found that some of these literature values exhibited large variation. For example, dispersion coefficients have been recorded from 0.02 to 44 m²/s (Peeters et al. 1996, Goodwin 1991, and Thomann and Mueller 1987) and raw sewage fecal coliform bacteria were reported in the range of 50,000 to 10,000,000 MPN/100mL (USEPA 2001). Based upon the wide range of literature values and the sensitivity of results to these values, the stakeholders identified parameters for which they felt site-specific data was necessary. For other less sensitive parameters, the stakeholder group chose values derived from literature or existing data (Table 13).

Table 13. Model parameter resolutions based on literature values or existing data

| | |
|--|--|
| Ratio of <i>E. coli</i> to Fecal Coliform | 0.7:1 |
| Non-point source (NPS) concentration in urban runoff | Fecal coliform count 16,048 MPN/100mL |
| Residential wastewater generation | 200 gpd/house |
| Bacteria decay rate at 15°C | 0.2/day |
| Temperature correction, $K = K_1 * \Theta^{(T - T_1)}$ Median summer temperature 28°C $\Theta = 1.07$ (Thomann and Mueller 1987) | |
| Bacteria decay rate @ 28°C | 0.5/day |

Three specific field evaluations were conducted to develop model parameter values (Table 14). These included (1) cove circulation studies to calculate dispersion coefficients (2) a bacteria concentration study for two waste water treatment plants (WWTPs) to calculate a representative raw sewage bacteria concentration and (3) a septic system leakage study to test the hypothesis that leaky septic systems contribute directly to the high bacteria concentrations in canals. The sampling protocol for these studies is described in the Lake Granbury Watershed Septic Tracer, Circulation Study, and Additional Water Quality Sampling, Quality Assurance Project Plan (BRA 2007).

Table 14. Model parameter resolutions based on field data

| | |
|---------------------------------|-------------------------------|
| Raw sewage <i>E. coli</i> count | 6.68 million MPN/100mL |
| Site-specific dispersion values | 0.02 to 0.18 m/s ² |

4.6.1 Cove circulation studies - Dispersion Coefficients

Espey Consultants, Inc. (EC) performed a circulation study February 18th through 22nd, 2008. The purpose of the circulation study is to develop field data from which to calculate dispersion coefficients in specific coves/canal areas. The circulation study was performed by releasing predetermined volumes of 20% solution of Rhodamine WT (RWT 20%) dye in several canal systems within Lake Granbury (details provided in Appendix C). The specific cove systems characterized by this field test were Oak Trail Shores, Sky Harbor, Port Ridglea East, Waters Edge, Indian Harbor, and Ports O' Call subdivisions. Each canal system was revisited multiple times to measure the concentration of the dye.

Circulation patterns, and therefore circulation studies, are sensitive to wind, flow and lake recreation in the study area. Inflows to and outflows from the lake were relatively low and decreasing during the period of the study (60 to 120 cfs). A temporary wind station was set up to collect wind data on-site during the study. Boat traffic inside the canals can potentially impact circulation dye studies, but boat traffic was negligible during the study period.. Disruption due to survey boat velocity was minimized by traveling at low velocity.

Several approaches can be used to estimate the dispersion parameter using conservative (non-reactive) dye as the tracer substance (Thomann and Mueller 1987, USGS 2002, Ward 1985). Ward (1985) performed a dye study for Texas bays, and methods used for that study were adopted to calculate the dispersion coefficients for Lake Granbury (Table 15). Dispersion

parameters for unvisited canals were estimated according to similarity to canals where field studies were conducted.

Table 15. Calculated Dispersion coefficients

| Subdivision | Dispersion Coefficients (m ² /s) |
|-------------------|---|
| Indian Harbor | 0.02 |
| Oak Trail Shores | 0.1 |
| Port Ridglea East | 0.125 |
| Ports O' Call | 0.09 |
| Sky Harbor | 0.18 |
| Waters Edge | 0.08 |

Dispersion coefficients for the Lake Granbury coves are comparably lower than most literature values, which is reasonable considering the more constrained condition in the canal systems. Wind speed between field tested and NCDC data for the Granbury area were compared (Appendix C). The wind speed is much lower over the cove/canal waterbodies compared with NCDC wind speed recorded at unobstructed stations 30 feet above ground.

4.6.2 Raw Sewage Bacteria Concentration Sampling

An important parameter for modeling direct discharge into the lake is the raw sewage bacteria concentration. Literature values of fecal coliform concentrations vary by location. Two wastewater treatment plants (WWTPs) in the Lake Granbury area that provide service to residential communities were sampled by Authority staff between March 5th and April 30th, 2008, for bacteria concentrations in raw sewage influent. The first WWTP discharges near the DeCordova Bend subdivision and the other near the Blue Water Shores subdivision. Over the nine week period, the WWTPs were visited every Wednesday for sampling. From each visit, at each plant, 20 bacteria analyses were carried out for both total coliform concentration and *E. coli* concentration.

The bacteria concentrations were determined by incubating the water sample for 24 hours and then counting the number of bacterial colonies that grew during that time. The unit for reporting fecal bacteria is "colony-producing units" (CPU) per 100 milliliters of water (CPU/100 mL). CPUs/100 mL is used interchangeably with "most probable number" (MPN) per 100 mL (MPN/100 mL).

A portion of the *E. coli* sampling data for DeCordova Bend plant are shown in Table 16 as an example.

Table 16. Raw Sewage E. Bacteria Concentration (100,000 MPN/100mL) for the DeCordova Bend WWTP

| E Coli (MPN*100,000) | 5-Mar-08 | 12-Mar-08 | 19-Mar-08 | 26-Mar-08 | 2-Apr-08 | 9-Apr-08 | 16-Apr-08 | 23-Apr-08 | 30-Apr-08 |
|----------------------|----------|-----------|-----------|-----------|----------|----------|-----------|-----------|-----------|
| DCB #1 | 86 | 10.8 | 26.5 | 96.0 | 34.5 | 81.6 | 39.7 | 88.2 | 51.2 |
| DCB #2 | 58.3 | 10.9 | 19.9 | <1 | 38.8 | 81.3 | 35.9 | 44.1 | 44.1 |
| DCB #3 | 75.4 | 3 | 27.2 | 98.8 | 46.2 | 58.3 | 35.9 | 63.8 | 69.7 |
| DCB #4 | 81.6 | 8.4 | 23.1 | 88.2 | 34.5 | 81.6 | 49.6 | 95.9 | 54.8 |
| DCB #5 | 62.7 | 8.6 | 23.1 | 84.2 | 49.5 | 79.8 | 50.4 | 56.5 | 49.6 |
| DCB #6 | 71.7 | 4.1 | 25.3 | 67.0 | 59.4 | 73.3 | 116.9 | 68.3 | 49.5 |
| DCB #7 | 65.7 | 14.4 | 33.1 | 90.8 | 50.4 | 81.6 | 35.9 | 73.3 | 65.7 |
| DCB #8 | 39.3 | 3.1 | 18.5 | 66.3 | 36.9 | 77.1 | 31.3 | 104.6 | 59.1 |
| DCB #9 | 51.2 | 9.7 | 17.1 | 88.4 | 39.3 | 55.6 | 113.7 | 52.9 | 79.4 |
| DCB #10 | 52.1 | 8.5 | 23.3 | 78.9 | 27.5 | 129.6 | 72.7 | 70.0 | 62.7 |

Arithmetic mean (average) of 360 samples (20 analyses, 9 visits, two plants) was calculated as 6,688,176 MPN/100mL. This value was adopted for model use for the Lake Granbury area *E. coli* concentration in raw sewage.

4.6.3 Septic Tracer Dye Study

The septic tracer study was performed on April 7 through 11, 2008, by injecting predetermined volumes of a 20% solution of Rhodamine WT (RWT 20%) dye into residential septic systems (generally via kitchen sink or bathtub drain) and then running water to flush the dye through the system. The entire process for one residence took approximately 30 minutes. Once the injection was complete, the drain field (yard) and the adjacent cove was monitored for the next few days, once in the morning and again in the evening, to determine the amount of time necessary for the colored dye to show up in the water around the cove. The intention of this test was to characterize normal or abnormal water movement from septic systems into the nearby canals. The details of the data collection methods and results are located in Appendix C.

In all of the subdivisions visited, study participants were concerned about water quality in the lake, citing a range of reasons such as property values, aesthetics, swimming and fishing. As a statistical summary, 16% of participants did not know when their septic system was last serviced; 30% knew their systems had not been serviced within the last 5 years; and 11% had new systems less than 5 years old at the time of the survey.

In 44 systems tested in this septic study, leakage was found in two systems, one in Oak Trail Shores and one in Port Ridglea East. In both cases, pooling on the ground surface were observed following laundry loads, which indicated that there was minor leaking of the septic system. Before the tests, both systems were thought by participants to be properly functioning as they had performed maintenance or repairs within the last two years. This indicated that septic systems exhibited imperfect functions sooner than residents expected; regular inspection and maintenance could alert owners of necessary repairs.

Water quality monitoring was conducted as a component of this study in the subdivisions visited. *E. coli* concentrations tested on April 10, 2008, are listed in Table 17 for each subdivision. Despite on-ground pooling at two locations, and subsequent precipitation events during the study, no dye was observed entering the canals. This indicates that the systems tested were not significant contributing sources to bacteria levels at the time of the study.

Table 17. *E. coli* concentration monitored on 04/10/2008

| Subdivision | <i>E. Coli</i> Conc. (MPN/100mL) |
|----------------------|----------------------------------|
| Oak Trail Shores | >2000 |
| Rolling Hills Shores | >1635 |
| Port Ridglea | PRE 416/ PRW 297 |
| Sky Harbor | >1875 |

4.6.4 Adopted Modeling Resolutions

Considering sensitivity of selected model inputs, stakeholders adopted resolutions related to specific model inputs.

1. The site-specific conversion of 1 FC:0.7 *E. coli* was adopted in this study. The current pathogen indicator for fecal contamination is reported in *E. coli* concentration (MPN/100mL). In the past, fecal coliform was the indicator bacteria used for monitoring bacteria; therefore, more data is available and more research has been performed for the fecal coliform indicator making available model inputs from literature based on fecal coliform concentrations. To make fecal coliform literature relevant to this study, a conversion factor between fecal coliform and *E. coli* concentrations is needed to compare modeling results and monitoring data. As a local reference the Brazos River Authority (BRA) reported a ratio of 1:0.6 to 1:0.7 (fecal: *E. coli*) for monitoring data at Lake Granbury between 2002 and 2004. The ratio 1:0.7 was adopted for this study.

2. *E. coli* concentration in runoff used in lake modeling is calculated as 11,234 MPN/100 mL. In the City of Austin Environmental Criteria Manual (2007), fecal coliform concentration in a multi-family residence area is 8,400 colonies/100 mL; CRWR (1996) quoted fecal coliform concentration for residential areas as 20,000 colonies/100 mL; and CCBNEP (1996) reported fecal coliform as 19,743 colonies/100 mL for high density residential areas. The average fecal coliform concentration from the above references, 16,048 colonies/100 mL, was adopted as the FC concentration for the Lake Granbury area. Using Bacteria FC:EC conversion factor of 1:0.7, *E. coli* concentration in runoff used in lake modeling is calculated as 11,234 MPN/100 mL.

3. Site-specific dispersion values range between 0.02 and 0.18 m²/s for the coves modeled in this WPP effort. As described previously, field circulation studies were conducted in February 2008 to calculate site-specific dispersion coefficients.

4. The value of 6,688,176 MPN/100mL was adopted as the Lake Granbury area *E. coli* concentration in raw sewage. An important parameter for modeling direct discharge into the lake is the raw sewage bacteria concentration. The broad range of literature values indicates the bacteria concentrations found in raw sewage may be dependent upon location. To establish a site specific reference for the Lake Granbury area, bacteria sampling were conducted from March 5 through April 30, 2008, at two WWTPs in the Lake Granbury area: DeCordova Bend and Blue Water Shores. The arithmetic mean (average) of 360 *E. coli* samples (20 analyses, 9 visits, two plants) was calculated as 6,688,176 MPN/100mL.

4.7 WATERSHED MODEL SOURCE IDENTIFICATION

4.7.1 Watershed Delineation

The Lake Granbury Watershed was delineated into subwatersheds (Figure 21) using ArcSWAT (SWAT, 2005). EC created a custom landuse classification by modifying the BRA 2007 landuse shapefile (Figure 22 **Error! Reference source not found.**), for use in the watershed model using the most recent aerial photography, and merging with the National Land Cover Database (NLCD) 2001 (Figure 23).

