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Bacteria Total Maximum Daily Load Task Force Final Report

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Texas Water
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make every drop count

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Executive Summary

In September 2006, the Texas Commission on Environmental Quality (TCEQ) and Texas State Soil and Water Conservation Board (TSSWCB) charged a seven-person Bacteria Total Maximum Daily Load (TMDL) Task Force with:

- examining approaches that other states use to develop and implement bacteria TMDLs,
- recommending cost-effective and time-efficient methods for developing TMDLs,
- recommending effective approaches for developing TMDL Implementation Plans (I-Plans),
- evaluating a variety of models and bacteria source tracking (BST) methods available for developing TMDLs and I-Plans, and recommending under what conditions certain methods are more appropriate, and
- developing a roadmap for further scientific research needed to reduce uncertainty about how bacteria behave under different water conditions in Texas.

The Task Force, assisted by an Expert Advisory Group of approximately 50 stakeholders and agency staff, held two two-hour meetings/teleconferences and developed two drafts of the report. These drafts were shared by e-mail and on a Web site and feedback received from the Expert Advisory Group was also made available on the Web site.

The Task Force report describes the characteristics, as well as some of the strengths and weaknesses of several models that have been used and/or are under development to assist bacteria TMDL and I-Plan analysis. These include:

- load duration curves (LDC),
- spatially explicit statistical models, including Arc Hydro, SPARROW and SELECT,
- the mass balance models BLEST and BIT, and
- the mechanistic hydrologic/water quality models HSPF, SWAT, SWMM and WASP.

The Task Force report also describes and makes recommendations for effective use of BST methods that have been used in Texas and elsewhere for TMDL development. These include ERIC-PCR, Ribotyping, PFGE, KB-ARA, CSU and *Bacteroidales* PCR. Based on recent experience in Texas and elsewhere, the Task Force recommends using library-independent methods like *Bacteriodales* PCR for preliminary qualitative analyses and more expensive and time-consuming library-dependent methods if more quantitative data are required for TMDL or I-Plan development.

Based on the discussions of bacteria models and source tracking, as well as extensive input from the Expert Advisory Group, the Task Force recommends a three-tier approach to implementing bacteria TMDLs and I-Plans.

Tier 1 is a one-year process that includes the formation of a representative stakeholder group, development of a comprehensive geographic information system (GIS) of the watershed, a survey of potential bacterial sources, calculation of load duration curves from existing monitoring data and analysis by agency personnel and stakeholders of data collected for Tier 1. After reviewing information from Tier 1, the group may choose to complete and submit a draft TMDL for agency approval, request an evaluation of the designated use of the water body (an use attainability analysis) or proceed to Tier 2.

Tier 2 is a one-to-two-year effort designed to collect targeted monitoring data to fill gaps in previously collected data, conduct qualitative library-independent BST data to determine whether humans and/or a few major classes of animals are sources and develop simple spatially explicit or mass balance models of bacteria in the watershed. After analysis of Tier 1 and Tier 2 data, the group may chose to complete and submit the draft TMDL (or I-Plan if a TMDL was developed after Tier 1), request an evaluation of the designated use (an use attainability analysis), or initiate a “phased TMDL” and proceed with Tier 3 analysis.

Tier 3 is a two-to-three-year process designed to continue strong stakeholder involvement, implement more extensive targeted monitoring, conduct quantitative library-dependent BST analysis and develop a detailed hydrologic/water quality model for the watershed. Tier 3 should be implemented only when this level of detailed analysis is needed for I-Plan development or for TMDL development for particularly complex watersheds for which consensus cannot be reached after Tier 2.

The Task Force emphasizes that the agencies and stakeholders may choose to deviate from these recommendations if they reach consensus that a more time- and cost-effective approach is feasible.

The Task Force concludes its report by summarizing a number of research activities needed to strengthen the scientific tools available for TMDL and I-Plan development. The needed research falls into the following categories: characterization of sources, characterization of kinetic rates and transport mechanisms, enhancements to bacteria fate and transport models and bacteria source tracking, determination of effectiveness of control mechanisms and quantification of uncertainty and risk.

Finally, the report includes a number of references to relevant scientific literature and studies, as well as five appendices:

Appendix 1	Bacteria TMDL Task Force Members and Expert Advisors
Appendix 2	Models Used in Bacteria TMDLs as Described in EPA Publications
Appendix 3	EPA Bacteria TMDL Guidelines
Appendix 4	State Approaches to Bacteria TMDLs
Appendix 5	Comments from the Expert Advisory Group

Introduction

As of January 2006, 197 water bodies in Texas were impaired because they did not meet bacteria criteria established by the state to protect contact recreation use (freshwater and saltwater) and/or oyster water use. The freshwater contact recreation use criterion used to determine impairment includes both a geometric mean for *Escherichia coli* (*E. coli)* of 126 colonies per 100 ml and a single sample maximum of 394 colonies per 100 ml. The saltwater contact recreation use criterion includes both a geometric mean for *Enterococci* of 35 colonies per 100 ml and a single sample maximum of 89 colonies per 100 ml. Finally, the oyster water use criterion includes a median fecal coliform concentration of 14 colonies per 100 ml and no more than 10% of samples may exceed 43 colonies per 100 ml. TCEQ is currently considering a variety of potential changes to Texas water quality standards. According to the TCEQ Web site, these "revisions to the standards and Standards Implementation Procedures are needed to:

- incorporate recently developed site-specific standards for individual water bodies,
- incorporate new research on the toxicity of specific chemicals,
- improve the way that standards are used and applied."

As required by Section 303(d) of the Clean Water Act, Texas has committed to complete TMDLs for these bacteria-impaired water bodies within 13 years of the listing date (i.e. 2017 for new bacteria impairments listed on the 2004 list). In order to identify the best and most cost- and time-effective methods to develop bacteria TMDLs and TMDL Implementation Plans (I-Plans), TCEQ and TSSWCB established a joint technical Task Force on Bacteria TMDLs on September 27, 2006. The Task Force was charged with:

- examining approaches that other states use to develop and implement bacteria TMDLs,
- recommending cost-effective and time-efficient methods for developing TMDLs,
- recommending effective approaches for developing I-Plans,

- evaluating the variety of models and bacteria source tracking (BST) methods available for developing TMDLs and I-Plans, and recommending under what conditions certain methods are more appropriate, and
- developing a roadmap for further scientific research needed to reduce uncertainty about how bacteria behave under different water conditions in Texas.

Task Force members are Drs. Allan Jones, Texas Water Resources Institute; George Di Giovanni, Texas Agricultural Experiment Station–El Paso; Larry Hauck, Texas Institute for Applied Environmental Research; Joanna Mott, Texas A&M University–Corpus Christi; Hanadi Rifai, University of Houston; Raghavan Srinivasan, Texas A&M University; and George Ward, The University of Texas at Austin. Dr. Allan Jones was named Task Force Chair by TCEQ and TSSWCB.

Approximately 50 Expert Advisors (Appendix 1) with expertise in bacteria-related issues have also provided significant input to the Task Force during the process. Included in this group are university scientists, environmental consultants and representatives of local, state and federal agencies with jurisdictions impacting bacteria and water quality.

Recommendations from the Task Force are intended to be used by the State of Texas, specifically TSSWCB and TCEQ, to keep Texas as a national leader in water quality protection and restoration.

Bacteria Fate and Transport Models

This section, coordinated by Drs. Hanadi Rifai and Raghavan Srinivasan, describes the strengths and weaknesses of several bacteria fate and transport models that have been used for TMDL and I-Plan development. The discussion is not intended to be a comprehensive review of the numerous models that have been or could be used for bacteria TMDL and I-Plan development. Instead, it briefly characterizes a few of the models that have been developed and/or used in Texas to assist in bacteria TMDL and I-Plan assessments.

Bacterial pollution in surface water bodies is difficult to model because bacterial sources and their fate and transport are complex. In addition, several fate and transport processes control their growth, decay and movement on the land and in streams. Indicators such as *E. coli, Enterococcus spp.*, and fecal coliform bacteria, although typically nonpathogenic, are used to identify the potential for the presence of other disease-causing organisms. These bacteria typically originate from mammalian and avian sources and are released into water bodies via point sources (such as wastewater treatment plant [WWTP] effluent and runoff from stormwater drainage networks) as well as dispersed (or nonpoint) sources (such as direct runoff from residential yards and streets, on-site sewage disposal, deposition from non-domestic animals and livestock, and re-suspension of bacteria from stream sediment). Bacteria are present in both water and sediment and experience survival, growth and decay within a water body. Furthermore, bacteria concentrations in streams vary spatially and temporally because of flow variability within the stream network and loads entering the streams from various sources at different times. Because of this complexity, most states use mathematical models to understand bacteria dynamics when developing bacteria TMDLs and I-Plans. Since numerous water quality models are available, selecting an appropriate model or combination of models for bacteria TMDLs is a challenge. Both the characteristics of each watercourse and the nature of its pathogen loads should be considered. Selection of a model or models is an important and critical step that should be undertaken early in the TMDL and I-Plan development processes in consultation with stakeholders and modeling experts.

Since bacteria TMDLs must estimate the maximum bacteria load that a water body can receive and still meet water quality standards, TMDL development involves estimating both existing and allowable loads, the instream water quality effects due to these loads, as well as the reductions that would be required to meet standards. I-plan development, however, involves designing realistic bacteria reduction strategies for different bacteria sources and examining the effects of these strategies on water quality. The different goals of TMDL development and I-Plan development may require the use of different bacteria models with different levels of complexity.

Efforts to formulate useful TMDLs have led to the development of many predictive tools for the estimation of necessary reductions to meet water quality goals. States required to develop TMDLs as part of consent decrees have been under a great deal of pressure to produce TMDLs quickly and cost-effectively to comply with federal law. States faced with budgetary constraints need an economical means to develop TMDLs to restore impaired waters. As a result, relatively simple and cost-effective approaches to identify sources of pollution and allocate loads are needed to identify bacteria load reductions to meet water quality standards.

These approaches include load duration curves, spatially explicit statistical models and mass balance models that rely on available flow and water quality data. In other cases states have chosen to use more complex mechanistic (process or physically based) hydrologic/water quality models combined with landscape-loading models. Some of the most common models used for bacteria TMDLs and I-Plans are described below. Other modeling tools described in EPA publications are summarized in Appendix 2.

Load Duration Curve (LDC) Models

Load Duration Curve (LDC) methodologies are acknowledged as a cost-effective, useful tool for addressing bacteria impairments because they are easy to understand, produce reasonable results and have minimal data requirements (Cleland 2002 and 2003, Bonta 2002, Stiles 2001).

LDCs graphically represent streamflow data in terms of pollutant loadings. The analysis begins with a flow duration curve where the x-axis is based on the frequency of exceedance of specific flows (y-axis) during the entire period of record represented in the data (Figure 1). The resulting graph depicts the range of flows (expressed as an exceedance frequency) experienced at a single monitoring over time.