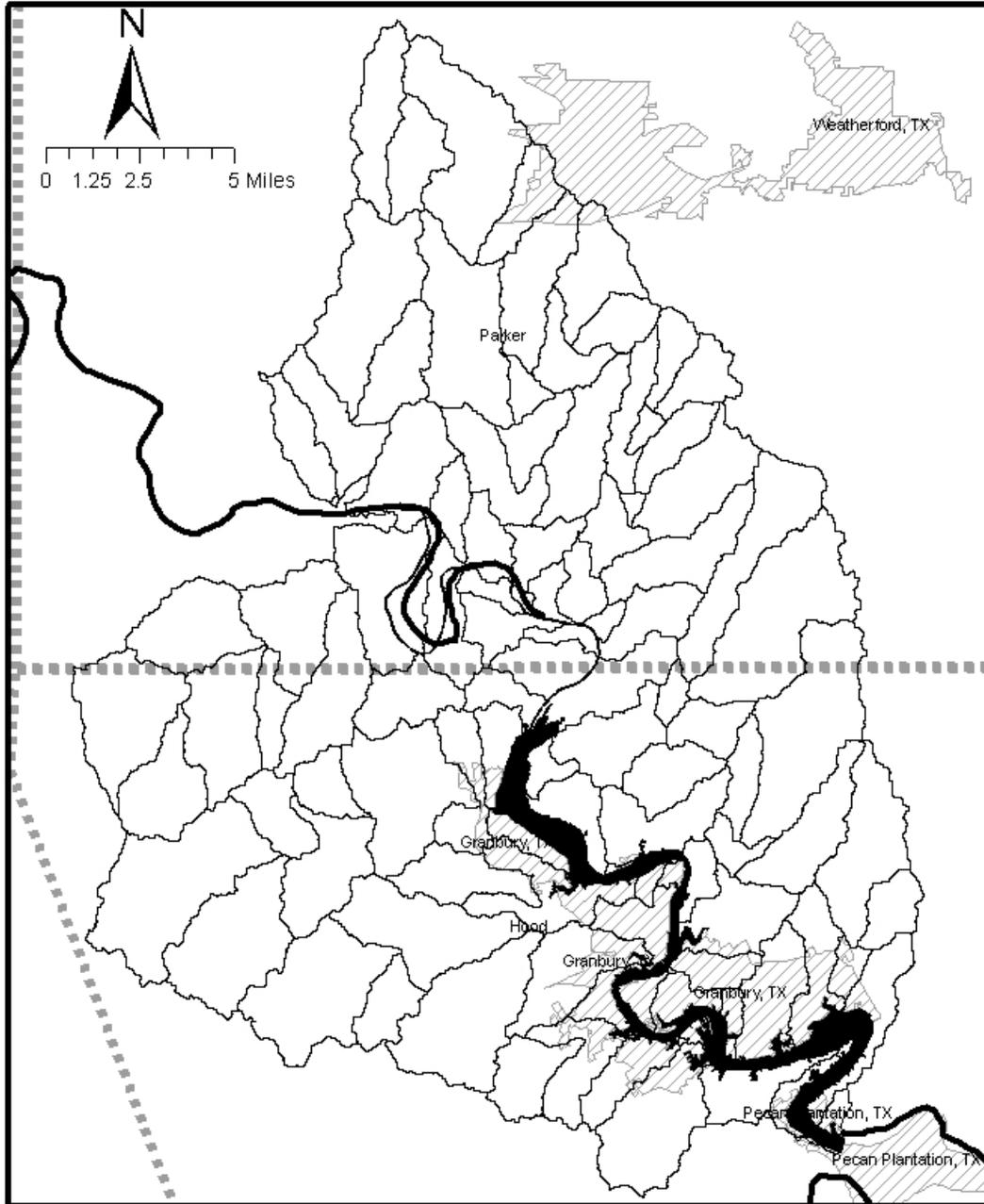


Figure 21. Location of Lake Granbury with Subwatersheds Delineated using SWAT.

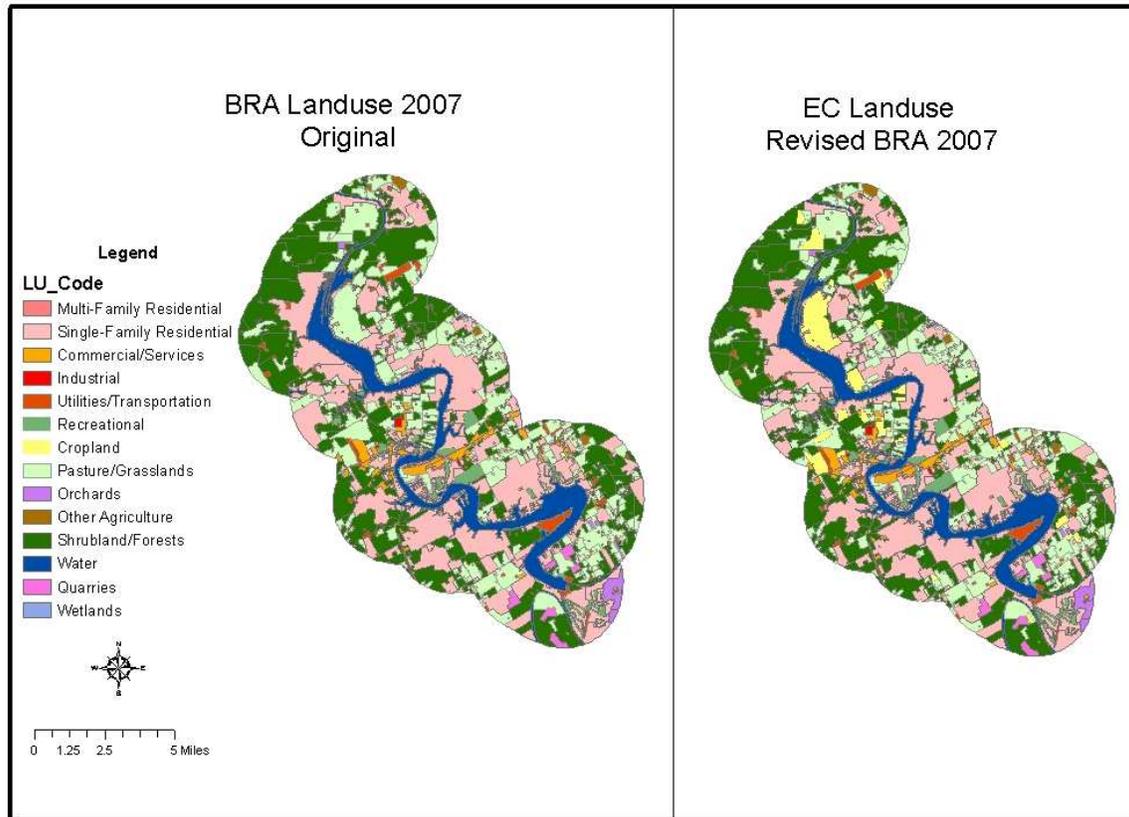


Figure 22. BRA 2007 Landuse and EC Revisions to the BRA 2007 Landuse Classification File.

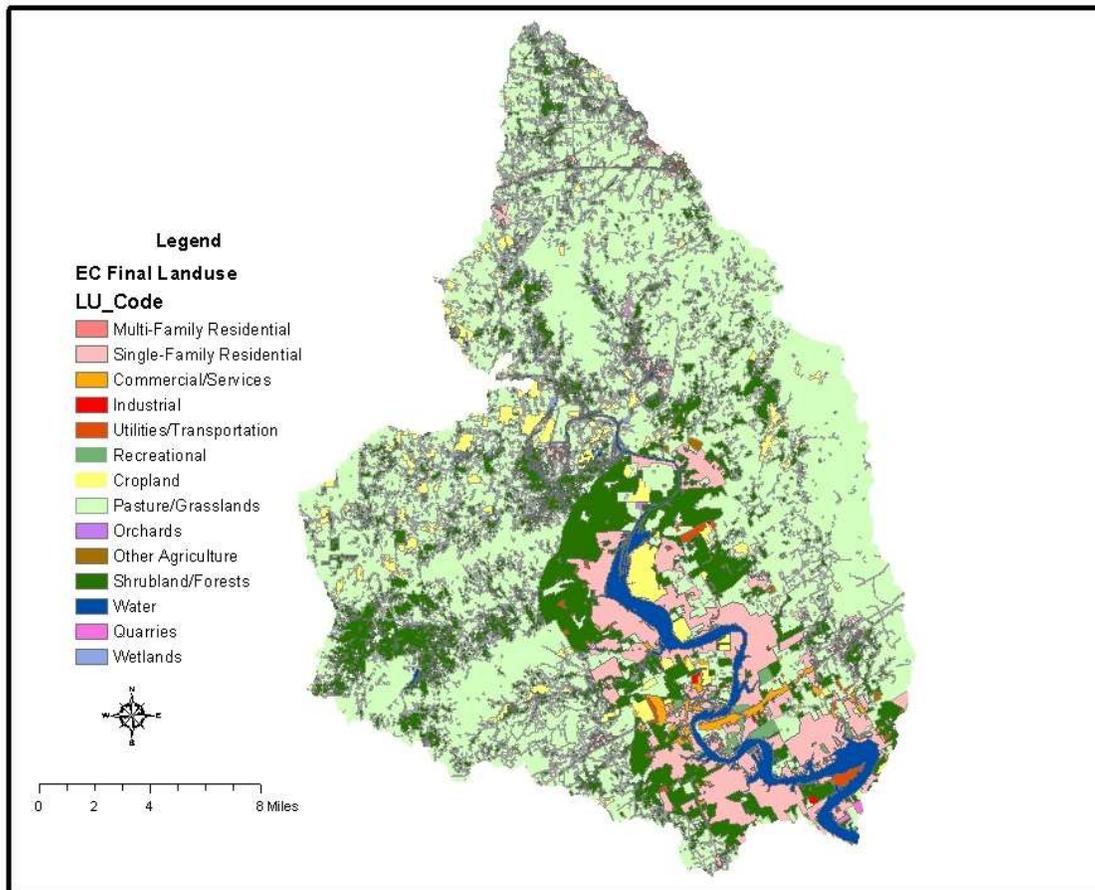


Figure 23. Landuse Classification of Lake Granbury Watershed (EC/BRA 2007 merged with NLCD 2001).

Modeling of large subwatersheds provided information on potential bacteria loads across the entire area of coverage (Appendix D). Since distant watersheds may have limited effects on Lake Granbury waters, microwatersheds pertinent to priority subdivisions were delineated for investigation (Figure 24) based upon site visits and topographic maps to determine drainage patterns. Identification of priority subdivisions were based on analysis of available monitoring data where bacteria levels were found to be elevated; these areas included Rolling Hills Shores, Oak Trail Shores, Indian Harbor, Sky Harbor, Port Ridglea East and Blue Water Shores. While data does not indicate current high bacteria levels, additional areas Arrowhead Shores, Ports O' Call and Nassau Bay are identified in historical reports as having potential bacteria concerns; microwatersheds for these subdivisions were also evaluated. The land use analysis for all microwatersheds surrounding Lake Granbury can be found in Appendix B.

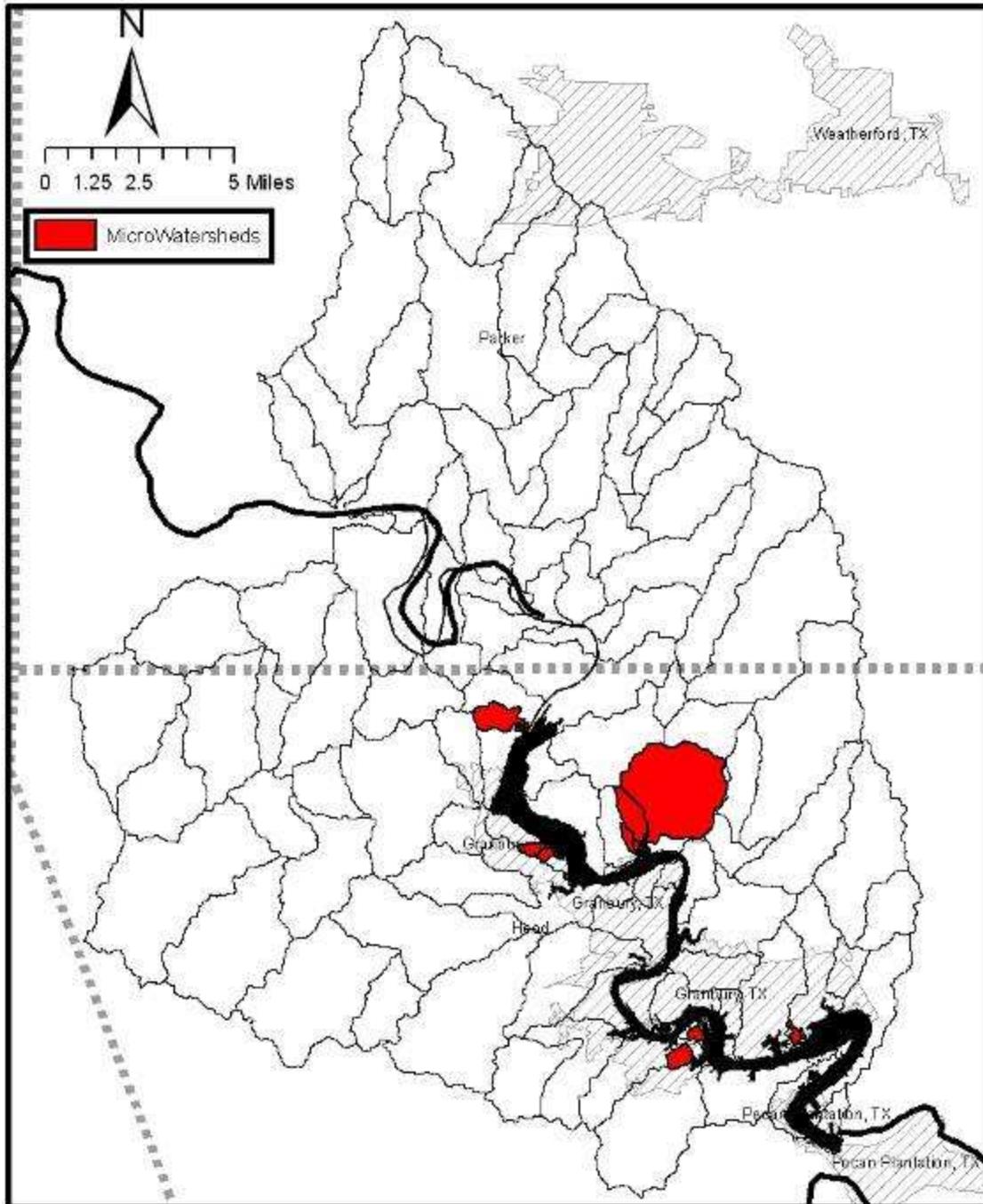


Figure 24. Location of Microwatersheds in the Greater Lake Granbury Watershed

4.7.2 Methodology

Application of SELECT helped stakeholders identify the areas potentially contributing to pathogen contamination of waterbodies without using complex hydrologic models. An additional pollutant connectivity factor (PCF) component was developed (Riebschleager 2008) based on three indicative factors for contamination: a) potential pollutant loading, b) runoff potential, and c) travel distance to streams and other waterbodies.

The SELECT approach for characterizing the *E. coli* sources is similar to the methodology developed by Teague (2007) for the Plum Creek Watershed Protection Plan, with the exception of on-site wastewater treatment systems (referred to here as OWTS, sometimes referred to as on-site sewage facilities). The approach outlined here for SELECT represents on that is expanded, revised, and automated for extending its application to diverse watersheds (Riebschleager 2008).

To characterize the production and distribution of waste and associated pathogens, sources contributing to contamination were determined by using agricultural census information provided by National Agriculture Statistics Service (NASS); talking to the local extension agents and wildlife experts; obtaining permitted Waste-Water Treatment Plants (WWTP) discharges from the EPA Envirofacts Data Warehouse; and researching previous pathogen TMDLs and WPPs. Land use is the factor that has the greatest effect on potential *E. coli* loading because the type of land use / land cover dictates whether the area is suitable for pollutant contribution. For example, it can be assumed that cattle will be confined to pasture and grazing lands and will not be found in cultivated cropland or residential neighborhoods. The fecal production rates for the various sources can be calculated using the EPA Protocol for Developing Pathogen TMDLs (USEPA, 2001) which includes a summary of source-specific pathogen and fecal indicator concentrations.

In SELECT the potential loading on a daily time scale is calculated by estimating the source populations, distributing the sources uniformly across suitable habitats, applying daily fecal production rates, and then aggregating to the level of interest for analysis. In the case of Lake Granbury, potential loading was determined for both the larger subwatersheds (Figure 21) and the micro-watersheds (Figure 24) associated with the subdivisions of interest.

SELECT simulated potential *E. coli* load resulting from cattle, deer, feral hogs, pets (dogs), malfunctioning OWTS, and Waste-Water Treatment Plants. The default fecal production rate values used for this project were chosen as the highest from the range of values provided in the EPA Protocol for Developing Pathogen TMDLs (USEPA 2001) for all *E. coli* sources identified in the Lake Granbury Watershed (Table 18). Default values for *E. coli* concentrations were used for all sources except malfunctioning OWTS; the stakeholder resolutions on raw sewage effluent were used for this source.

Details related to SELECT model assumptions are located in Appendix D.

Table 18. Calculation of *E. coli* Loads from Source Populations

| Source | Calculation |
|------------|--|
| Cattle | $E.coli = \#Cattle * 10 * 10^{10} cfu / day * 0.7$ |
| Deer | $E.coli = \#Deer * 3.5 * 10^8 cfu / day * 0.7$ |
| Feral Hogs | $E.coli = \#Feralhogs * 1.1 * 10^{10} cfu / day * 0.7$ |
| Dogs | $E.coli = \#Households * \frac{0.8dogs}{Household} * 5 * 10^9 cfu / day * 0.7$ |

| | |
|------------------------|--|
| Malfunctioning OWTS | $E.coli = \#OWTSs * MalfunctionRate * \frac{9.554 \times 10^6 \text{ cfu}}{100mL} * \frac{200 \text{ gal}}{\text{household / day}}$ $* \frac{3785.4mL}{gal} * 0.7 * 0.133$ |
| WWTP | $E.coli = PermittedMGD * \frac{126 \text{ cfu}}{100mL} * \frac{10^6 \text{ gal}}{MGD} * \frac{3785.4mL}{gal}$ |

4.7.3 Pollutant Connectivity Factor

The pollutant connectivity factor (PCF) was developed to weigh the influence of the driving forces of contamination with the total pollution present. The PCF indicates areas within the watershed vulnerable to contributing bacteria to waterbodies. This component of the model utilizes the curve number, which directly relates to runoff potential, and the distance to streams, which directly relates to fate and transport. The total pollutant connectivity factor was calculated using a weighted combination of the normalized potential loading, curve number grid, and the inverse of the normalized flow length to streams (Figure 25). This allowed stakeholders to identify areas of greatest concern for water quality impairment. The flow length is derived from a digital elevation model (DEM) using ArcHydro Tools within ArcGIS. The curve number grid is created from intersecting the SSURGO soils hydrologic soil grouping (HSG) and the NRCS 2001 land use classification and then using a NRCS Curve Number Lookup Table. The resulting PCF is a ranking of potential contribution from subwatershed without considering any detailed fate and transport processes in the watershed. The following is the weighted overlay expression for determining the pollutant connectivity factor (PCF):

$$PCF = W_p \times P_I + W_R \times R_I + W_D \times I / D_I \tag{Equation 1}$$

Where,

PCF = Pollutant Connectivity Factor

W_P = weighting factor for the pollutant indicator, P_I

P_I = pollutant indicator, normalized pollutant load on scale from 0 to 100

W_R = weighting factor for the runoff indicator, R_I

R_I = runoff indicator, curve number

W_D = weighting factor for the distance indicator, D_I, and

D_I = distance indicator, normalized flow length on scale from 0 to 100

Appropriate weighting should be based on best knowledge available or expert opinion. Alternatively, sensitivity of weighting factors can be determined by running multiple trials of the pollutant connectivity factor across a range of weighting schemes (Table 19). If a particular subwatershed consistently is determined to be a 'hot spot' for contributing to contamination, then it is likely this subwatershed is of great concern and should be more readily addressed. On the other hand if a particular watershed is consistently rated low, then this watershed should not be of concern when determining management practices. The 'hot spot' evaluation approach was used for the Lake Granbury watershed.

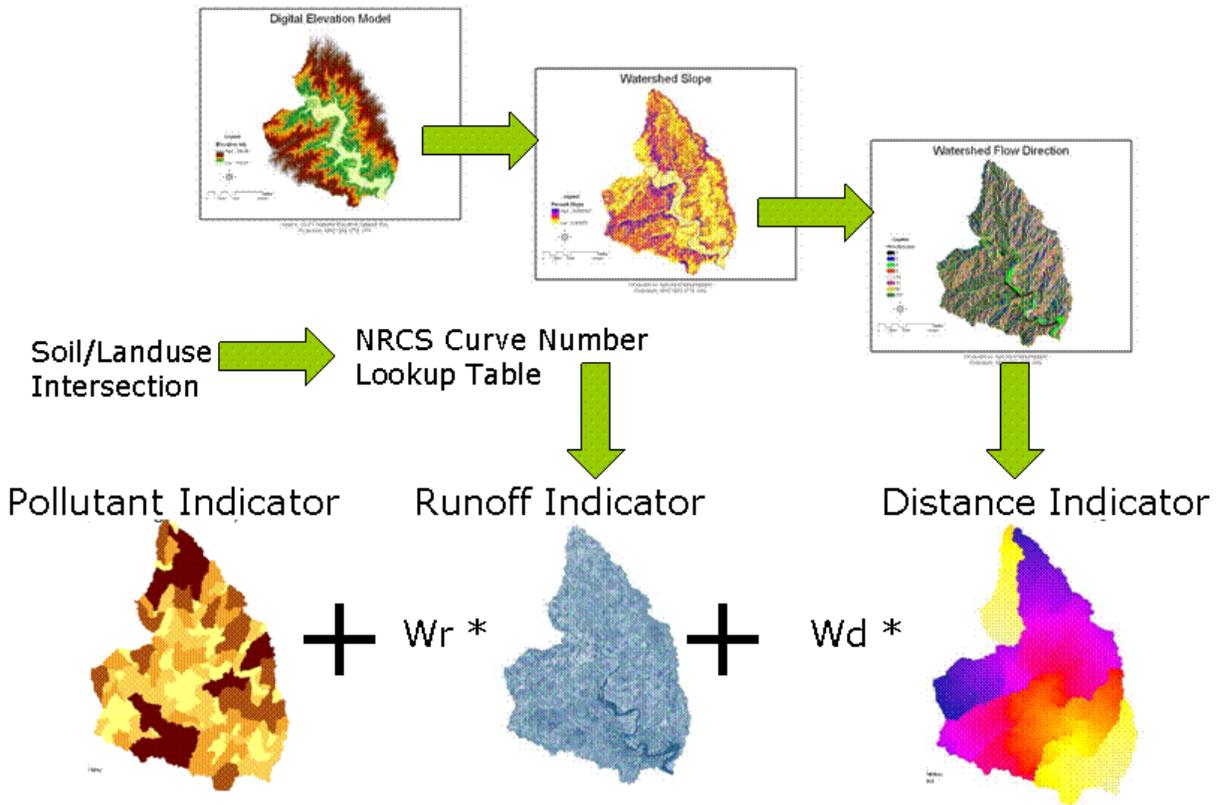


Figure 25. Spatial and Hydrologic Processes to Determine the Pollutant Connectivity Factor (PCF).

Table 19. Weighting Scheme for Sensitivity Analyses of Pollutant, Runoff, and Distance Indicators for determining the Pollutant Connectivity Factor (PCF).

| Trial Number | W_p | W_r | W_d |
|--------------|-------|-------|-------|
| 1 | 5 | 3 | 2 |
| 2 | 5 | 2 | 3 |
| 3 | 4 | 4 | 2 |
| 4 | 4 | 3 | 3 |
| 5 | 4 | 2 | 4 |
| 6 | 3 | 5 | 2 |
| 7 | 3 | 4 | 3 |
| 8 | 3 | 3 | 4 |
| 9 | 3 | 2 | 5 |
| 10 | 2 | 5 | 3 |
| 11 | 2 | 4 | 4 |
| 12 | 2 | 3 | 5 |
| 13 | 3.33 | 3.33 | 3.33 |

4.7.4 Results

The potential loading component of SELECT can help identify source contributions spatially distributed across the watershed. However, this is only a daily snapshot of the amount of *E. coli* potentially present in the watershed (Figure 26 and Figure 28). The Pollutant Connectivity Factor (PCF) applied weighting to important fate and transport factors such as runoff capabilities and travel distance to provide helpful information to determine whether *E. coli* from various sources potentially contaminate the waterbodies. For the Lake Granbury Watershed, PCF analyses was based on applying multiple weighting schemes (Table 19) and then ranking the subwatersheds (Figure 27 and Figure 29) for potential water quality problems due to bacteria. The resultant ranked PCF maps for each source can be found in Appendix D.