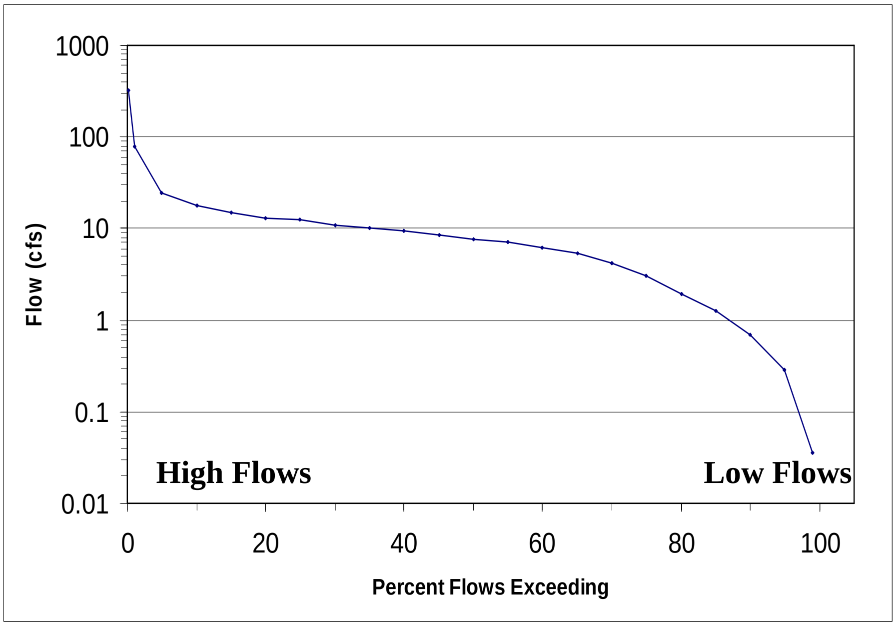

Figure 1: Example flow duration curve

In order to make this approach useful for TMDL purposes, it is necessary to convert the flow duration curve to an LDC. This conversion is accomplished by multiplying the flow (at each frequency interval) by the water quality criterion (Figure 2), in this case the single sample criterion. The resulting plot represents the maximum pollutant load for every flow experienced in the specific stream, in essence the total maximum daily load. The plotted line in Figure 2 is equal to the water quality criterion (in this case, for a single sample) times the flow.

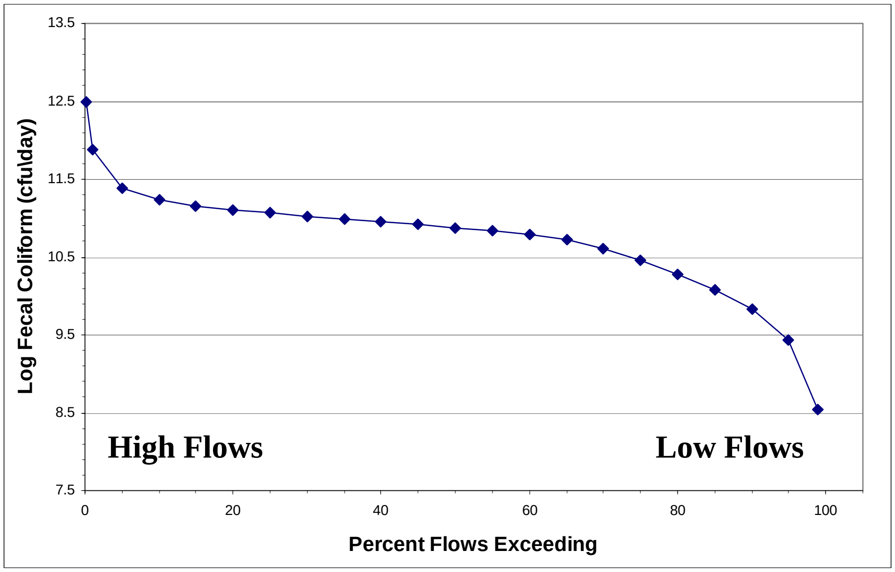

Figure 2: Example load duration curve using the single sample criterion

Monitoring data can be added to the graph to identify those flow conditions where pollutant levels may be above allowable loadings. This step is done by multiplying the water quality sample bacteria concentrations by the daily average flow that occurred when the sample was taken. The data points can then be plotted at the appropriate flow frequency and compared directly to the relevant water quality criterion obtained from the LDC (Figure 3).

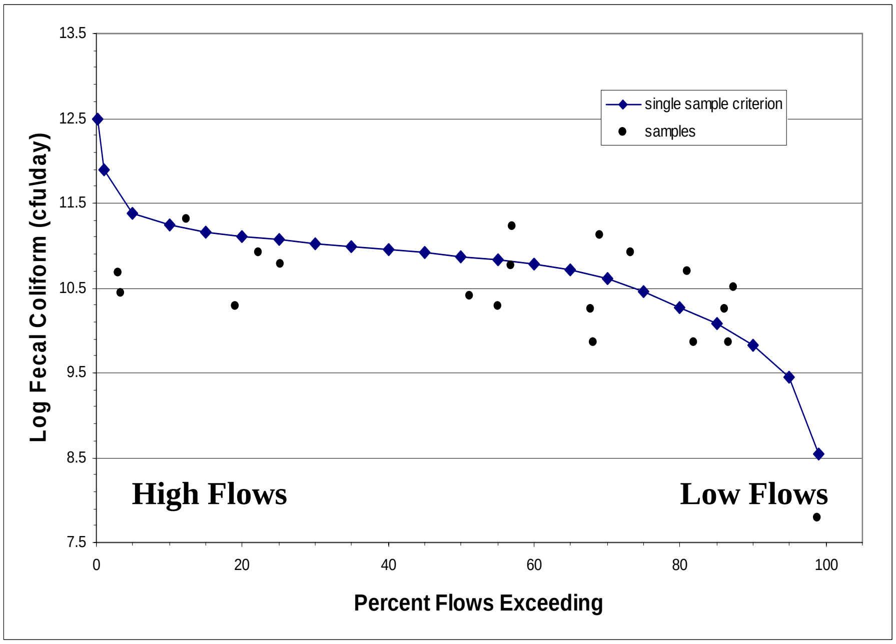

Figure 3: Data assessment using load duration curve

LDCs provide several types of useful information for the TMDL development process. An LDC can differentiate between point and nonpoint sources of bacteria related to different flow conditions (Figure 4). Generally speaking, monitored loads that exceed the allowable load at low flows (i.e., high frequency of exceedance) are likely to be the result of point source discharges, such as a WWTP discharging bacteria into a low flow stream. Resident populations of waterfowl could also contribute to chronic exceedances during low flows. In contrast, monitored loads exceeding the criteria at the mid-range and high flows are typically caused by nonpoint source inputs or point sources (such as stormwater systems) that channel rainfall runoff into water bodies. An example might be surface runoff carrying bacteria from livestock or non-domestic animal sources into a high flow stream. Finally, resuspension of indicator bacteria surviving in streambed sediments could produce exceedances under both high and low flow conditions.

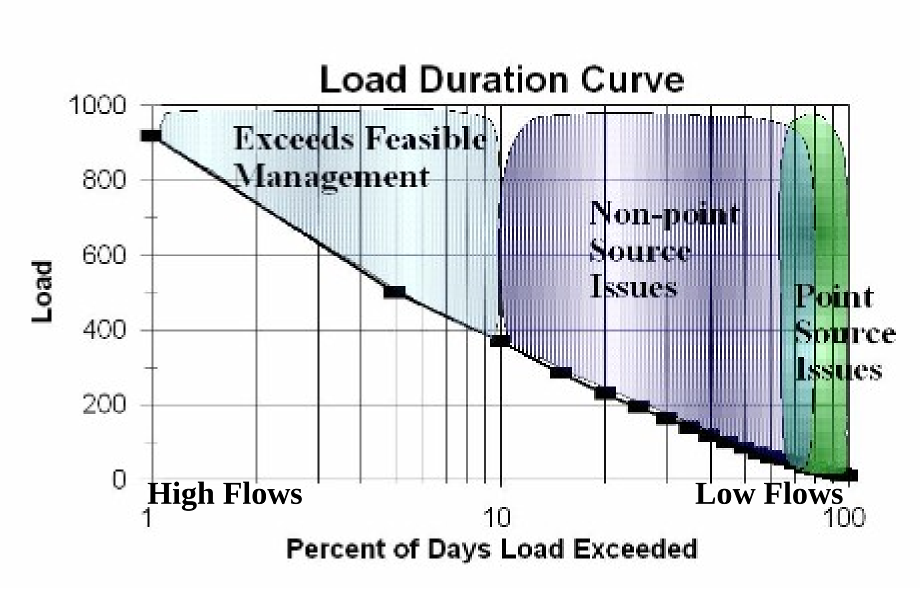

Figure 4: Source identification using load duration curve (Cleland 2003)

Developing load reduction scenarios based upon the LDC requires the examination of relationships between the data and the allowable loads expressed in the curve. This usually requires comparisons between statistical representations of the data (means, regression lines, confidence intervals) and the LDC, with the difference between the two values representing the required reduction. Statistical estimates of the data may include all of the loads or just those that exceed the TMDL line.

The segmentation of the LDC allows for the development of appropriate implementation strategies that target specific flow conditions (Cleland 2002). Exceedances occurring at the low flows may require regulatory actions to control point sources. At the mid range and high flows, management measures directed towards nonpoint sources could be developed. At some point in the flow frequency, control of pollutant sources becomes unfeasible. Pollutant loadings at these high flow events typically exceed design specifications for control actions. For this reason, it may be reasonable to exclude data and loadings that occur at flooding conditions.

Several states have developed bacteria TMDLs using LDCs and have produced reasonable scenarios to address impairments. Oklahoma developed TMDLs for bacteria in the Upper Canadian River in several nonpoint source-dominated watersheds. In Maryland, a TMDL for bacteria was developed for Cabin John Creek. Maryland also used BST to further refine source loadings. Kansas used the load duration methodology to develop a bacteria TMDL for the Kansas River. Texas is currently developing several TMDLs using LDCs to address bacteria impairments (Upper Oyster Creek, Gilleland Creek, Guadalupe River above Canyon Lake, among others).

Recognizing the importance and practical use of LDCs, the U.S. Environmental Protection Agency's Watershed Branch in the Office of Wetlands, Oceans and Watersheds is producing a detailed technical document on how to use LDCs for establishing TMDLs. The draft of "An Approach for Using Load Duration Curves in Developing TMDLs" is available on the Task Force's Web site at: http://twri.tamu.edu/bacteriatmdl/.

As with all predictive tools used in TMDL development, the LDC approach has both strengths and weaknesses. The primary strengths of this approach are the minimal data requirements (although large datasets are preferable in all cases), its simplicity and its usefulness as an illustrative model. The model's simple nature can also be considered a weakness in that very few inputs are considered for estimating resulting bacteria loads, potentially increasing uncertainty, though this could also be considered a strength in that other uncertainties are reduced by using fewer assumptions. This method also does not work very well in tidally influenced areas, and intermittent streams tend to produce truncated curves. Though the load duration approach can help differentiate between point and nonpoint sources, more mechanistic models provide more detailed assessments of specific sources of bacteria loads. On the other hand, specific source identification may not be necessary since a TMDL, in its most basic form, only requires differentiation between point (Waste Load Allocation [WLA]) and nonpoint (Load Allocation [LA]) sources.

Further refinements may be desirable for developing measures to control sources in the I-Plan following the TMDL. Additional tools (targeted monitoring, bacteria source surveys, BST and more complex models) used in conjunction with load duration methods have the potential to significantly refine source identification and increase the power of this analytical tool.

Spatially Explicit Statistical Models

The three models described below estimate the spatial distributions of potential pollutant sources throughout a watershed, estimate loadings from each source into water bodies and calculate the change in pollutant concentration within the water body. Key parameters are calibrated to mimic pollutant concentrations measured in the watershed.

Arc Hydro Model (Maidment)

The Arc Hydro Model, developed by Dr. David Maidment of the Center for Research in Water Resources at The University of Texas at Austin, can be defined as a geographic database containing a geographic information system (GIS) representation of a hydrological information system. Arc Hydro uses a case-specific database design that is extensible, flexible and adaptable to user requirements. It takes advantage of the next generation of spatial data in relational database management systems (an RDBMS-based GIS system), the geodatabase model. Conceptually, it is a combination of GIS objects enhanced with the capabilities of a relational database to allow for relationships, topologies and geometric networks.

This model has been used to develop bacteria TMDLs for Galveston and Copano Bays (Gibson, C.J. et al., 2006) The Copano Bay TMDL model input was developed within a GIS framework. Point sources were located in the GIS and accounted for in the model. Nonpoint source loadings were estimated from livestock, non-domestic animals and domestic animal populations per county. These populations were assumed to be equally distributed within their appropriate land use categories within each county. Loadings were then calculated by combining population, geographic and precipitation data. This information was used to estimate bacterial loadings for each watershed.

Septic systems were accounted for in a similar manner. It was determined, however, that systems located immediately adjacent to the bay were of particular interest. Increased efforts were made, therefore, to accurately account for systems in these areas.

A first order decay rate was assumed for bacterial degradation as pollutants moved through the watershed, into streams/channels and eventually into the bay. Once in the bay, degradation was modeled as four independent continuous flow, stirred tank reactors.

Once the loading to the bay was obtained, a Monte Carlo simulation was used to determine the necessary load reductions. Monte Carlo simulations use random number probability distributions to simulate random behavior, providing estimates of uncertainty in a given outcome. Accurate estimates of measured bacteria concentrations only required calibration of stream residence times and a multiplication factor.

SPAtially Referenced Regressions On Watershed attributes (SPARROW)

SPARROW is maintained by the U.S. Geological Survey. It spatially references various watershed components, such as stream monitoring data, pollutant sources, etc., to surface water flow paths that are defined by a digital drainage network. It then imposes mass balance constraints to empirically estimate terrestrial and aquatic rates of pollutant flux. Applications of SPARROW include estimation of the spatial distributions of pollutant yields, pollutant sources and the potential for delivery of those yields to receiving waters. This information can be used to:

- predict ranges in pollutant levels in surface waters,
- identify the environmental variables that are significantly correlated to the pollutant levels in streams,
- evaluate monitoring efforts for better determination of pollutant loads, and
- evaluate various management options for reducing pollutant loads to achieve water-quality goals.

SPARROW has been used previously to estimate the quantities of nutrients delivered to streams and watershed outlets from point and nonpoint sources over a range of watershed sizes (Smith et al., 1997; Alexander et al., 2000, 2001; Preston and Brakebill, 1999). This approach can be used for bacteria TMDLs because it not only uses process-based models to simulate transport of pollutants, but it also uses the actual historical monitoring data and known predictor variables to predict the various model input parameters. In this manner, a more realistic model can be developed that closely describes the conditions of the particular watershed (Schwarz, et al., 2006).

Spatially Explicit Load Enrichment Calculation Tool (SELECT)

SELECT (Teague 2007a, 2007b) spatially references the sources of bacteria contamination and is being developed under an ArcGIS 9 environment. SELECT will calculate and allocate bacteria loading to a stream from various sources in a watershed. All loads will be spatially referenced. In order to allocate the bacteria load throughout the watershed, estimations of the source contributions will be made. This, in turn, allows the sources and locations to be ranked according to their potential contribution. The populations of livestock, non-domestic animals and domestic pets will be calculated and distributed throughout the watershed according to appropriate land use. Furthermore, point sources will be identified and their contribution quantified based on flow and outfall concentration. Septic system contribution will also be estimated based on criteria including distance to a stream, soil type, failure rate and age of system. Once the watershed profile is developed for each potential source, the information can be aggregated to the sub-watershed level to identify the top contributing areas.

Mass Balance (MB) Methods

These methods, as the name implies, calculate a mass balance between bacteria loads entering the water body and bacteria loads within the stream. Sources are typically inventoried, quantified and compared to existing and allowable in-stream loads at specified points within the stream (typically, where the TMDL is sought) for different flow conditions. MB methods require more data than the LDC method, but are more amenable for use in TMDL implementation. These methods have typically been developed using spreadsheets. The main advantages of the MB methods are that they can be used for tidal and non-tidal water bodies, including both TMDL and I-Plan development. In addition, they can be used for watersheds where both point and nonpoint sources appear to contribute at both low flow and high flow conditions. The main disadvantage is that MB methods, like the LDC method, are static and do not consider temporal variations in loading. The MB method accounts for spatial variations since it estimates the various sources within the watershed. However, estimates of nonpoint source loadings may be difficult to obtain. The output from these methods can often be used in the development of more complex, mechanistic models discussed in the next section.

Bacteria Load Estimator Spreadsheet Tool (BLEST)

In Texas, one of the more recent MB applications is described in Petersen (2006) in which BLEST was used to calculate bacteria loads from all sources and land uses on a subwatershed basis for Buffalo and White Oak Bayous. The loads were accumulated by segment and calculated for low, median and high flow conditions in a stream. Sources include WWTPs, septic tanks, nonpoint source runoff, sanitary sewer overflows and bypasses, sewer leaks and spills, in-stream sediment and non-domestic animals and domesticated animals. BLEST was used to calculate existing loads and allowable loads and to estimate the load reductions that would be required to meet the standard. The limitations of this tool include the extensive amount of inventory data required, the use of literature values for some of its variables (for example, the rate of failure for septic systems) and the absence of attenuation or loss mechanisms that might affect loads before they reach the water body. Additionally, and due to its static nature, temporal variations in the source loads are not modeled.

Tools similar to BLEST have been developed elsewhere; for example, the Bacteria Source Load Calculator (BSLC) from the Center for TMDL and Watershed Studies at Virginia Tech (http://www.tmdl.bse.vt.edu/outreach/C85/).

Bacteria Indicator Tool (BIT)

Another MB tool is the BIT provided by EPA (http://www.epa.gov/waterscience/ftp/basins/system/BASINS3/bit.htm). The BIT is a spreadsheet that can be used to estimate the monthly accumulation rate of fecal coliform bacteria on four land uses (cropland, forested, built-up and pastureland). The tool also estimates the direct input of fecal coliform bacteria to streams from grazing agricultural animals and failing septic systems. Output from BIT can be used as input to the Hydrological Simulation Program Fortran (HSPF) water quality model in BASINS (Better Assessment Science Integrating Point and Nonpoint Sources). BIT has been used in Texas.

Mechanistic Hydrologic/Water Quality Bacteria Models

A number of simulation models have been used to describe (in mathematical form) the mechanisms of water movement as well as loading and transport of pollutants. Both researchers and managers desire to have a means to create scenarios to simulate environmental outcomes in response to specific management practices. Models are used to predict the water quality in a water body based upon changes in pollutant loading and various allocation strategies. Current models have been adapted for use in bacteria TMDLs from other models originally designed for more conventional pollutants (suspended sediments, nutrients, dissolved salts). These models can be used for both TMDL and I-Plan development to evaluate spatial and temporal variation of bacteria loading within a watershed. These models, however, have extensive data requirements and their level of sophistication requires a significant investment of resources for parameterization, calibration and training of personnel to use the models effectively.

In-stream water quality models are either steady-state or transient and are hydrologically driven (via rainfall) or hydrodynamically driven (via velocities in the water body). A steady-state model does not allow for variations over time and averages water quality over time. A dynamic or transient model, on the other hand, allows for changes over time and can be used to estimate bacteria loads and concentrations at different points in time anywhere in the stream.

Ward and Benaman (1999) identified a number of models as being appropriate for use in Texas TMDLs. Their list includes: ANSWERS, CE-QUAL-W2, DYNHYD, EFDC, GLEAMS, HSPF, POM, PRMS, QUALTX, SWAT, SWMM, TxBLEND and WASP. Their assessment categorized these models based on the watercourse type and the scale of resolution for time. For example, HSPF, SWAT, PRSM, SWMM and ANSWERS were characterized as watershed type models that can be used for "slow time variation" and "continuous time variation."

Of the above list of models identified by Ward and Benaman (1999) for use in Texas TMDLs, the most commonly used for bacteria include HSPF, SWAT, SWMM and WASP. HSPF has been the most commonly used of the four, but EPA specifically requested U.S. Department of Agriculture – Agricultural Research Service (USDA–ARS) scientists in Temple, Texas to develop bacteria fate and transport components for SWAT to facilitate its use in TMDL and I-Plan development. These models all require many input variables, a substantial cost and time investment in set-up, calibration and validation time and have a steep learning curve.

Hydrological Simulation Program – FORTRAN (HSPF)

HSPF has been in extensive use since the 1970s, and is distributed by EPA's Center for Exposure Assessment Modeling. This watershed hydrologic model has been commonly used for TMDL development for a variety of conventional water quality parameters in Texas (for indicator bacteria and for dissolved oxygen) and also in other states. The required data include land use; watershed and subwatershed boundaries; location and data for rainfall gages and surface water quality monitoring stations; detailed descriptions of stream geometry and capacity; detailed information about sources within the watershed; sedimentation and re-suspension characteristics and bacteria die-off rates, to name a few. Development of an HSPF model for a given watershed is both complex and time-consuming and involves substantial calibration and validation. HSPF can be used for most types of watersheds (except possibly tidally influenced streams) regardless of the land use, but it requires extensive input from hydrologic and hydraulic models as well as GIS data layers. HSPF allows for a detailed spatial resolution within the watershed and allows for estimation of bacteria loads from runoff from the land surface as well as re-suspension from the streambed and from direct deposition sources. Disadvantages include the inherent difficulty in its application, its poor documentation and inadequate simulation of bacteria fate and transport processes. For example, transport of bacteria associated with sediment, sedimentation and re-suspension, regrowth and die-off processes are simplified and modeled using variables that difficult to measure in field settings. These variables are commonly treated as calibration variables during model development.