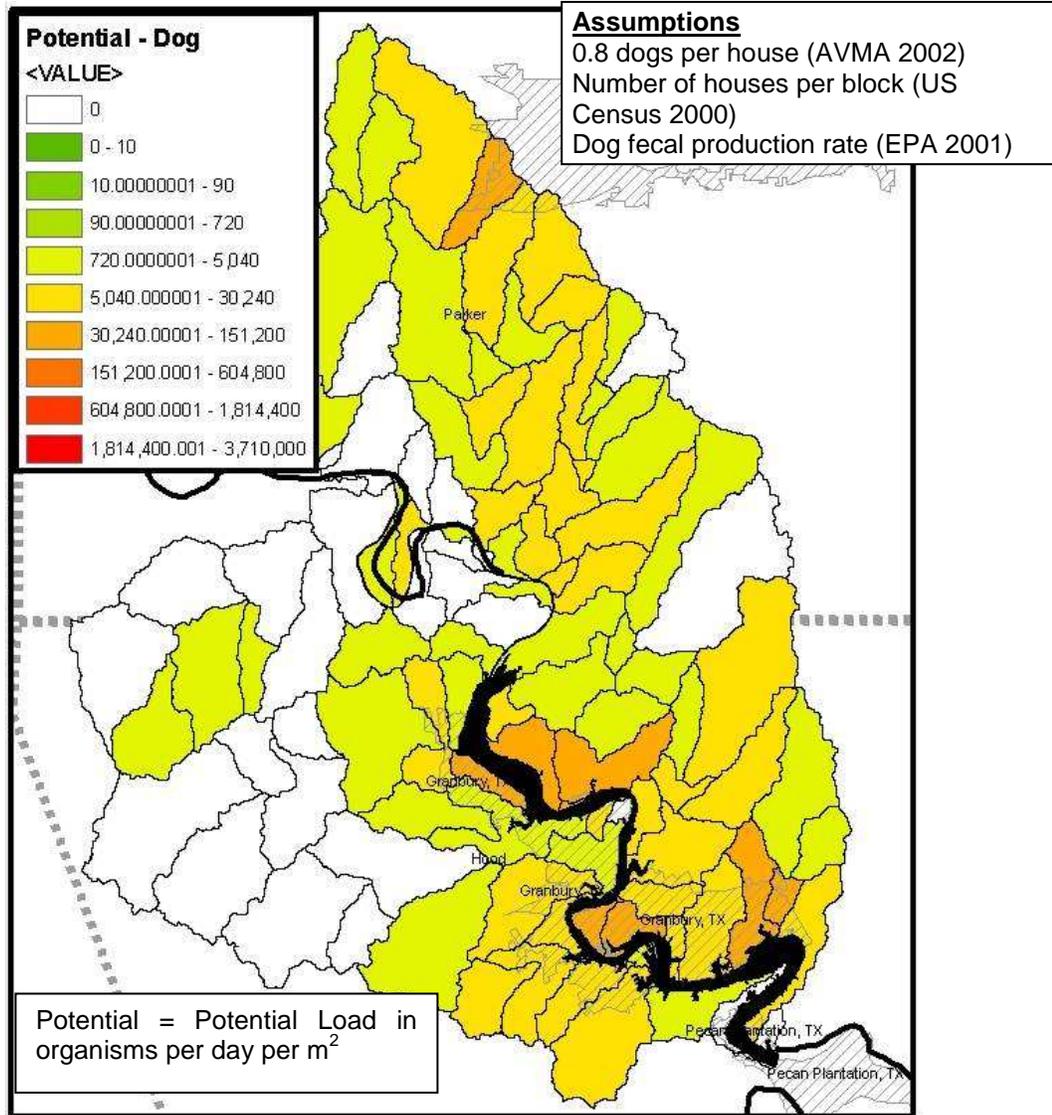


Figure 26. Area Weighted Potential *E. coli* Loading from Dogs

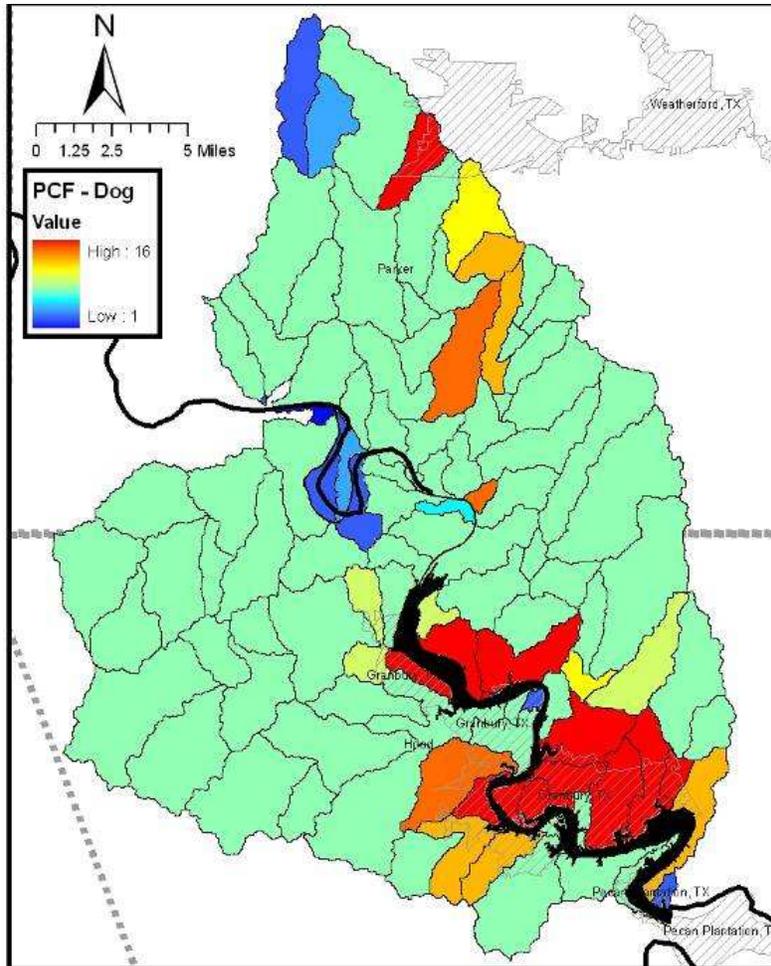


Figure 27. Ranked PCF using Area Weighted Potential *E. coli* Loadings from Dogs

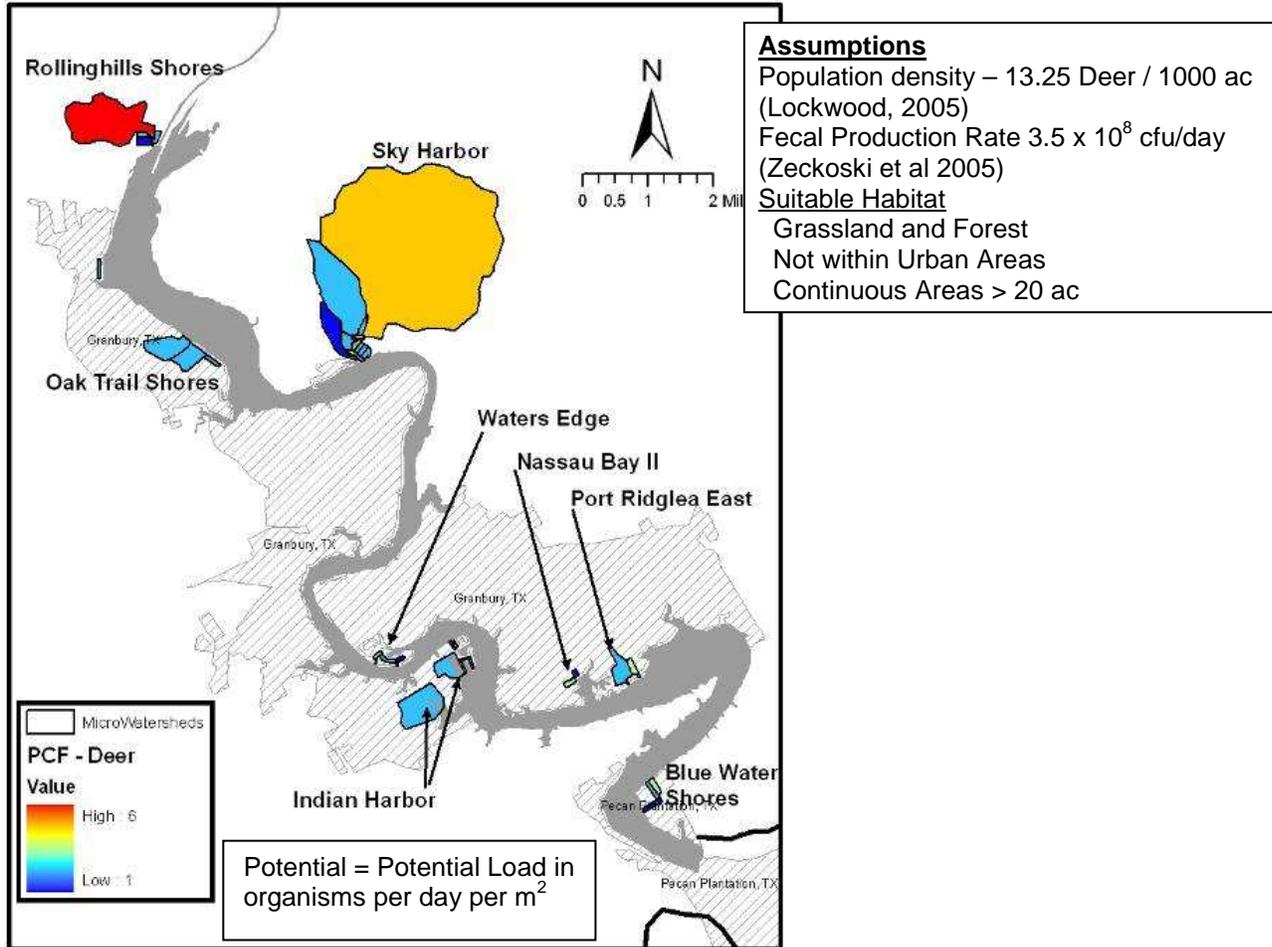


Figure 28. Microwatershed Area Weighted Potential *E. coli* Loading from Deer

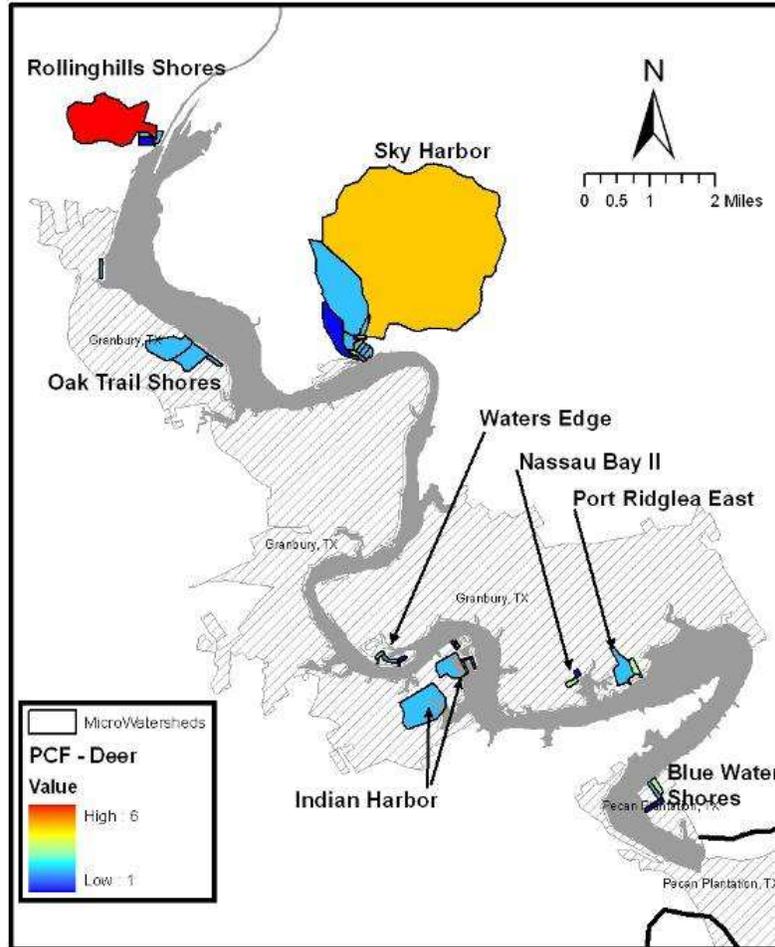


Figure 29. Microwatershed Ranked PCF using Area Weighted Potential *E. coli* Loading from Deer

Seven wastewater treatment plant facilities operate within the watershed (Figure 30). These facilities contribute large amounts of treated effluents if unintentional release of improperly treated wastewater was to occur.

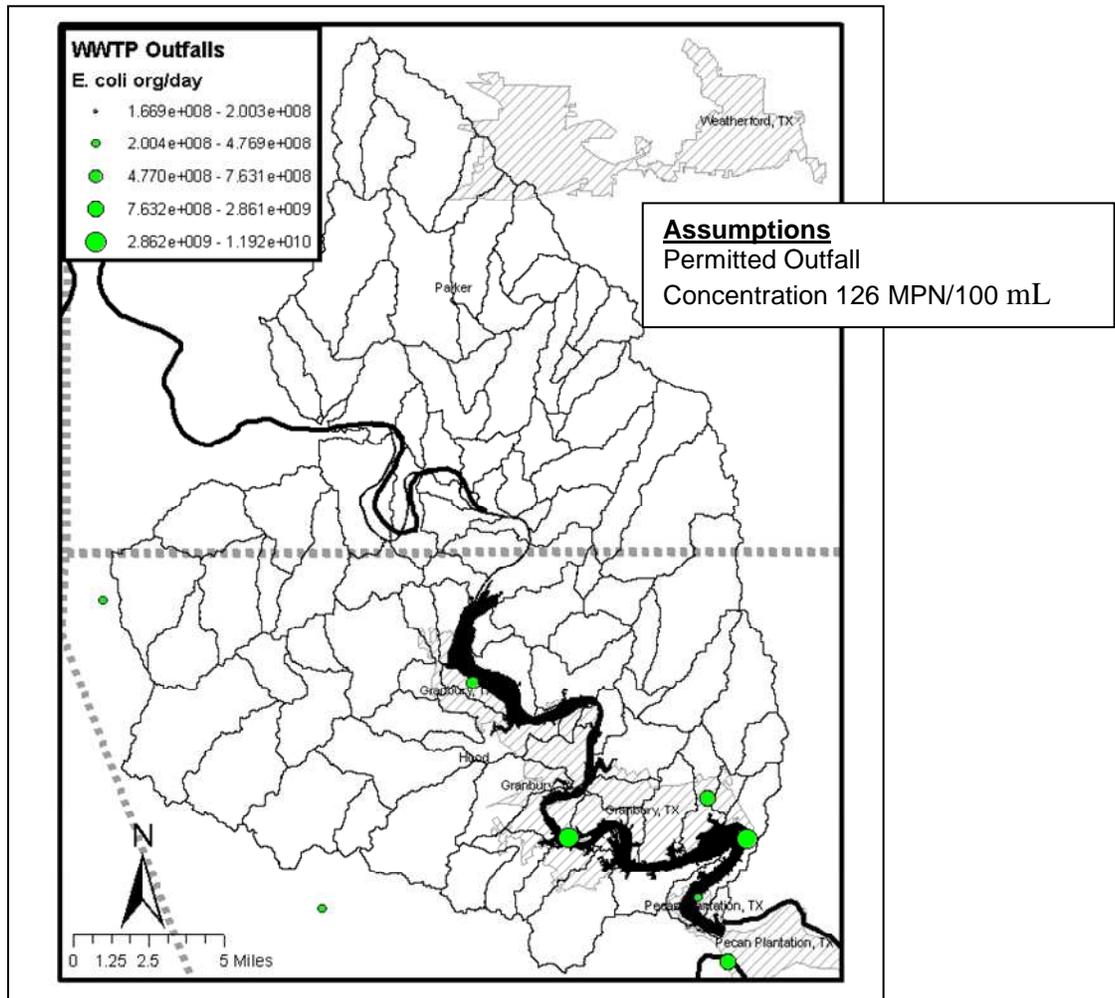


Figure 30. Potential *E. coli* Loading from Wastewater Treatment Plants.

4.8 LAKE/COVE WATER QUALITY MODEL SOURCE IDENTIFICATION

4.8.1 Methodology

Given the shallow depths (generally less than 6' deep) in each of the residential cove/canal systems, vertical stratification is not considered a driving issue for consideration of bacteria in this project. Thus a segmented well-mixed mass balance spreadsheet model is used for modeling of each canal system. The lake/cove model considers longitudinal gradients of concentration from the lake boundary to the dead-end reaches of a canal system, and considers time-varying inflow conditions. Several assumptions for the mass balance model are listed as follows:

- The simple segmented mass balance model applies to the canals or coves; i.e., canal waters are well-mixed and homogeneous within a given segment.
- Boundary conditions, i.e., exchanges between the canal and the lake main body, can be suitably applied to each canal's simple segmented mass balance model.
- Wave-induced circulation patterns in the canals are insignificant and resultant mixing could be modeled indirectly with diffusion (particle motion or turbulent mixing) and/or dispersion (variation in velocity) coefficients.

Assume segment 1 is in connection with segment 2. The mass balance equation for segment 1 is expressed as (Thomann and Mueller 1987):

$$V_1 \frac{ds_1}{dt} = W_e + Q_r s_r - Q_{12} s_1 + E'_{12} (s_2 - s_1) - V_1 K_1 s_1 \quad \text{Equation 2}$$

Where:

- V_1 – Volume for segment 1
- s_1 – Concentration of segment 1
- t – Time
- W_e – Mass input rate
- Q_r – Runoff inflow
- s_r – Runoff concentration
- Q_{12} – Flow between segment 1 and 2
- s_2 – Concentration of segment 2
- K_1 – Decay rate for segment 1

E'_{12} - Bulk exchange coefficient; $E'_{12} = \frac{E_{12} A_{12}}{\Delta x_{12}}$

The following is a list of the required input data for each canal model:

- Inflow timeseries (from local watershed runoff or stream flow)
- Depth
- Volume
- Segmentation
- Exchange between segments and boundary

Cross sectional area and distance between segments
Dispersion coefficient
Bacteria concentration/loading
Bacteria decay rates

The mass balance model is generally completed using a spreadsheet approach. Mass balance models were developed for 10 representative subdivisions as shown highlighted on the subdivision map for Lake Granbury area in Figure 31. The chosen canals include:

Rolling Hills Shores
Arrowhead Shores
Oak Trail Shores
Ports O' Call
Indian Harbor
Nassau Bay
Sky Harbor
Port Ridglea East
Blue Water Shores
Waters Edge

These subdivisions were chosen for modeling by Stakeholders because they exhibit a range of conditions (length, width, orientation, and depth) that allow inferences to be made on other canal systems with similar configurations. Moreover, based on analysis of available monitoring data, bacteria levels in the canals of these subdivisions were found to be currently or historically high, with the exception of Waters Edge, and therefore have most potential for improvement. Waters Edge subdivision was chosen for modeling as a control, to show applicability of the model framework at low bacterial concentrations.

Model segmentation was assigned according to flow directions and canal geometry. Take Oak Trail Shores as an example, the canal system is divided into five segments as shown in Figure 32. Mass balance using Equation 1 is calculated for each segment in the spreadsheet model. The flow directions are: 1→2, 2→5, 3→4, 4→5, 5→lake. Approximate dimensions and volumes of each segment are tabulated in Table 20 for Oak Trail Shores.

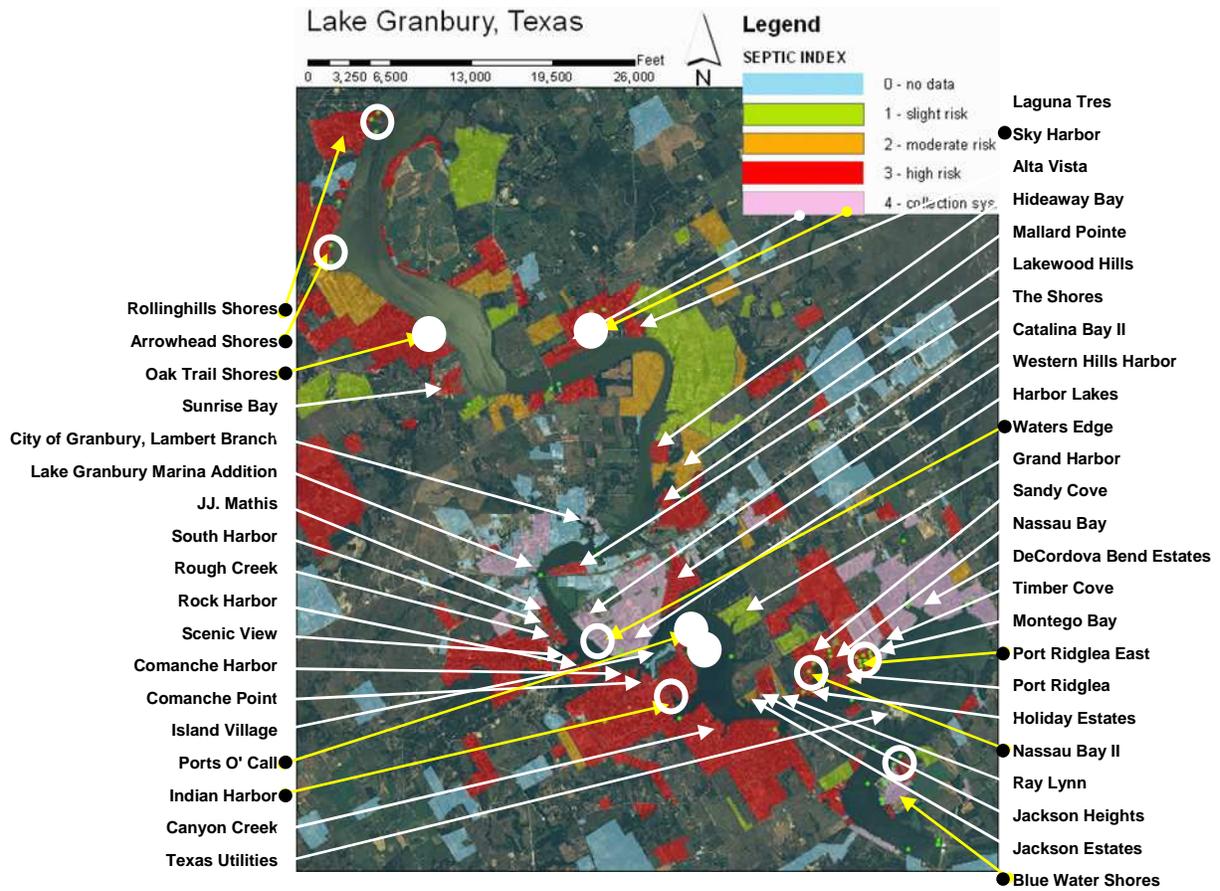


Figure 31. Aerial photo and subdivision map with septic index



Figure 32. Segmentation of Oak Trail Shores for Canal Modeling

Table 20. Dimensions and Volumes for each segment in Oak Trail Shores

| Segment | 1 | 2 | 3 | 4 | 5 |
|--------------------------|---------|---------|---------|---------|---------|
| Length (m) | 169.3 | 161.6 | 173.7 | 183.7 | 107.3 |
| Width (m) | 8.9 | 9.5 | 9.8 | 9.8 | 9.2 |
| Depth (ft) | 3.4 | 3.4 | 3.7 | 3.7 | 4.5 |
| Depth (m) | 1.04 | 1.04 | 1.13 | 1.13 | 1.37 |
| Volume (m ³) | 1561 | 1591 | 1920 | 2030 | 1354 |
| Volume (L) | 1561496 | 1590958 | 1919741 | 2030261 | 1353989 |

Similar segmentation and modeling processes were conducted for the other nine subdivisions. The segmentation illustration for each subdivision can be found in Appendix E.

4.8.2 Lake/Cove Model Scenarios

The mass balance model for each subdivision is executed for four bacteria loading situations: continuous septic point source, intermittent septic point source, lake source and local watershed non-point source. The initial condition for all scenarios is for the initial waterbody bacteria concentration to be zero.

4.8.2.1 Direct Discharge (Septic Point Source) Scenario

Two generalized modeling scenarios have been developed to evaluate septic systems as a point source of bacteria pollution to lake and cove water bodies.

The first scenario is continuous direct discharge from a point source, without rainfall events. If one residence discharges into the canal continuously, total daily point load of 5.06×10^{12} MPN is applied to the corresponding segment and is distributed evenly in time across each time increment (typically 6 minutes). In the water quality model, once this continuous point load is added, bacteria concentration for every segment would reach a steady state value in a short period of time. To continue using Oak Trail Shores as an example, with 1 residence discharging continuously to segment 1, the steady state concentration in segment 1 after 10-15 days is predicted at about 482,700 MPN/100mL (Figure 33).

However in most cases, a complete malfunction, reflecting 100% of daily discharge contributed to the canal, does not occur. Rather, partial malfunction of the septic system is more common, e.g., where a tank overflows with rainwater or where a portion of drainfield malfunctions. Thus a malfunction percentage can be introduced into the model for either whole or part of the modeling period. If the malfunction percentage is 10%, the steady state concentration in segment 1 is achieved in 10-15 days as 48,270 MPN/100mL (Figure 34). Additionally, bacteria concentration in the opposite end of the canal (Segment 3) is predicted to exhibit concentrations higher than state standards.

For selected subdivisions, a second scenario was modeled to evaluate an intermittent point source. This scenario represents a short-duration septic system discharge into the cove water, as may be expected from a failure resulting from an overloaded system on laundry day once per week. This event was estimated as a 33.3 gallon discharge of raw sewage into the canal, which is

also consistent with 4 hours (or 1/6 of a day's effluent) for one residential household. A maximum predicted canal/cove concentration of approximately 500 MPN/100mL is predicted by the Oak Trail Shores model, with concentration exceeding the stakeholder goal of 53 MPN/100ml in segment 1 for a duration of 3.5 days following the one-time discharge in segment 1 (Figure 35).

Model results at this location indicate that a local concentration far in excess of the state water quality standards (geometric mean of 126 MPN/100mL) can be achieved with only one residence continuously discharging all sewage directly to the canal (Figure 33). In addition, intermittent, short duration discharges from a single residence can result in locally-high bacteria concentrations that exceed stakeholder goals (Figure 35). Results across all modeled subdivisions (see Appendix E) are consistent with these general conclusions.

Considering bacteria monitoring does not indicate concentrations as high or as persistent as those predicted by the continuous discharge scenario, a continuous and complete septic system malfunction is not likely a typical failure mode in this area. Rather, order-of-magnitude comparisons of data and model predictions indicate that a more typical failure mode is one that is intermittent (occurs only under certain high-stress conditions, e.g., during a large family gathering), a failure mode that is incomplete (only a small proportion of sewage is emitted) and/or a combination of intermittent/incomplete failures by one or more systems.

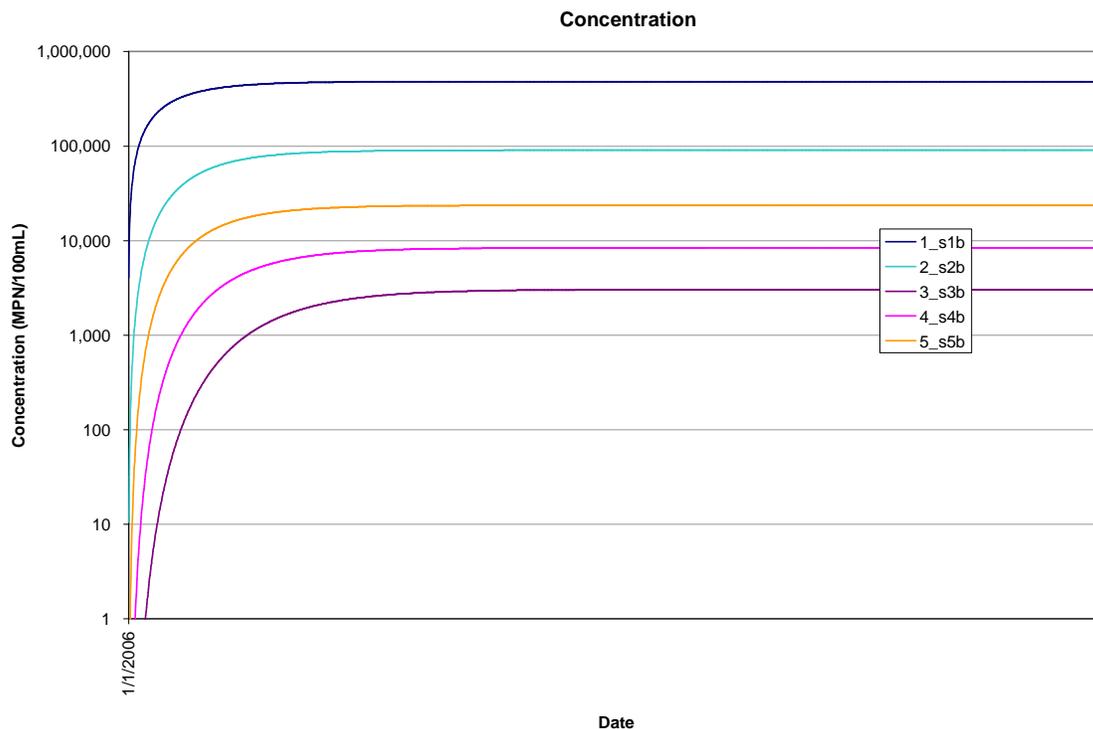


Figure 33. Bacteria concentration for each segment for continuous direct discharge scenario (1 residence)

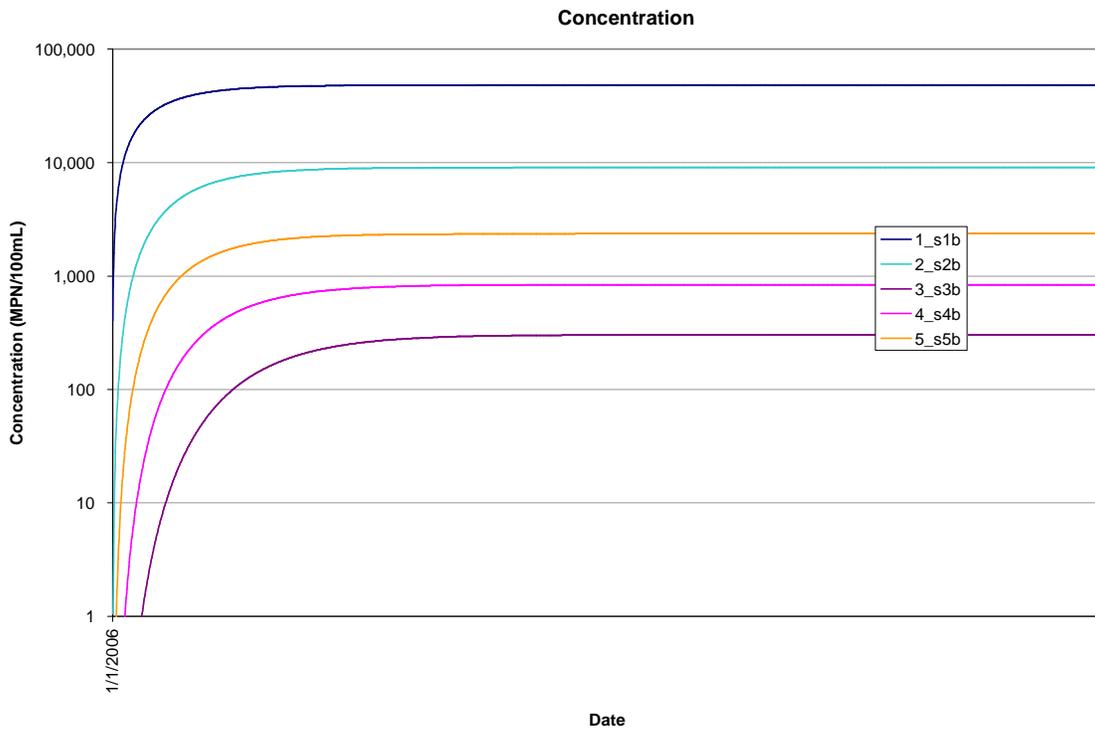


Figure 34. Bacteria concentration for each segment for continuous discharge with 10% malfunction percentage (1 residence)