Soil and Water Assessment Tool (SWAT)

The SWAT model is a continuation of nearly 30 years of modeling efforts conducted by the USDA-ARS at Temple, Texas. SWAT has gained international acceptance as a robust interdisciplinary watershed modeling tool as evidenced by regular biennial international SWAT conferences (Gassman 2005a), SWAT-related papers presented at numerous other scientific meetings, and dozens of articles published in peer-reviewed journals. The model, like HSPF, has been adopted as part of the EPA Better Assessment Science Integrating Point and Nonpoint Sources (BASINS) software package and is being used by many federal and state agencies, including the USDA within the Conservation Effects Assessment Project (CEAP). Reviews of SWAT applications and/or components have been previously reported, sometimes in conjunction with comparisons with other models (i.e., Arnold and Fohrer, 2005; Borah and Bera, 2003; Borah and Bera, 2004; Steinhardt and Volk, 2003; Gassman, et. al 2005b).

SWAT was developed primarily to estimate loads from rural and mainly agricultural watersheds; however, the capability for including impervious cover was accomplished by adding urban buildup/washoff equations from SWMM. At the request of EPA, a microbial sub-model was incorporated to SWAT for use at the watershed or river basin levels. The microbial sub-model simulates (1) functional relationships for both the die-off and regrowth rates and (2) release and transport of pathogenic organisms from various sources that have distinctly different biological and physical characteristics. SWAT has been used in Virginia and North Carolina for bacteria TMDL development.

Storm Water Management Model (SWMM)

SWMM was developed primarily for urban areas. It is most commonly used to simulate real storm events based on meteorological and watershed data, although it can also be used for continuous simulations. While SWMM was developed with urban watersheds in mind, it can be used for rural watersheds. The biggest advantage of SWMM is in its ability to model urban infrastructure including drains, detention basins, sewers and related flow controls. However, SWMM does not simulate the in-stream water quality. Linking it to WASP can circumvent this limitation. Perhaps the best application for SWMM is to characterize the bacterial pollution from the urban drainage infrastructure, but this limits its usefulness within a bacterial TMDL context to implementation rather than development.

Water-quality Analysis Simulation Program (WASP)

This model is also distributed by EPA’s Center for Exposure Assessment Modeling and is a well-established water quality model incorporating transport and reaction kinetics. Unlike HSPF, however, WASP is driven by flow velocity rather than rainfall, thus it is usually coupled with a suitable hydrodynamic model such as DYNHYD, EFDC or SWAT. WASP is typically used for main channels, reservoirs and bays and estuaries and not for modeling watershed-scale processes. Problems studied using WASP include biochemical oxygen demand and sources of bacteria, dissolved oxygen dynamics nutrients and eutrophication, organic chemical and heavy metal contamination.

Important Considerations for Bacteria Modeling

- The expectations from using a model for TMDL development or implementation must be realistic and commensurate with the level of data and information available for the watershed in question. The model used will only be as good as the data used to develop it.
- Models should be used as part of the TMDL framework and not as an only tool for decision-making. Models should continually evolve as the knowledge base used in developing them changes.
- In-stream sediment settling and re-suspension processes are not well represented in most models available to date and their roles in bacterial concentrations in water bodies are poorly understood.
- Bacteria regrowth and decay are also not well represented in presently available models. Bacteria death is typically approximated using first-order expressions, and the first-order decay constant is determined from controlled laboratory and/or field experiments.
- Transient (time-varying) models such as HSPF provide bacterial concentrations on a very detailed time scale (minutes or hours), whereas most bacterial measurements are made much less frequently (once a week or once a month or once a quarter) thus complicating calibration and validation of the model.
- The models that are hydrologically driven such as HSPF are biased toward high flow conditions since rainfall is the main driver for flow in the water body. These models have to be fine-tuned to represent bacterial sources in dry weather conditions (under mostly effluent dominated conditions).

- The main advantage of simple models such as LDC, SELECT, BLEST or BIT is in determining required reductions to meet the standard.
- The main value of detailed models is that they allow for spatial and temporal analysis of different reduction strategies (i.e., BMPs) and their effectiveness in improving in-stream water quality.
- Sensitivity and uncertainty in data, parameters and models should be considered and assessed.
- The results of modeling exercises are heavily dependant on the precision of the model as determined by calibration activities. For this reason, calibration specifications for model application should be explicitly stated and standardized throughout all applications.

Table 1 (below) is a matrix describing the applicability and capability of typically used models.

Table 1 Bacteria Modeling Matrix

Model		**LDC**	**Spatial Explicit Statistical Models**			**Mass Balance Models**			**Mechanistic/Hydrologic/WQ**			
			ArcHydro	**SPARROW**	**SELECT**	**BLEST**	**BSLC**	**BIT**	**HSPF**	**SWAT**	**SWMM**	**WASP**
Watercourse Type	Watersheds		x	x	x	x	x	x	x	x	x	
	River/Stream	x	x	x	x	x	x	x	x	x		x
	Lake/Reservoir		x	x	x	x	x	x				x
	Fresh/Saltwater Estuarine		x	x	x	x	x	x				x
TMDL Phase	Development	x	x	x	x	x	x	x	x	x		x
	Implementation		x			x			x	x		x
Model Type	Analytical	x	x	x	x	x	x	x				
	Numerical								x	x	x	x
Spatial Dimensions	1-D	▨	▨	x	x	▨	▨	▨	x	x	x	x
	2-D	▨	▨	▨		▨	▨	▨				x
	3-D	▨	▨	▨		▨	▨	▨				x
Time Scale	Steady-state	▨	▨	x		▨	▨	▨		x		x
	Time Varying	▨	▨	▨		▨	▨	▨	x	x	x	x
	Single Storm Event	▨	▨	▨	x	▨	▨	▨	x	x	x	
	Continuous in time	▨	▨	x		▨	▨	▨	x	x	x	x
Watershed Characteristics	Rural	x	x	x	x	x	x	x	x	x		▨
	Urban	x	x	x	x	x	x	x	x	x	x	▨
	Sediment transport	▨	▨	x	x	▨	▨	▨	x	x		x
In-Stream Processes	Bacteria Regrowth	▨	▨	▨		▨	▨	▨				
	Bacteria Die-off	▨	▨	x		▨	▨	▨	x	x		
	Settling	▨	▨	▨		▨	▨	▨	x	x		
	Re-suspension	▨	▨	▨		x	▨	▨	x	x		
WLA Sources	WWTF	▨	▨	x	x	x	▨	▨	x	x		x
	Storm Sewers	▨	▨	x	x	x	▨	▨	x	x		x
LA Sources	Septic Tanks	▨	▨	x	x	x	x	x	x	x		
	Direct Deposition	▨	▨	▨		x	x	x	x	x		x
	Bed Sediment	▨	▨	▨		x	▨	▨	x			x
Cost		$	$$			$$			$$$			

Notes: 1. Shaded areas: not applicable.

Bacteria Source Tracking (BST)

This section, coordinated by Drs. George Di Giovanni and Joanna Mott, describes the strengths and weaknesses of several BST tools that have been used. The EPA has also issued a microbial source tracking guidance document (USEPA 2005) which provides technical details on many different BST methods, quality control measures, discussion of library size and representativeness, statistical analysis, project design and case studies. No consensus has been reached for most of these issues by the source tracking scientific community, and detailed discussions of these topics are outside the scope of this report. However, where appropriate, brief discussion of these issues have been included in this document and considered in the recommendations presented below.

The premise behind BST is that genetic and phenotypic tests can identify bacterial strains that are host specific so that the original host animal and source of the fecal contamination can be identified. Often *E. coli* or *Enterococcus spp*. are used as the bacteria targets in source tracking, as this provides a direct link with water quality standards which are usually based on one of these two indicators (for example, [Parveen, Portier et al. 1999; Dombek, Johnson et al. 2000; Graves, Hagedorn et al. 2002; Griffith, Weisberg et al. 2003; Hartel, Summer et al. 2003; Kuntz, Hartel et al. 2003; Stoeckel, Mathes et al. 2004; Scott, Jenkins et al. 2005]). While there has been some controversy concerning host specificity and survival of *E. coli* in the environment (Gordon, Bauer et al. 2002), this indicator organism has the advantage that it is known to correlate with a probability of gastrointestinal illness and is used for human health risk assessments. BST of *E. coli,* therefore, has the advantages of direct regulatory significance and availability of standardized culturing techniques for water samples, such as EPA's Method 1603 (USEPA 2005).

Description of Methods

There have been many different technical approaches to bacterial source tracking (Scott, Rose et al. 2002; Simpson, Santo Domingo et al. 2002; Meays, Broersma et al. 2004), but there is currently no consensus on a single method for field application. Genotypic (molecular) tools appear to hold promise for BST, providing the most conclusive characterization and level of discrimination for isolates. Of the molecular tools available, ribosomal ribonucleic acid (RNA), genetic fingerprinting (Ribotyping), repetitive element polymerase chain reaction (rep-PCR), and pulsed-field gel electrophoresis (PFGE) are emerging as a few of the versatile and feasible BST techniques. Antibiotic resistance analysis (ARA), a phenotypic characterization method, also has the potential to identify the human or animal origin of isolates, and variations of this technique have been applied in several BST studies. Carbon source utilization (CSU) is another phenotypic method that has been used in Texas, as well as other states, as a source tracking method.

Four years ago, a review of BST methods was performed before initiating the BST study for Lake Waco and Belton Lake. At that time, and still today, there is no consensus among BST experts as to the best approach or technique. The enterobacterial repetitive intergenic consensus sequence polymerase chain reaction (ERIC-PCR), RiboPrinting, pulsed field gel electrophoresis (PFGE) and Kirby-Bauer antibiotic resistance analysis (KB-ARA) were chosen for the Texas study because they appeared promising from previous BST and other scientific studies, and cover the spectrum in cost, ease of use, and discriminatory ability. This allowed researchers to not only evaluate the practical application of these methods for the identification of human and animal sources of fecal pollution, but also to perform a comprehensive comparison of the methods and composite data sets for further consideration and use in future studies. Additionally, CSU has been used in Texas in conjunction with KB-ARA. Each of these five methods has its strengths and weaknesses, which are described below. A disadvantage of each of these techniques is that reference libraries of genetic or phenotypic fingerprints for *E. coli* isolated from known sources (i.e., domestic sewage, livestock and non-domestic animals) are needed to identify the sources of bacteria isolated from environmental water samples. Thus, the development of an identification library can be a time consuming and expensive component of a BST study. Libraries of isolates from various parts of Texas have been developed using these methods following the same protocols for comparability.

ERIC-PCR

Enterobacterial repetitive intergenic consensus sequence polymerase chain reaction (ERIC-PCR), a type of rep-PCR, has moderately high ability to resolve different closely related bacterial strains (Versalovic, Schneider et al. 1994). Consumable costs for ERIC-PCR are inexpensive and labor costs for sample processing and data analyses are moderate. ERIC-PCR is a genetic fingerprinting method used in previous BST studies (i.e., McLellan, Daniels et al. 2003; Leung, Mackereth et al. 2004; Casarez, Pillai et al. 2006) as well as many microbial ecology and epidemiological studies. ERIC elements are repeat DNA sequences found in varying numbers and locations in the genomes of different bacteria such as *E. coli*. The PCR is used to amplify the DNA regions between adjacent ERIC elements. This generates a DNA banding pattern or fingerprint which looks similar to a barcode pattern. Different strains of *E. coli* bacteria have different numbers and locations of ERIC elements in their bacterial genomes, and therefore, have different ERIC-PCR fingerprints. ERIC-PCR is useful as a screening technique for library development because of its moderate cost and moderately high ability to resolve different strains of the same species of bacteria. Though rep-PCR banding patterns for isolates tend to be generally stable, differences in fingerprint image processing and PCR protocols between laboratories may result in reduced between-laboratory reproducibility and pose a challenge to generating a composite library in multiple laboratories. Rigorous quality control and quality assurance, standardized protocols for PCR and image processing, and adequate training of personnel is crucial for generation of comparable data. Two analytical strategies that enhance data comparability between laboratories are the use of horizontal fluorophore-enhanced rep-PCR (HFERP; Johnson et al., 2004), or a commercially packaged product such as the DiversiLab system (http://www.bacbarcodes.com/).

Ribotyping

Ribotyping is a genetic fingerprinting method used in previous BST studies (i.e., Parveen, Portier et al. 1999; Scott, Parveen et al. 2003; Moore, Harwood et al. 2005), as well as many microbial ecology and epidemiological studies (i.e., Verduin, Kools-Sijmons et al. 2000; Clark, Kruk et al. 2003), although there is not a consensus as to the best protocol. Ribotyping has a moderate ability to resolve different strains of the same bacteria species. An automated ribotyping system (DuPont Qualicon RiboPrinter) is available, which saves labor costs and requires little training, but the initial investment and the consumable cost per isolate are expensive. The RiboPrinter was originally developed for use in identification and BST of microbial isolates for the food industry. An endonuclease enzyme (i.e., *Hin*dIII) selectively cuts *E. coli* DNA wherever it recognizes a specific DNA sequence. The resulting DNA fragments are separated by size and probed for fragments containing particular conserved ribosomal RNA gene sequences, which results in DNA banding patterns or fingerprints that look similar to barcode patterns. Different strains of *E. coli* bacteria have differences in their DNA sequences and different numbers and locations of enzyme cutting sites, and therefore have different ribotyping fingerprints. By automating the process, the RiboPrinter System can analyze up to 32 samples per day, whereas manual ribotyping methods, which require highly trained and experienced personnel, may require up to several days to complete. All bacteria isolate sample processing is automated using standardized reagents and a robotic workstation, providing a high level of reproducibility. Since the system employs standardized methods and reagents, results obtained from other laboratories using the system are directly comparable.

Pulsed-Field Gel Electrophoresis (PFGE)

PFGE is another leading genetic fingerprinting method used in BST. PFGE has very high resolution and can discriminate between closely related bacteria strains. The entire bacterial genome is fragmented using an infrequent cutting restriction endonuclease enzyme (i.e., *Xba* I) which cuts DNA wherever it recognizes a specific rare sequence. All the DNA fragments are separated by size and stained to visualize the resulting genetic fingerprint that resembles a barcode. Different strains of *E. coli* bacteria have differences in their DNA sequences and different numbers and locations of enzyme cutting sites and therefore, have different PFGE fingerprints. PFGE is currently being used by the Centers for Disease Control and Prevention (CDC) to track foodborne *E. coli* O157:H7 and *Salmonella* isolates. CDC currently uses this standardized protocol as the basis of its "PulseNet" outbreak surveillance network that allows public health laboratories nationwide to quickly compare their PFGE fingerprints to the CDC central reference library. Although it requires more training and cost, PFGE has very high resolution and can discriminate between closely related strains. While this level of resolution allows higher confidence in the matches made, fewer identifications of water isolates can be made, and an unrealistically large (and costly) library would be needed for field application. In addition, some bacterial strains have genomic DNA in configurations that do not permit effective restriction endonuclease digestions and cannot be analyzed by PFGE.

Kirby-Bauer Antibiotic Resistance Analysis (KB-ARA)

Antibiotic Resistance Analysis was one of the first approaches developed for BST and has been used for many TMDL studies in the United States. It relies on the principle that bacteria from intestinal tract of different animals have been exposed to different antibiotics and will exhibit different profiles of resistance to a panel of antibiotics. Several methods have been used for antibiotic resistance analysis; however all rely on the same principle and the data are usually statistically analyzed using discriminant analysis to categorize isolates. The KB-ARA technique follows procedures used in the clinical laboratory for evaluating the antibiotic resistance of bacteria isolates and has the advantage of strong quality assurance/quality control requirements. The method involves measuring the diameter of the zone of inhibition of bacterial growth around a filter disk impregnated with a specific antibiotic. By comparison to resistant and susceptible control strains, the response of the *E. coli* isolates can be determined. In the procedure used in several studies in Texas (Mott) to further standardize and automate the assay, an image analysis system is used to measure the zones of inhibition and provide electronic archival of data. The KB-ARA profile for an isolate consists of the measurements of the zones of inhibition in response to 20 antibiotics, each at a standard single concentration. Among

ERIC-PCR, RiboPrinting, PFGE and KB-ARA, the KB-ARA method has the lowest ability to discriminate closely related bacteria strains. However, it also has the lowest initial and per sample cost and takes the least time and training.

Carbon Source Utilization (CSU)

CSU is another phenotypic method and is less widely used than ARA. It is based on the principle that bacteria from different animals have been exposed to a range of carbon sources (dietary differences between animals). It is most commonly conducted using the Biolog Microbial Identification System (MIS) (Biolog, Inc., 3939 Trust Way, Hayward, CA 94545). Bacteria are grown on specific media and then transferred to 96 well microplates, with each well containing a different carbon source and an indicator that changes color if the source is utilized. The plates are incubated and read using an automated plate reader, which can provide color intensity data for each well. The profiles of utilization of the carbon sources of unknown source isolates are compared to the profiles of known source isolates (the library) and discriminant analysis is used to categorize isolates. This approach has been used both in Texas, in conjunction with KB-ARA, and in other states as a stand-alone method. In Texas, CSU profiles of *E. coli* were used in conjunction with ARA of the same isolates for a study of sources of contamination in White Oak and Buffalo Bayous (Mott and Lehman, with Dr. Rifai, University of Houston). Combining both profiles provided increased accuracy in terms of rates of correct classification for the library.

Table 2 compares several BST techniques.

Table 2. Relative comparison of several bacterial source tracking techniques

Technique	Acronym	Target organism(s)	Basis of characterization	Previously Used or in Progress in Texas	Used in other states	Accuracy of source identification	Size of library needed for water isolate IDs	Capital cost	Cost per sample (reagents and consumables only)	Ease of use	Hands on processing time for 32*** isolates	Time required to complete processing 32 isolates
Enterobacterial repetitive intergenic consensus sequence polymerase chain reaction	ERIC-PCR	*Escherichia coli* (*E. coli*) and *Enterococcus* spp.	DNA fingerprint	Yes (Di Giovanni)	Yes	Moderate	Moderate	$20,000 ($15,000 BioNumerics software, $5,000 equipment)	$8	Moderate	3 h	24 h**
Automated ribotyping (RiboPrinting)†	RP	*E. coli* and *Enterococcus* spp.	DNA fingerprint	Yes (Di Giovanni)	Yes	Moderate	Moderate	$115,000 ($100K RiboPrinter, $15K BioNumerics software)	$40	Easy	1 h	24 h
Pulsed field gel electrophoresis	PFGE	*E. coli* and *Enterococcus* spp.	DNA fingerprint	Yes (Pillai and Lehman)	Yes	High	Large	$30,000	$40	Difficult	10 h	5 days
Kirby-Bauer antibiotic resistance analysis‡	KB-ARA	*E. coli* and *Enterococcus* spp.	Phenotypic fingerprint	Yes (Mott)	Yes	Moderate*	Moderate	$35,000	$15	Easy	3 h	24 h**
Carbon source utilization	CSU	*E. coli* and *Enterococcus* spp.	Phenotypic fingerprint	Yes (Mott)	Yes	Moderate	Moderate	$15,000	$10	Easy	4 h	24 h**
Bacteriodales polymerase chain reaction	*Bacterio-dales* PCR	*Bacteriodales* species	Genetic marker presence or absence (not quantitative)	Yes (Di Giovanni)	Yes	Moderate to high for only human, ruminant, horse, and pig sources	Not applicable	$5,000	$8	Easy to moderate	3 h	8 h**
Enterococcus faecium surface protein polymerase chain reaction or colony hyb.	*E. faecium* esp marker	*E. faecium*	Genetic marker presence or absence (not quantitative)	Yes (Di Giovanni)	Yes	High for only human	Not applicable	$8,000	$8 to $12	Easy to moderate	3 to 6 h	8 to 24 h**
ERIC and RP 2-method composite	ERIC-RP	*E. coli*	DNA fingerprints	Yes (Di Giovanni)	No	Moderate to high	Moderate	$120,000	$48	Moderate	4 h	24 h
ERIC and KB-ARA 2-method composite	ERIC-ARA	*E. coli*	DNA and phenotypic fingerprints	Yes (Di Giovanni)	No	Moderate to high	Moderate	$55,000	$23	Moderate	6 h	24 h
KB-ARA and CSU 2-method composite	ARA-CSU	*E. coli* and *Enterococcus* spp.	Phenotypic fingerprints	Yes (Mott)	Yes	Moderate to high	Moderate	$50,000	$23	Easy to moderate	7 h	24 h

†A manual ribotyping version is also used by some investigators (i.e. Dr. M. Samadpour with IEH Laboratories and Consulting Group in Seattle), but no detailed information is available for comparison.

‡A variation of this technique using replica plating and +/- scoring of growth on media with different concentrations of antibiotics, called ARA, has been used extensively in Virginia for TMDLs.

*This technique is better for distinguishing broader groups of pollution sources. For example, “wildlife” and “livestock” as opposed to “avian wildlife”, “non-avian wildlife,” “cattle,” etc.

**With sufficient personnel, up to approximately 150 isolates can be analyzed in 24 h.

***Thirty two isolates selected for comparison because it is the maximum throughput per day of the RiboPrinter, which is the only automated system described.

Method Comparisons and Composite Data Sets in a Previous Texas Study

As mentioned above, a BST project was completed for Lake Waco and Belton Lake in which *E. coli* isolates were analyzed using RP, ERIC-PCR, PFGE and KB-ARA. For this study, BST analyses were performed using the individual techniques, as well as composite data sets (Casarez, Pillai et al. 2006). The congruence (concordance) between the groupings of isolates from known fecal sources by individual BST methods and different combinations of composite data sets was determined using the same statistical software (BioNumerics, Applied Maths, Austin, Texas) and Pearson's product moment correlation coefficient. The four-method composite library generated the most desirable BST results in regards to accuracy, blind quality control study results, library quality measures and ability to identify water isolates. However, as few as two methods in combination may 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. ERIC-ARA has the lowest cost for consumables and has high sample throughput, but requires a considerable amount of hands-on sample and data processing. Due to the high cost of RiboPrinting consumables and instrumentation, ERIC-RP has a higher cost than ERIC-ARA. However, ERIC-RP has the advantage of automated sample processing and data preprocessing that the RiboPrinter system provides.