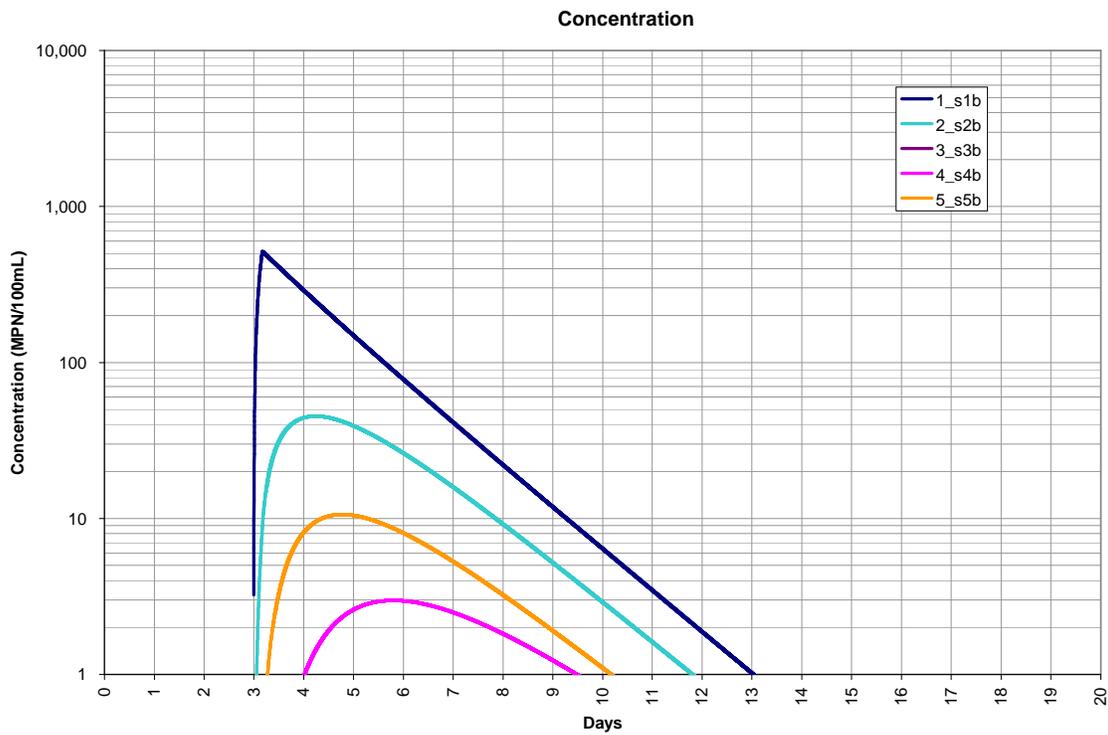


Figure 35. Bacteria concentration by segment for intermittent, one-time point discharge (1 residence)

4.8.2.2 Lake-source of Bacteria Scenario

This modeling scenario tests the hypothesis that high bacteria concentrations in the main body of Lake Granbury can cause high bacteria concentrations in the coves. Historically, bacteria concentration at long-term lake monitoring locations has been well below the state standard. The maximum values recorded at the three long-term stations were evaluated to develop an unlikely scenario that concentration in the lake could be 300 MPN/100mL. Using this concentration as a lake boundary condition in selected lake/cove models can test how bacteria may travel through natural dispersion processes from the lake into the upper reaches of the coves.

Given sustained conditions (more than 4 days) of high-concentration bacteria in the lake, concentration in Oak Trail Shores canal segments located away from the lake may get as high as the stakeholder goal of 53 MPN/100mL (Figure 36). For the selected canals evaluated, lake waters are not considered a likely source of bacteria within distal ends of canals.

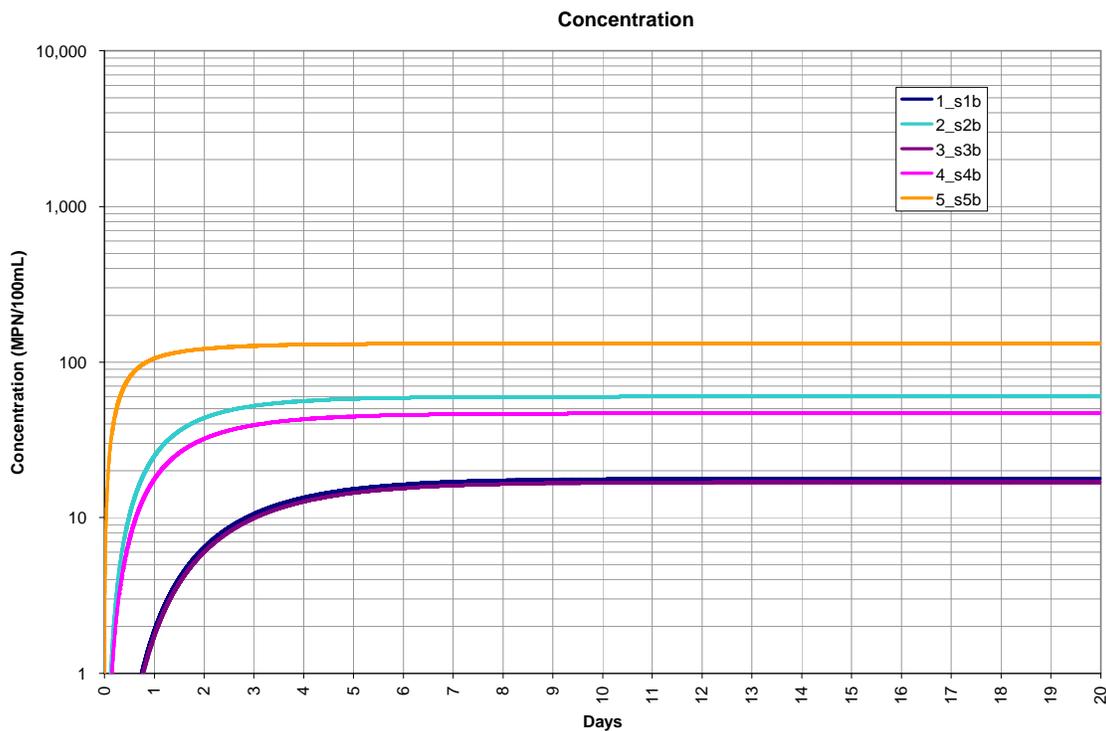


Figure 36. Bacteria concentration by segment in Oak Trail Shores- Lake Granbury as bacteria source

4.8.2.3 Nonpoint Source Surface Runoff Scenario

To evaluate how bacteria concentration in the canal may be tied to non-point source pollution and upper-watershed sources resulting from rainfall events, a time-series model scenario was developed for each subdivision for the period July 2002 through July 2008. Bacteria concentration in runoff water is assumed to be the only bacteria source for this scenario. Methods used to determine bacteria load are described below. Development of this time-series model

based upon precipitation events observed near the study area allows comparison to observed monitoring data.

Surface runoff is estimated using the SCS curve number procedure (Neitsch 2002). The SCS runoff equation is an empirical model that was developed to provide a consistent basis for estimating the amounts of runoff under varying land use and soil types.

$$Q_{surf} = \frac{(R_{day} - I_a)^2}{(R_{day} - I_a + S)} \quad \text{Equation 2}$$

Where

Q_{surf} – Accumulated runoff or rainfall excess (mm H₂O)

R_{day} – Rainfall depth for the day (mm H₂O)

I_a – Initial abstractions which includes surface storage, interception and infiltration prior to runoff (mm H₂O)

S – Retention parameter (mm H₂O), approximately $I_a = 0.2S$

$$S = 25.4 \left(\frac{1000}{CN} - 10 \right) \quad (4.3)$$

CN – curve number for the day

CN is a function of the soil's permeability, land use and antecedent soil water condition. For Lake Granbury residential district, the average lot size is 1/8 acre or less, average percent impervious area is 65% and hydrologic soil is regarded as group C or D (high runoff potential). Thus a curve number $CN = 90$ is used for surface runoff calculation.

Runoff on a particular day occurs only when the depth of rainfall exceeds the initial abstractions, $R_{day} > I_a$. For Lake Granbury in this study, it is estimated runoff occurs when $R_{day} > 0.22$ inch.

The one day rainfall is expressed as a 6 hour hyetograph. As an example, a 0.5 inch rainfall hyetograph is shown in Figure 37 (Williams-Sether 2004). Historical precipitation data for Lake Granbury is available from 1985 to date, enough for the modeling period of July 2002 to July 2008.

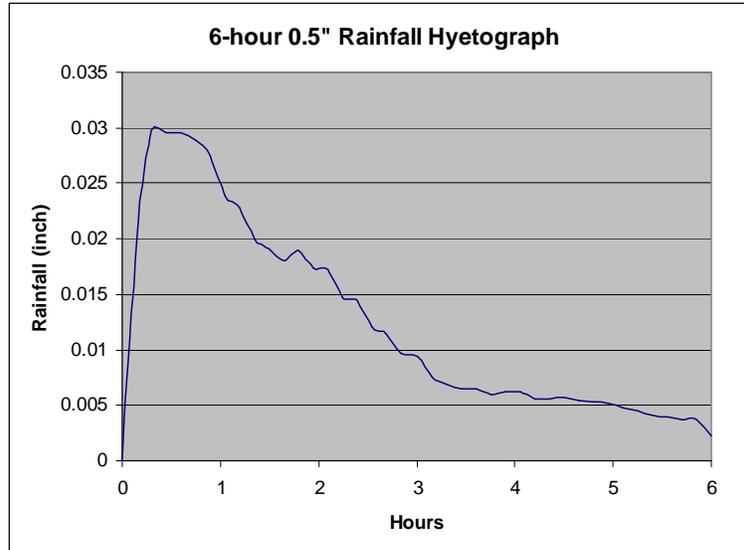


Figure 37. Hyetograph of a conceptual 6 hours 0.5” rainfall

As explained in Equation 2, accumulated runoff or rainfall is expressed in the format of precipitation depth. Therefore, the watershed area needs to be determined to calculate the runoff discharge in volume. Multiplication of precipitation depth and watershed area gives the value of runoff discharges in L/day. In this way, runoff non-point source load series were developed and applied to the water quality model.

To illustrate an example, three micro-watersheds exist near the Oak Trail Shores canal system (Figure 38), which are numbered as Watershed 1 (red polygon), 2 (yellow polygon) and 3 (green polygon). The respective areas for Watersheds 1, 2, and 3 are 110 acres, 76 acres and 58 acres.

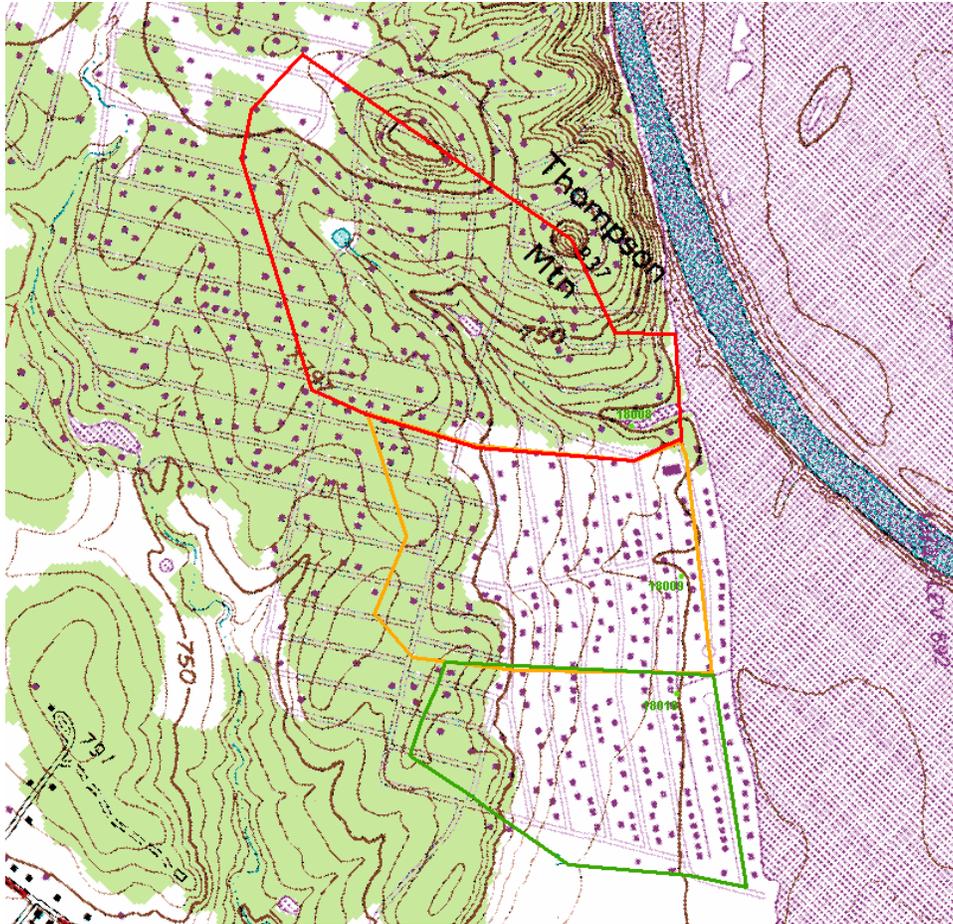


Figure 38. Micro-Watersheds at Oak Trail Shores

Because of drainage patterns observed on-site, runoff flows for Watershed 2 and 3 were applied to segment 1 and segment 3 as non-point source flow, with runoff *E. coli* concentration of 11,233.6 MPN/100ml at the same time periods of rainfall events. Resultant predicted bacteria concentration in Oak Trail Shores is shown in Figure 39 along with bacteria *E. coli* concentration monitoring data.

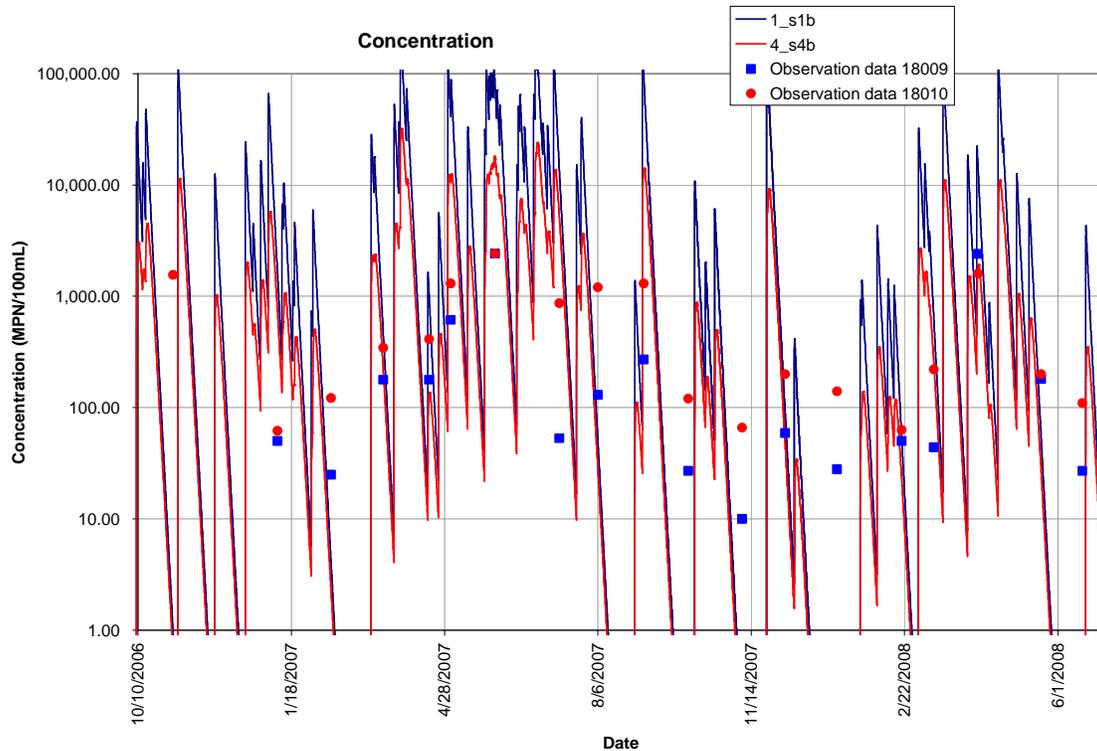


Figure 39. Predicted bacteria concentration from assumed potential non-point sources at Oak Trail Shores canal

Evaluation of time-series runoff-based model predictions was conducted by comparing bacteria predictions with observed data in coincident spatial-temporal locations. Both visual, graphical comparisons and residual analysis were used to estimate the degree of correspondence between runoff-based bacteria predictions and observations.

Figure 39 illustrates the graphical depiction of bacteria concentration modeling results at Oak Trail Shores for model segments coincident with monitoring locations. The modeling results graphics for all 10 subdivisions are shown in Appendix E. While the figures illustrate correspondence between observed values and model prediction values, the graphics provide only qualitative comparisons.

Additional quantitative validation was conducted through residual analysis. Residual analysis is performed to evaluate differences between model predictions and field observations. Residuals were calculated between on-site observed bacteria concentration and model predicted bacteria concentration within a window of time. Recognizing that analysis of bacteria field samples limited the upper *E. coli* concentration reported to 2,420 MPN/100mL (or, to a reporting value of >2,420 MPN/100mL) and the lower reporting value to <1 MPN/100mL, an alternative residual analysis was conducted by evaluating the differences “horizontally” on the time axis. For each observed bacteria concentration, a horizontal (time axis) check was performed to determine when the model prediction catches the same concentration with the smallest backward-looking time difference. This time difference was recorded for each observed data point and plotted on

the residual graph (e.g., Figure 40). Given uncertainty in timing of rainfall events, only model results before the monitoring time or within 1 day following were compared. Model output greater than one day after a monitoring observation is not coincident.

Residual plots of non-point source loads from Oak Trail Shores are shown in Figure 40 and Figure 41. The time difference between monitoring bacteria concentration at station 18009 and the model predicted bacteria level in segment 1 is illustrated in Figure 40. The time difference between monitoring bacteria concentration at station 18010 and the model predicted bacteria level in segment 4 is plotted in Figure 41.

The plots are indicators of correspondence between runoff-induced model predictions and observed bacteria concentration, and provide indication of the degree of correspondence between rainfall-induced events and observed high bacteria concentration. The highest observed concentration events in the Oak Trail Shores area do correspond to predicted rainfall-induced non-point source loadings (Figure 40 and Figure 41). Lower persistent bacterial levels (< 250 MPN/100mL) in this area are evident at times more removed from runoff events indicating other bacteria factors exist nearer to the canal water body like intermittent discharge of systems (e.g. Figure 35) or pets.

For comparison to the Oak Trail Shores example, Sky Harbor station 18014 more strongly indicates a relationship between runoff and observed concentration (Figure 42). With one exception, all high bacteria events >150 MPN/100mL occur within 3 days of a model-derived, runoff-induced bacteria model prediction and concentrations remain low without runoff events. Conversely, the Port Ridglea East example (Figure 43) illustrates little correspondence to the runoff event model, indicating that the source of bacteria is less keyed to rainfall/runoff processes and more keyed to local, direct sources.

A range of results were observed for other subdivisions, as presented in Appendix E.

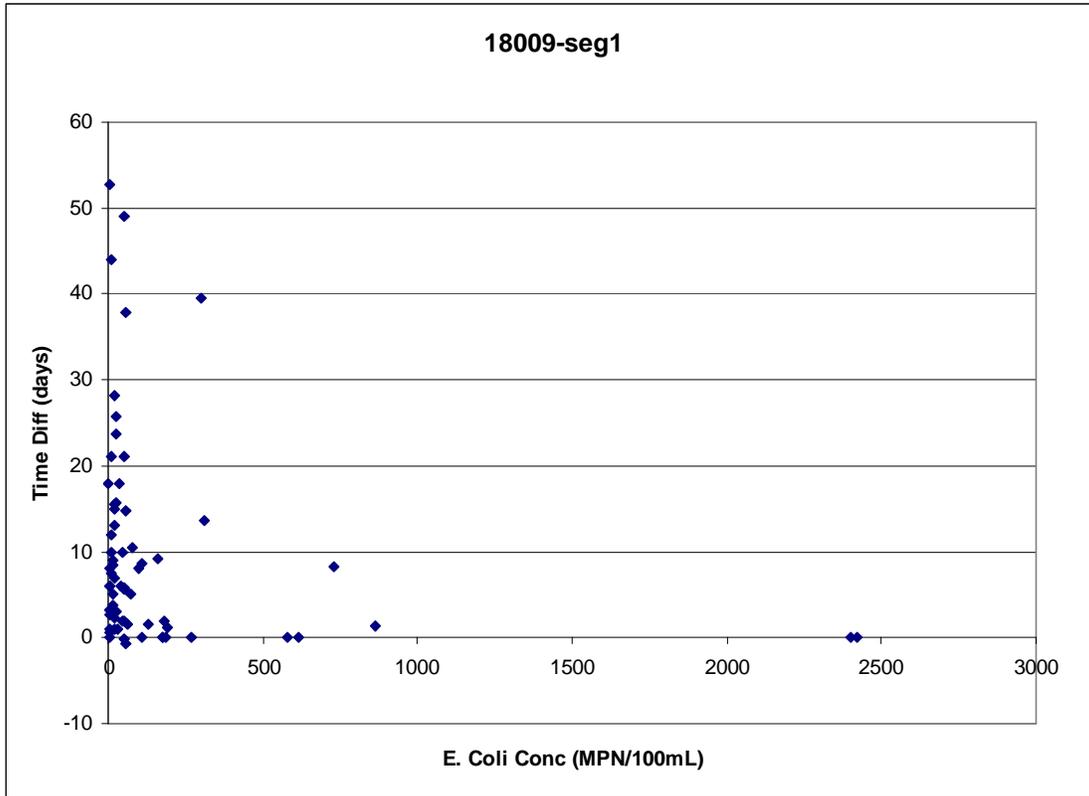


Figure 40. Residual plot for monitoring station 18009 at Oak Trail Shores

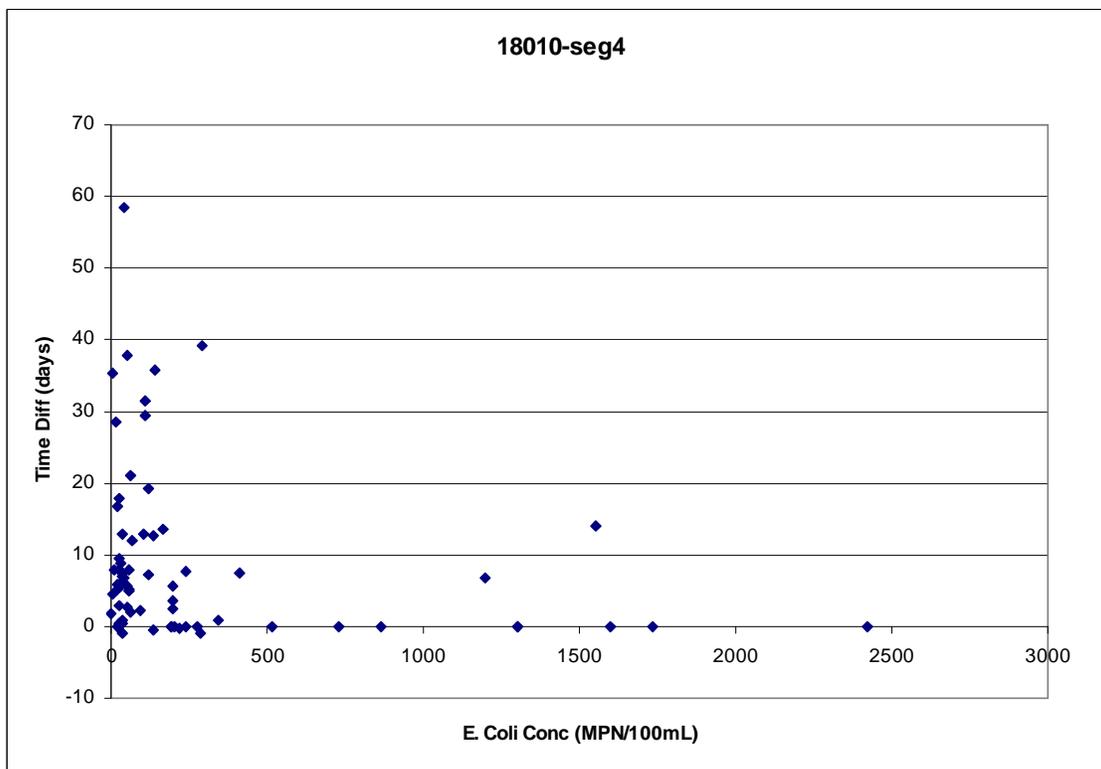


Figure 41. Residual plot for monitoring station 18010 at Oak Trail Shores

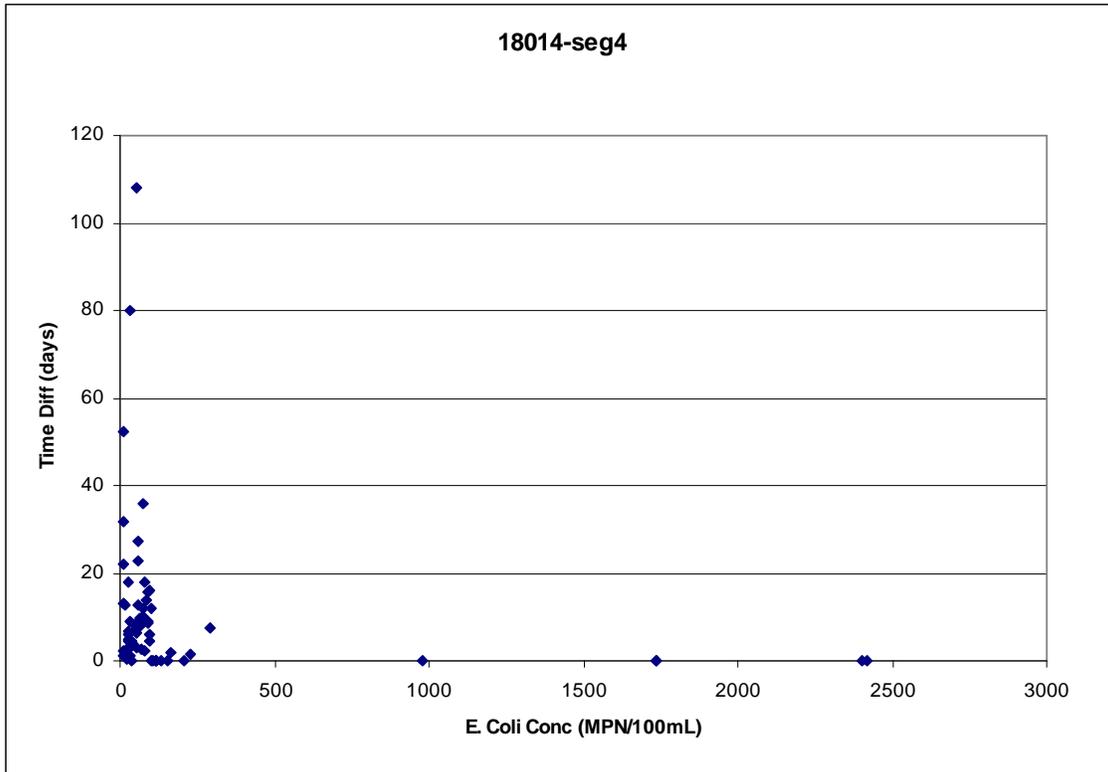


Figure 42. Residual plot for monitoring station 18014 at Sky Harbor

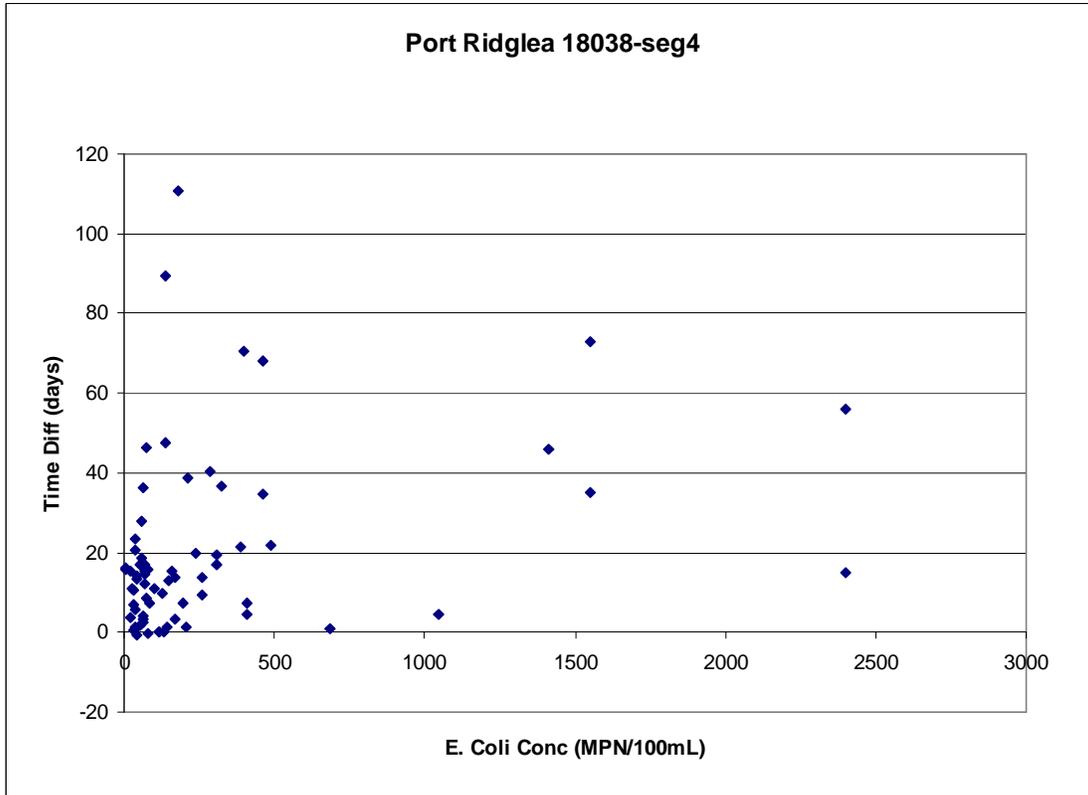


Figure 43. Residual plot for monitoring station 18038 at Port Ridglea East

4.9 MOST LIKELY BACTERIA SOURCES: COMBINED WATERSHED AND LAKE/COVE MODELING

The modeling results of both watershed potential loading models and lake/cove water quality models are combined and aggregated in this section to investigate the most likely bacteria sources for the 12 modeled subdivision areas and the three streams. Based upon these findings, possible best management practices can be identified and recommended for each of these locations.