Regulatory Expectations and Capabilities of BST Methods

Regulatory agencies continue to have high hopes and expectations for BST in aiding them to address water quality issues. BST may not be needed, or may not be suitable for all TMDL studies. In some cases, more rigorous monitoring of water bodies and determination of *E. coli* levels may identify the major sources of pollution. No BST method developed to date can provide 100% accuracy of pollution source identification in field studies. In many cases, the reduced accuracy often does not justify the high cost of some of the analyses.

In addition, the issue of indicator bacteria regrowth in the environment has been raised. There are many uncertainties surrounding this issue and there is a lack of scientific evidence that demonstrates regrowth occurs naturally in subtropical and temperate environments. However, because of the obvious implications for regulatory efforts (particularly for *E. coli*), the survival and regrowth of fecal indicator organisms in the aquatic environment, sediments and soils will need to be addressed not only for source tracking, but the concept of bacterial fecal indicators. While no BST method has specifically been developed to identify environmentally adapted indicator organisms, *ex post facto* analysis of BST data for environmental water isolates may provide some insight into this issue.

Ideally, agencies and stakeholders would prefer identification of pollution sources to the level of individual animal species. Performing a three-way split of pollution sources into domestic sewage, livestock and non-domestic animals source classes would likely be more scientifically justified with the current levels of accuracy and confidence of BST techniques in general. The division of host sources into the seven classes in the Lake Waco study was a compromise between the capabilities of the *E. coli* BST techniques and their practical application. Rates of correct classification (RCCs, measurements of library internal accuracy) are calculated using jackknife statistical analyses in which a single known source isolate is removed from the identification library, treated as an unknown, and is tested against the remaining library isolates to determine the percent of correct source identification. Comparisons of the RCCs for two- or three-way splits of host sources show high accuracy in distinguishing human from animal sources (83% and 95% RCCs, respectively); and distinguishing domestic sewage, livestock and non-domestic animals (83%, 72% and 73% RCCs, respectively). The RCCs for the seven-way split of source classes ranged from 22% to 83%, although those classes of particular interest (domestic sewage and cattle) were relatively high (83% and 60%, respectively). It is important to note that these RCCs for each of the source classes were three- to seven-fold greater than random chance based on library composition. Identifying pollution loading down to the sampling station level would require collecting hundreds of water samples per sampling site to analyze a statistically significant number of *E. coli*, making this approach not feasible. More realistic for BST is identification of fecal pollution sources at the watershed level. Alternatively, a higher number of *E. coli* isolates (i.e., 50) can be analyzed from fewer water samples to identify statistically significant differences in pollution sources. However, this will only provide pollution source identification on limited time scales, and will not provide an overall assessment of the water body.

Although quantitative allocation of fecal contamination to source categories is a goal of most TMDL projects, uncertainty in classification limits our capacity for absolute quantification. In some cases, library-dependent methods may enable identification of a source that contributes more fecal contamination than other sources, or identification of sources for which there is no credible evidence of substantial contamination. The results of library-dependent classification are conservatively seen as semi-quantitative and suitable for sample-level classification of sources as “contribution not detected” or “contribution detected” with possible refinement to “contribution detected greater than (alternative source).” This information may not be suitable for incorporation into quantitative water-quality models. However, most library-independent methods are even less quantitative than library-dependent methods, and the correlation between the fecal pollution indicators targeted by these methods and regulated contaminants (i.e., *E. coli*) is uncertain.

Another issue is that BST typically only identifies the major sources of pollution for a water body, not the entry pathways of the fecal pollution. This can be an important issue when developing implementation actions for different watershed stakeholders. This emphasizes the importance of sampling station selection and upstream/downstream targeted sampling of suspected pollution sources.

Future Direction

As described above for the EPA CWA §319(h) funded study for Lake Waco and Belton Lake, a cost-effective alternative to using multiple BST methods for each study is to use the two-method combination of either ERIC-PCR and RiboPrinting (ERIC-RP), or ERIC-PCR and Kirby-Bauer antibiotic resistance analysis (ERIC-ARA). Based on other studies in Texas, CSU and KB-ARA may also be a suitable combination. It is important to note that in nearly all cases, no single BST method should be solely relied upon. This is particularly true with the phenotypic methods, such as KB-ARA, which alone cannot provide the resolution needed for most BST studies. A factor to be considered when choosing the methods includes the level of resolution needed for the particular study. In some cases, it may be critical to determine specific animal groups, while in other cases broad categories may provide the level of resolution needed for management decisions. Cost constraints, equipment needs and expertise available are other factors that should be considered in the decision.

Since the Lake Waco study was initiated, there have been significant developments in library-independent BST methods, including bacterial genetic markers specific to different animal sources and humans (i.e., Bernhard and Field 2000; Dick, Bernhard et al. 2005; Scott, Jenkins et al. 2005; Hamilton, Yan et al. 2006). Library-independent methods are cost-effective, rapid and potentially more specific and accurate than library-dependent methods. Concerns with many of the recently developed library-independent approaches include uncertainties regarding geographical stability of markers and the difficulty of interpreting results in relation to regulatory water quality standards and microbial risk, since some target microorganisms are not regulated. More importantly, these library-independent methods can only detect a limited range of pollution sources and are currently not quantitative. For example, the *Bacteroidales* PCR (Bernhard and Field 2000; Dick, Bernhard et al. 2005) can detect fecal pollution from ruminants, humans, dogs, horses and pigs; but no further discrimination is possible. This method involves the concentration of 100 ml water samples, extraction of bacterial DNA, and detection of animal group-specific *Bacteroidales* bacteria genetic markers using the PCR.

This method is qualitative (presence/absence), and does not identify sources of *E. coli*, but rather the potential sources of fecal pollution that may contribute *E. coli*. Despite these limitations, this method may be useful for a rapid assessment of the possible sources of fecal pollution for a water body and are currently being applied to BST studies in Texas. Another example is the detection of optical brighteners used in laundry detergent using fluorometry. This approach can be used in real-time for the detection of leaking septic systems and sewage releases, is ideal for lakes and beach waters but obviously cannot identify other sources of fecal pollution.

Identification libraries consisting of thousands of isolates from different geographical regions in Texas have already been established for ERIC-PCR, PFGE, RiboPrinting, CSU and KB-ARA patterns. In addition, several thousand more *E. coli* isolates from source samples have been archived and are available to researchers. Library development is one of the most costly components of BST studies. It would be most economical to build upon the libraries already established in Texas. It is recommended that agencies use contractors that use BST methods that will strengthen and expand the current Texas library and follow previously approved standard operating procedures (SOPs) for performing analyses. However, further research is needed to determine if a regional library built from different projects using the same protocols may be useful for the identification of water isolates from other watersheds. That is, geographic and temporal stability of the existing *E. coli* library will need to be explored. Currently, the Di Giovanni laboratory at the El Paso Agricultural Research and Extension Center is cross-validating the libraries generated in the Lake Waco study and the San Antonio watershed study in an attempt to explore issues of geographical and temporal stability of BST libraries, refine library isolate selection and determine accuracy of water isolate identification. By selecting *E. coli* source isolates that are correctly identified in both watershed libraries, we hope to find more geographically universal and host-specific isolates, resulting in more accurate source tracking.

The infrastructure for BST work in Texas needs to be expanded for both library dependent as well as library independent methods. More laboratories with trained personnel and equipment are needed. This could be facilitated by the use of automated systems for BST analyses. In addition to the RiboPrinter, an automated system for repetitive element PCR (repPCR) using BOX primers (Diversilab, Athens, Georgia) has been developed and may be an alternative to ERIC-PCR. For just the *E. coli* isolates selected through cross-validation of existing libraries, funding is needed to develop a complete data set using BST techniques selected for use in Texas.

For future TMDL studies, an assessment phase using a “toolbox” approach is recommended. The assessment phase should include targeted monitoring of suspected pollution sources, use of library-independent methods to identify the presence of domestic sewage pollution and screening of water isolates from the new watershed against the existing library to determine the need for collection of local source samples and expansion of the library.

Recommended Approach for Bacteria TMDL and Implementation Plan Development

With the background provided by the preceding sections on BST and modeling, as well as extensive input from the expert advisory group, the task force recommends that TCEQ and TSSWCB implement the following integrated approach to the TMDL and I-Plan development.

The task force recognizes that no single process is appropriate for all bacteria impairments, given the variations in: (1) the severity of the bacteria impairments, (2) the complexity of watershed land uses and development, and (3) the interests of stakeholders and the regulated community affected. For these reasons, we propose a tiered approach that identifies alternate procedures to accommodate the site-specific factors that will emerge in each assessment. The three-tiered approach to developing bacteria TMDLs and I-Plans described in this section incorporates adaptive management, phased TMDLs and phased implementation to the extent allowable by EPA. The objectives of Tiers 1 and 2 are to ensure that each TMDL is developed using a scientifically credible, cost-effective process with strong stakeholder involvement. Tier 3 is designed to develop a feasible I-Plan, and, for some complex TMDLs, expands the information available for TMDL development. Figure 5 summarizes the three-tier approach.

Tier 1 should be required of all bacteria TMDLs to provide the minimum level of technical analysis and stakeholder input needed to make sound decisions regarding load reductions and allocations. Tier 2 provides a more in-depth and extensive assessment of the water body in question. We anticipate that it will provide sufficient scientific content and stakeholder involvement to develop most bacteria TMDLs. Tier 3 should provide additional information regarding bacteria sources and impacts of best management practices. We anticipate that for most contaminated water bodies Tier 3 activities will be limited to I-Plan development, though in some cases Tier 3 may be required for TMDL development.

TMDLs requiring Tier 3 could include: (1) those requiring large reductions in bacteria loads (e.g. >75 %), (2) those with highly uncertain and conflicting results, (3) those with large implementation costs or (4) those that have not obtained stakeholder acceptance. The decision to move to Tier 3 is strictly at the discretion of the TCEQ and TSSWCB, but with adequate scientific and stakeholder input.

The tiered framework presented here is intended to be flexible to ensure it best fits the complexity of the watershed sources, availability of data, degree of impairment and level of accuracy required.

TIER 1

Tier 1 is a one-year analysis required for all TMDLs. It provides for early stakeholder involvement, development of a comprehensive geographic information system of watershed information, surveys of potential bacteria sources, development of a load duration curve and analysis of the assembled information by agency staff, agency consultants and stakeholders.

1.1 - Stakeholder Involvement

TCEQ, with the TSSWCB and other key agencies, have been developing TMDLs in consultation with watershed-based stakeholder groups. The process includes extensive efforts to identify and involve diverse and sometimes competing interests. The task force believes it is essential to preserve and enhance these processes. Leaders within the watershed should be enlisted to participate at the outset of the project (after listing on the 303(d) list) and collaborate on all aspects of the TMDL development. County commissioners courts; soil and water conservation districts; community leaders; non-governmental environmental, agricultural and civic organizations; TPDES permit holders; cities and water districts (especially with MS4 permits); watershed landowners; and other potential contributors should form the basis for the stakeholder group. In most cases, the TCEQ should initiate a TMDL project with a planning meeting of state and local entities (such as TSSWCB, Texas Department of Agriculture [TDA], Texas Parks and Wildlife Department [TPWD], Texas Cooperative Extension, key municipalities, county commissioners and soil and water conservation districts) and the appropriate river authority to develop an initial outreach strategy whereby agency representatives will solicit the commitment and involvement at the local level of key leaders.

Figure 5: Recommended Three-Tier Approach for Bacteria TMDL Development

Tier 1 Analysis (T1) (one-year)
Required for all bacteria TMDLs.

1. Form TMDL stakeholder advisory group.
2. Develop comprehensive GIS inventory for watershed.
3. Implement source survey for watershed.
4. Calculate load duration curves (LDCs).
5. Analyze Tier 1 data with stakeholder advisory group.

Decision 1 (D1) *Are data and analysis adequate?*
Yes → Go to D2.
No → Go to T2.

Decision 2 (D2) *Are needed load reductions socially and economically attainable?*
Yes → Complete and submit draft TMDL for agency approval.
No → Complete and submit a draft TMDL that includes a recommended change in designated use (i.e. Use Attainability Analysis).

Tier 2 Analysis (T2) (one-to-two years)_
Implemented for most bacteria TMDLs. May be adequate for I-Plan development for non-controversial TMDLs.

1. Implement targeted monitoring to fill data gaps.
2. Perform library-independent BST and limited library-dependent BST analysis.
3. Develop simple LDC, GIS and/or Mass Balance Models.
4. Analyze Tier 2 data with stakeholder advisory group.

Decision 3 (D3) *Are data and analysis adequate?*
Yes → Go to D4.
No → Initiate a “phased TMDL” and go to T3.

Decision 4 (D4) *Are needed load reductions socially and economically attainable?*
Yes → Complete and submit draft TMDL (or I-Plan) for agency approval.
No → Complete and submit a draft TMDL that includes a recommended change in designated use (i.e. Use Attainability Analysis).

Tier 3 Analysis (T3) (two-to-three years)
Normally used for I-Plan development. May be required for development of complex “phased TMDLs.”

1. Assure extensive stakeholder involvement.
2. Implement extensive targeted monitoring.
3. Perform extensive library-dependent BST analysis.
4. Complete mechanistic modeling.
5. Analyze Tier 3 data with stakeholder advisory group.

Decision 5 (D5) *Are needed load reductions socially and economically attainable?*
Yes → Complete and submit draft I-Plan (or revise “phased TMDL”) for agency approval.
No → Complete and submit a draft TMDL that includes a recommended change in designated use (i.e. Use Attainability Analysis).

The identified stakeholder participants and agencies should be invited by TCEQ (or, when appropriate, TSSWCB and other participating organizations) for a kick-off meeting. The meeting will discuss the project goals, the existing water quality, relevant water quality standard(s) not met, the time line and process for TMDL development and what implementation strategies are typical for addressing bacteria impairments. Stakeholder participants should understand the complexity of the watershed, the uncertainty associated with bacteria monitoring and analysis and what may be required of the regulated community during implementation, as well as the typical voluntary or incentive-based strategies needed for implementation. Either at a kick-off meeting or soon after, the TCEQ (and TSSWCB) should discuss with stakeholders and seek consensus on the overall project's design, including the tools, models and monitoring that would be used in Tier 1 of the TMDL assessment. Attentive efforts to receive broad input, involvement and consensus should pay off in the end, particularly with groups representing entities that are not regulated point sources, to improve the water quality. Stakeholders can provide insight into sources and solutions that may not be apparent to those living outside the watershed. Since stakeholders will ultimately be responsible for helping achieve TMDL goals, it is appropriate that they be involved throughout TMDL development.

1.2 - Comprehensive Geographic Information System

A comprehensive geographic information system should be developed for the watershed, including available land use, elevation, soil, stream network, reservoir, road, municipality and satellite or aerial photographic information. In addition, locations of other relevant information (such as wetlands, sewage treatment plants, subdivisions, confined animal feeding operations, etc.) should be included for use by scientists, agencies and other stakeholders. In most cases, almost all data layers required for Tier 1 analysis can be obtained from readily available public sources. Locations of potential bacteria sources (identified in 1.3 below) should be incorporated into the GIS.

1.3 - Surveys of Potential Bacteria Sources

Conducting a potential source survey is an important Tier 1 activity. Texas and other states have conducted these surveys to better characterize the pollutant sources that contribute loadings that cause impairments. As with many efforts of this nature, there is a substantial range of costs and investigative activities that could occur, dependent on the project design, complexity of land uses and geographic size of the target watershed. For instance, in the Buffalo and White Oak Bayous in the Houston area, the TCEQ and its contractors spent several years and substantial funds to assure the watershed (with its intensive land use, dense population and hundreds of point sources) was adequately characterized.

The potential source survey should be representative of warm and cool seasons and, if possible, low and high flow conditions. The survey should be conducted by an integrated team including stakeholders, TPWD biologists, TDA/TCE personnel, Texas Department of State Health Services, TCEQ Regional Office staff, local governments and SWCD and TSSWCB personnel in order to identify all potential contamination sources. Point sources like wastewater treatment plants and industrial outfalls, nonpoint sources, stream sediment sources (especially those below wastewater outfalls) and other possible bacteria sources should be evaluated. According to a study by Harris County *E. coli* in fully disinfected WWTP effluent can regrow a thousand-fold over the course of four days. It is possible that in many effluent-dominated streams, regrowth is a major source of *E. coli*. To complete this evaluation, it will be important to examine permit compliance issues, residences and businesses on central sewage collection systems, septic systems and livestock and non-domestic animal concentrations.

1.4 - Data Analysis / Load Duration Curves

Note: For bacteria impairments in reservoirs or estuaries, the load duration curve method is not usually applicable.

The fourth component of Tier 1 includes analysis of ambient bacteria concentrations using statistical methods and LDCs. LDC development at this point in the process will use existing data and provide stakeholders insight into when exceedences occur, potential reductions needed, and potential sources. This will help stakeholders develop monitoring methodologies needed for the next tier. LDCs should be developed (using the methods described earlier in the document) for all sites having at least 24 bacteria data points (including at least three high flow points). For those sites with large data sets, only the most recent five years of data should be used. As additional data become available following targeted monitoring in Tier 2, this initial LDC should be updated. The analysis of the data should include an assessment of the degree of impairment, expressed as a percentage exceedance of the standard. This will help identify the course of action needed to address the impairment. In addition, this will provide some indication of the need for a UAA, particularly in areas where large exceedances of the criteria are unlikely to be resolved by revised criteria.

1.5 - Analysis of Tier 1 Information

Components 1.1 through 1.4 should be implemented simultaneously during the first year of TMDL development. As information from components 1.1 through 1.4 is collected, it should be shared with interested stakeholders, scientists and agency personnel. In addition to organizational meetings at the beginning of Year 1, at least one meeting with stakeholders should be held in the watershed approximately halfway through Year 1 to share information collected to that point. As the end of Year 1 approaches, accumulated data and recommendations of agency staff and consultants should be collected and shared with stakeholders. A meeting should be held in the watershed to discuss the data and recommendations of experts, and consensus should be sought regarding future activities.

At the meeting, consensus should be sought concerning whether data and analysis are adequate to develop a draft TMDL, including target reductions in bacteria loads and waste loads. If data and analysis from Tier 1 are not adequate, Tier 2, a one- to two-year period of additional data collection and analysis, should begin. If Tier 1 data and analysis are sufficient, the group must consider the question of whether the required reductions in bacteria waste loads and loads are socially and economically attainable. If they are attainable, a draft TMDL can be completed and submitted to the agencies for approval. However, in some cases, reaching the required waste load and load reductions may not be socially and economically attainable. In those cases, the group may reach consensus that the agencies should consider changing the designated use of the water body in order to meet alternative standards (see Figure 5).

A provisional TMDL should be drafted when a UAA is under way. A final TMDL may be required to comply with the new standard. In this case, the provisional TMDL should be adopted by the TCEQ and TSSWCB to meet the water quality standard in effect at that time and remain in place while standards issues are addressed. However, I-Plan development and implementation for these TMDLs should not proceed until the standards evaluation is completed. Once the standards are resolved, the provisional TMDL would be replaced by the final TMDL and an I-Plan developed.

TIER 2

If Tier 1 does not produce a consensus that data and analysis are adequate, the process should move to Tier 2, a one- to two-year effort to develop sufficient information to implement the needed TMDL or change the designated use of the water body. We recommend that Tier 2 include targeted monitoring to complement data collected in Tier 1, library-independent bacterial source tracking, statistical and mass balance modeling and development of a consensus draft TMDL.

2.1 - Targeted Monitoring

Agency personnel, expert consultants and stakeholders should develop a targeted monitoring plan to fill data gaps (for example, provide additional high flow samples or sample additional locations in the water body), evaluate the magnitude and impacts of possible waste loads or loads identified in Tier 1, and/or evaluate bacteria fate and transport within the water body. For example, point sources could be sampled at their outfalls. Additional sampling points more representative of the watershed or stream segment than public access points could be sought. Measurements of waste loads and loads could be made and substituted for literature values or estimates used in Tier 1. More intensive (biweekly or monthly) monitoring could be implemented for stream segments at greatest risk for fecal pollution.

2.2 - Library-Independent BST

To further assess bacteria sources, BST analysis should be conducted in conjunction with the targeted monitoring to determine if livestock, humans and/or non-domestic animals are contributing bacteria to the water body. Fifty to 100 samples should be analyzed using the library-independent PCR genetic test for the *Bacteroidales* markers for human, ruminants, horse and swine sources.

If sufficient funds are available, *E. coli* isolates from 50 to 100 different water samples should be analyzed using the BST methods described in the Tier 3 BST discussion and compared with isolates from the previously developed Texas *E. coli* source library to determine the need for development of a local source library (see component 3.2 below). These analyses are needed to confirm that the sources of *E. coli* and *Bacteroidales* are comparable. If these *E. coli* analyses are not done in Tier 2, they should be included in subsequent Tier 3 activities.

2.3 - Spatially Explicit Statistical and Mass Balance Modeling

Spatially explicit statistical models and/or mass balance models should be used in combination with the LDC developed in Tier 1 to provide multiple lines of evidence for bacteria sources. This report does not recommend specific spatially explicit statistical models or mass balance models. We consider that the quality of model calibration, input data quality and the experience of the modeling team are as important as the choice of model used. Therefore, we recommend that agency staff and their expert consultants evaluate the characteristics of the water body, its watershed and the data available for analysis, and then select the most appropriate model and modeling team.