4.9.1 Most Likely Bacteria Sources

Using the lake/cove models, most likely bacteria sources were identified by evaluating loading schema to determine which scenarios most likely resulted in the observed measurement concentrations of bacteria (Table 21). These scenarios considered the contributing watershed size, rainfall events, and cove geometries. The loading scenarios considered near-canal sources discharging waste to the canals (“Near-canal/septic”) or a generic non-point source (“NPS”) urban bacteria loading within the watershed away from the canal waterbody. Some canal water bodies exhibit correspondence to both loading scenarios; like Oak Trail Shores that exhibits both a strong correspondence of high bacteria levels to precipitation events (noted as NPS) while lower background bacteria levels are persistent even without antecedent rainfall (noted as Near-canal/Septic). The lake/cove modeling source evaluation does not differentiate the species of potential sources, but does provide information on near-canal sources vs. more distant watershed sources that require a rainfall event to transport bacteria to the canals.

Table 21. Most Likely Bacteria Sources identified by lake/cove modeling scenarios

| Subdivision | Most likely sources |
|----------------------|----------------------------|
| Rolling Hills Shores | Near-canal/Septic + NPS |
| Arrowhead Shores | Near-canal/Septic + NPS |
| Oak Trail Shores | Near-canal/Septic + NPS |
| Sky Harbor | NPS |
| Nassau Bay II | Near-canal/Septic + NPS |
| Waters Edge | No problem exhibited; NPS |
| Ports O’ Call | Near-canal/Septic |
| Indian Harbor Cove | Near-canal/Septic |
| Indian Harbor Canal | Near-canal/Septic + NPS |
| Port Riddlea East | Near-canal/Septic |
| Blue Water Shores | Near-canal/Septic |

Using the watershed SELECT model, area-weighted potential bacteria watershed loads were ranked for several watershed sources of bacteria, including cattle, deer, feral hogs, pets and septic system malfunction, for each studied subdivision (Table 22). This ranking was based on relative load magnitude from each potential source influencing the watershed(s) and the source species likely to be present within the watershed.

Table 22. Most Likely Bacteria Sources identified by watershed modeling of potential sources

| Area | Most likely sources |
|------------------------|---|
| Rolling Hills Shores | 62% Septic, 38% Cattle, <1% Pets, <1% Deer |
| Arrowhead Shores | 99% Septic, <1% Pets, <1% Deer |
| Oak Trail Shores | 54% Septic, 46% Pets |
| Sky Harbor | 82% Cattle, 13% Septic, 4% Pets, 2% Feral Hog |
| Nassau Bay II | 98% Septic, 2% Pets |
| Waters Edge | Very low potential; Pets |
| Ports O' Call | >99% Septic, <1% Pets |
| Indian Harbor Cove | 99% Septic, 1% Pets |
| Indian Harbor Canal | 98% Septic, 2% Pets |
| Port Ridglea East | >99% Septic, <1% Pets |
| Blue Water Shores | Pets |
| Long Creek - Watershed | <98% Cattle, 2% Feral Hog, <1% Pets, <1% Deer |
| Long Creek - Cove | >99% Septic, <1% Pets |
| Walnut Creek | 96% Cattle, 2% Feral Pets, <1% Pets, <1% Deer |
| McCarthy Branch | 94% Cattle, 3.5% Pets, 2% Feral Hog, <1% Septic |

Combining both the watershed and cove modeling approaches (Table 23) provides greater insight into the most likely sources using a multi-pronged approach to source identification. The benefit of combining these approaches is we can evaluate the types of loading scenarios occurring, relate them to monitoring data and consider watershed characteristics to further evaluate relative contributions of particular sources to the total pollutant loads.

Table 23. Model results to evaluate most likely potential sources by subdivision studied.

| Subdivision | Most likely potential sources | |
|------------------------|-------------------------------|----------------------------------|
| | Lake/cove model | Watershed model |
| Rolling Hills Shores | Near-canal/Septic + NPS | Septic, Cattle, Dogs, Deer |
| Arrowhead Shores | Near-canal/Septic + NPS | Septic, Dogs, Deer |
| Oak Trail Shores | Near-canal/Septic + NPS | Septic, Dogs |
| Sky Harbor | NPS | Cattle, Septic, Dogs, Feral hogs |
| Nassau Bay II | Near-canal/Septic + NPS | Septic, Dogs, Feral hogs |
| Waters Edge | No problem exhibited; NPS | Very low potential; Dogs |
| Ports O' Call | Near-canal/Septic | Septic, Dogs |
| Indian Harbor Cove | Near-canal/Septic | Septic, Dogs |
| Indian Harbor Canal | Near-canal/Septic + NPS | Septic, Dogs |
| Port Ridglea East | Near-canal/Septic | Septic, Dogs |
| Blue Water Shores | Near-canal/Septic | Dogs |
| Long Creek - Watershed | | Cattle, Feral hogs, Dogs, Deer |
| Long Creek - Cove | | Septic, Dogs |
| Walnut Creek | | Cattle, Feral hogs, Dogs, Deer |
| McCarthy Branch | | Cattle, Dogs, Feral hogs, Septic |

4.9.1.1 Rolling Hills Shores

Malfunctioning holding tanks are a potential persistent source of bacteria in the coves of this subdivision; however, watershed sources, particularly livestock, are indicated as a significant potential source contributed from the upper watershed. Enforcement actions and typical septic system configurations do not rule out septic discharges as a potential source. The cove modeling schemes indicate that both continuous near-canal and runoff-event non-point source contributions do relate to the observed concentration data. Thus both models and anecdotal evidence suggests that septage is the largest contributing source followed by either livestock or wildlife from the upper watershed after runoff events.

4.9.1.2 Arrowhead Shores

The contributing watershed for the Arrowhead Shores subdivision is small. The model results indicate near-canal/septic and NPS contributions to bacteria. Since the watershed contributing to the canal in this area is small, the contributions are likely from septic systems proximal to the canal or from localized NPS (dogs, deer or other wildlife).

4.9.1.3 Oak Trail Shores

The fit of the canal model with monitoring data suggests that highest bacteria loading occurs during rainfall events; however, persistent elevated background levels also exist between rainfall events. The most likely sources are pets and OWTF/septic malfunctions. The location of malfunctioning septic contributions, whether in the watershed or adjacent to the canals, is not known.

4.9.1.4 Sky Harbor

The Sky Harbor subdivision is characterized by high population density areas with localized watersheds near the finger canals; however, less populated, large rural watersheds also drain to the main canal system. The models evaluations indicate watershed non-point sources such as livestock and wildlife appear most likely. Cattle, pets, septic, and feral hogs all have high potential for contributing NPS bacteria loadings.

4.9.1.5 Nassau Bay II

The Nassau Bay II subdivision has a small contributing watershed. The canal model indicates localized NPS or pipe leakage are the most likely sources. Further, the model indicates continuous direct discharge from residence is not the bacteria source in this area since direct discharge scenario predicts an *E. coli* concentration much higher than observed concentrations, even with discharge from just one residence. The watershed model identified the most likely sources as septic effluent, dogs, and feral hogs.

4.9.1.6 Waters Edge

No problems exhibited. This subdivision has a small contributing watershed. Direct discharge (WWTP), leaking collection system pipes, or local non-point source (pets, runoff from yards adjacent to canal) would be the most likely potential sources if a problem were to exist.

4.9.1.7 Ports O' Call/Indian Harbor

The Ports O' Call and Indian Harbor subdivisions have small watersheds comprised of residential lots adjacent to the canal water bodies. The sources of bacteria found in the canals are most likely from direct discharge (septic) or localized non-point sources (pets, runoff from yards adjacent to canal).

4.9.1.8 Port Ridglea

The Port Ridglea subdivision has small localized watersheds with some off-site runoff that enters the canals. Direct discharge from septic systems is the most likely potential source, based upon the lake/cove model since high persistent bacteria values are exhibited in absence of rainfall events. The high density of residences also indicates potential for local non-point source runoff from pet waste contributed from yards adjacent to canal. Ducks and geese in specific areas have been reported in high numbers by residents, although waterfowl count studies by BRA and TPWD did not indicate sufficient numbers of fowl to cause a problem. Though a fowl source was not modeled, the anecdotal evidence suggests management measures to address waterfowl would be beneficial.

4.9.1.9 Blue Water Shores

Blue Water Shores subdivision exhibits a small contributing watershed and residences in the area are served by a sewage collection and treatment facility. Based upon the watershed modeling, the most likely source of bacteria is from local non-point source runoff from high-density, high impervious cover yards adjacent to canal, most likely from pet waste. There is not evidence of WWTP pipe leakage, but this potential source should be investigated in further detail, given the persistence of elevated bacteria levels in absence of rainfall events.

4.9.1.10 Long Creek

Due to elevated bacteria concentrations observed at station 20220 after the start of the bacteria assessment modeling studies, the stakeholders requested further investigation of potential sources for the Long Creek Watershed. It should be noted that the Long Creek watershed does not actually include the Long Creek subdivision located downstream of the monitoring station. The stakeholders indicated that migratory water fowl congregate in adjacent headwaters of the lake. While migratory birds are not included in the models, this could be a major source of contribution during migratory season but fowl counts by BRA and TPWD did not indicate sufficient numbers to be of concern. The watershed modeling exercise indicates livestock (modeled as cattle though could be from some other type of livestock) and wildlife (primarily feral hogs and deer) as the most likely potential sources of bacteria contributing to Long Creek.

Bacteria from human activities (septic and pets) is not considered likely due to the relatively small number of residences, distance from the streams, and size of properties.

4.9.1.11 Walnut Creek

Bacteria concentration measurements at station 20229 in Lake Granbury at the mouth of Walnut Creek indicate rising bacteria concentrations that have exceeded the stakeholder goal of 53 MPN/100 mL. This noted rise in bacteria compelled the stakeholders to request further investigation into the Walnut Creek Watershed potential sources of bacteria. The Walnut Creek Watershed can be divided into four subwatersheds: Walnut Creek above the confluence with Ike Branch, the McCarthy Branch, the Ike Branch, and Walnut Creek near the DeCordova subdivision. Several pond structures exist along the McCarthy Branch reach near the confluence with Walnut Creek near the lake as well as near the creek further up in the watershed and on the golf course. These pond structures are observed to host water fowl, a potential localized source of nonpoint source pollution. Watershed contributions are likely from some type of livestock (modeled here as cattle) in upper watershed, from dogs from the DeCordova and Acton Meadows subdivisions, and feral hogs attracted to the undeveloped land and water features in these watersheds.

4.10 SUMMARY OF BACTERIA SOURCE IDENTIFICATION EFFORTS

Stakeholders and cooperators applied a multi-pronged approach in evaluating potential bacteria sources. Current and historical data indicates differences in bacteria trends for different areas across the Lake Granbury watershed (Table 1, Figure 5 and EC 2009), and investigation of spatial patterns in land use indicates a range watershed sizes and land uses for areas with elevated bacteria concentrations (Figure 9 through Figure 11). To dissect likely potential causes of elevated bacteria across the spectrum of unique areas, and to provide information to feed forward into the decision-making process, stakeholders and cooperators conducted many site-specific studies, including (1) on-site data collection; (2) bacterial source tracking studies; (3) SELECT watershed modeling bacteria assessment; and (4) lake/cove modeling within affected water bodies.

The results of the watershed efforts and the lake/cove modeling efforts were chosen to be used as basis for identification of bacteria sources. The Stakeholders carefully considered the results of site-specific bacterial source tracking (BST) studies, but decided further development of BST methodologies would be warranted before BST results could be used.

The SELECT watershed modeling approach identifies potential bacteria loading across a range of sub-watersheds considering soils, slope, land use and bacteria source species. This approach was used to identify areas of high bacteria contribution potential, and to identify what sources of bacteria (e.g., human/ossf, pets or wildlife) are most suspect within each area.

Waterbody modeling within the lake/cove waters allowed evaluation of how different potential sources could affect the magnitude and timing of bacteria concentration in the water body. Considering each area's cove/canal geometry and watershed hydrology in response to localized rainfall events, the lake/cove models helped identify whether distant upper watershed sources

(e.g., wildlife or urban sources transported via runoff) or nearby watershed sources (e.g., direct discharge of residential sewage from septic/OSSF systems) were most likely to produce bacteria concentrations similar to concentrations reported in monitoring data.

From the multi-pronged approach, specific results were developed to indicate the most likely source of bacteria for each area around the lake. These results were fed forward into evaluation and identification of appropriate management measure priorities for the Lake Granbury WPP watershed.