The main value of LDC and mass balance models such as BLEST and BIT is in determining load reductions required to meet the water quality standard. Spatially explicit models such as Arc Hydro, SELECT or SPARROW should be used to estimate contaminant loads from various sources in a watershed.

Models should be run using the highest quality, readily available input data for the watershed. Every effort should be made to use measured loadings from wastewater treatment plants and other point and nonpoint sources. Data collected through the targeted monitoring in Tier 2.3 should be used to update the LDC as well as for providing the data needed to initialize, calibrate and validate the model(s) used. Updated LDCs should be developed (using the methods described earlier in the document) for all sites having at least 24 bacteria data points (including at least three high-flow points). At each step, confidence intervals for model inputs and outputs should be estimated and reported.

The principal reason for recommending that simpler spatially explicit statistical models and mass balance models be used in Tier 2 rather than more complex hydrologic/water quality models is that the simpler models should be more economical to implement. This may not be the case in the future as baseline simulations are developed by USDA with SWAT. If such baseline, partially calibrated models are available, agency personnel may choose to implement them for Tier 2 analyses.

2.4 - TMDL Development

Components 2.1 through 2.3 should be implemented simultaneously. As during Tier 1, at least one meeting with stakeholders should be held in the watershed approximately halfway through Tier 2 activities to share information about progress to date. As the end of Tier 2 approaches, a meeting should be held in the watershed to discuss the data and recommendations of experts, and consensus should be sought regarding future activities.

We anticipate that for most impacted segments, consensus will be reached by the end of Tier 2 to complete development a draft TMDL, including target reductions in bacteria loads and waste loads. If consensus is reached that Tier 2 data and analysis are sufficient, the group must consider whether the required reductions in bacteria waste loads and loads are socially and economically attainable. If the required reductions are attainable, a draft TMDL can be completed and submitted to the agencies for approval. However, if the required waste load and load reductions are not socially and economically attainable the agencies should consider conducting a Use Attainability Analysis (UAA) and changing the designated use of the water body in order to meet alternative standards (see Figure 5).

A provisional TMDL should be drafted when a UAA is under way. A final TMDL may be required to comply with the new standard. In this case, the provisional TMDL should be adopted by the TCEQ and TSSWCB to meet the water quality standard in effect at that time and remain in place while standards issues are addressed. However, I-Plan development and implementation for these TMDLs should not proceed until the standards evaluation is completed. Once the standards are resolved, the provisional TMDL would be replaced by the final TMDL and an I-Plan developed.

If Tier 2 data and analysis are not sufficient to reach consensus, a "phased TMDL" should be completed. TCEQ staff (with TSSWCB, as appropriate) will be responsible for deciding when consensus cannot be achieved.

The phased TMDL should consist of draft "phase 1" TMDL based on data gathered during Tiers 1 and 2. In addition, the draft "phase 1" TMDL should include a commitment to collect and analyze additional data during Tier 3 I-Plan analysis. This approach allows implementation of the TMDL (beginning with BMPs most socially and economically acceptable) while additional data are collected to reduce uncertainty. The TMDL may be reopened to consider new information that suggests that the WLA or LA should be modified. If standards are not met by target dates established by the stakeholders, increasingly stringent measures should be implemented in a phased manner over a period of years.

TIER 3

Tier 3 analyses will normally be required for development of I-Plans and, if necessary, phased TMDLs. Tier 3 should normally consist of a two- to three-year effort consisting of extensive watershed monitoring, library-dependent bacteria source tracking, mechanistic hydrologic modeling and I-Plan or phased TMDL development.

We recommend the use of "adaptive management" for the I-Plan process. During the multi-year course of development and execution of an I-Plan, changes in water quality, infrastructure and agency policies can be expected. As a result, the I-Plan or TMDL should be subject to revision as conditions change. Agency personnel and stakeholders should also remain sensitive to the need for identifying and implementing cost-effective BMPs. Costly BMPs can have adverse economic impacts on stakeholders and taxpayers, and they should be avoided if possible, especially when good scientific evidence of their effectiveness is lacking.

3.1 - Watershed Monitoring

Extensive watershed monitoring should be initiated to identify bacteria sources, quantify loading and provide the data needed for calibration and validation of watershed scale mechanistic models. Watershed monitoring should be targeted to fill information gaps identified in Tiers 1 and 2. At a minimum, monthly sampling for one year should be conducted, although greater frequency (weekly) and duration (two years) is preferred. Monitoring should include measurement of bacteria levels and flows from all wastewater treatment plants and other point sources that are suspected of contributing significant bacteria loads. Sampling sites should be carefully selected, and samples should represent spatial variability, seasonal fluctuations and typical (low, medium and high) flows. A minimum of 100–200 isolates from approximately 40 water samples should be collected in conjunction with the watershed monitoring effort for library-dependent BST analysis. These samples should be collected at carefully selected and representative sites, seasons and flow conditions (see 3.2 below).

3.2 - Library Dependent Bacteria Source Tracking

The isolates collected during the watershed monitoring described in component 2.2 (above) should first be analyzed using ERIC-RP, ERIC-ARA or CSU-ARA combination methods. Isolates should first be identified using the Texas Source Library. If the Texas Source Library does not provide 80% identification then a local library should be developed using *E. coli* isolates from known sewage and animal sources. The sampling design should be determined using data from the component 2.2 assessment.

At least 300 *E. coli* colonies from approximately 100 known fecal samples should be characterized by the selected combination method (i.e. ERIC-RP, ERIC-ARA, CSU-ARA). The *E. coli* isolates obtained from ambient water samples should be characterized using the selected method. DNA patterns of those isolates should be compared to the individual watershed *E. coli* source library as well as Texas library and identified to cattle, other livestock, avian and non-avian non-domestic animals, domestic sewage and pet sources. Identified sources and unknown sources should be expressed as percentages of total isolates with appropriate confidence intervals.

3.3 - Mechanistic Hydrologic / WQ Modeling

For Tier 3 analyses, a mechanistic hydrologic water quality model or combination of models (such as HSPF, SWAT, SWMM and/or WASP) should be used to model watershed hydrology and fate and transport of *E. coli* within the watershed. The main value of these detailed models is that they allow for spatial and temporal analysis of the effectiveness of different best management practices in improving in-stream water quality. The selected model(s) should be run using the highest quality, readily available input data for the watershed.

The model(s) should be calibrated and validated for flows using long-term weather and stream flow gauges within (or near) the targeted water body. Once the model(s) are calibrated and validated for flow, baseline *E. coli* loads and concentrations should be calibrated and validated using monitoring data previously collected from the impacted segment. Finally, recommended best management practices (BMPs) identified by the stakeholder committee and/or cooperating agencies should be evaluated for their impacts on bacteria loads. At each step, confidence intervals for model inputs and outputs should be estimated and reported.

Every effort should be made to use measured loadings from wastewater treatment plants and other point and nonpoint sources for model calibration. This caution is particularly important if the effectiveness of BMPs is not well understood or monitored. Where effluent limits are specified as BMPs rather than loads that can be verified (as in the case of NPDES-regulated municipal and small construction storm water discharges), monitoring or other scientifically acceptable BMP performance data should be obtained to assess if the expected load reductions attributed to the BMP are achieved. Otherwise, adaptive management will be limited by our understanding of BMP effectiveness.

3.4 - IP-Plan and Phased TMDL Development

We anticipate that in most cases Tier 3 data collection and analysis will be used for IP-Plan development. However, for some complex and/or controversial water bodies, Tier 3 assessments will be required for phased TMDL development.

As pointed out above, we recommend the use of “adaptive management” for the I-Plan process. During the multi-year course of development and execution of an I-Plan, changes in water quality, infrastructure and agency policies can be expected. As a result, the I-Plan should be subject to revision as conditions change. We recommend that TCEQ identify a watershed coordinator to facilitate the communication, education and coordination needed during I-Plan development, revision and execution.

Adaptive management of I-Plans should facilitate progress toward achieving water quality goals while using new data and information to reduce uncertainty and adjust implementation activities. Adaptive management can include immediate implementation of BMPs, success monitoring, use of improved monitoring data and modeling, new experimental results and revision of the implementation plan.

Phased TMDLs are an example of the adaptive implementation approach because each new phase utilizes new information to reevaluate the original TMDL. However, even for TMDLs where there is little uncertainty regarding the loading capacity of the water body and the necessary load reductions, an adaptive implementation approach can be a useful tool. Implementation of TMDLs can take many years, and uncertainty about the effectiveness of implementation activities usually exists. Follow-up monitoring addresses uncertainty in the efficacy of implementation actions and can provide assurance that implementation measures are succeeding in attaining water quality standards, as well as in inform the ongoing TMDL implementation strategy. If adaptive implementation activities reveal that TMDL loading capacity needs to be changed, the revision may require EPA approval. In most cases, however, adaptive implementation is not anticipated to lead to the re-opening of a TMDL. Instead, it is a tool used to improve implementation strategies.

The I-Plan describes the actions that the TCEQ, TSSWCB and the project's stakeholders will undertake to achieve restoration of the water body's use. Implementation strategies specify actions to meet the load allocations assigned to all point sources and nonpoint sources identified in the TMDL report. Action strategies may be selected from a menu of possible measures based on an evaluation of feasibility, costs, support, timing and other factors. Activities may be implemented in phases with evaluation of progress and success before proceeding to a subsequent phase.

In addition to the actions taken to reduce pollutant loads from sources, an I-Plan includes provisions to track the progress of the plan using both implementation and water quality indicators. The I-Plan identifies in-stream monitoring at specific locations and targets constituents that will be used to evaluate whether the water quality criterion is achieved. It includes tracking using a schedule identified in the I-Plan for evaluating whether administrative actions undertaken to improve water quality actually occurred.

An I-Plan includes a review strategy that will consider when and if the I-Plan needs to be revised, or as mentioned earlier, whether a subsequent phase of implementation is needed. The review strategy implements adaptive management into the planning process by providing decision points in the process for such consideration. The review strategy accounts for unexpected changes in implementation of controls. In some special circumstances, the I-Plan may include strategies to evaluate the underlying water quality standard and its appropriateness as a goal driving implementation. Recommended changes to a standard could drive the need to re-evaluate and modify the TMDL itself.

Communication is necessary to ensure stakeholders understand the I-Plan and the progress that is being made to restore water quality conditions. The TCEQ disseminates information derived from tracking I-Plan activities to watershed stakeholders and others.

Agency personnel and stakeholders should also remain sensitive to the need for identifying and implementing cost-effective BMPs the effectiveness of which can be verified. Costly BMPs can have adverse economic impacts on stakeholders and taxpayers, and should be avoided if possible, especially when good scientific evidence of their effectiveness is lacking.

Research and Development Needs

This section, coordinated by Drs. Larry Hauck and George Ward, summarizes research and development needed in the next three to five years to improve the tools and methods available to TCEQ and TSSWCB for bacteria TMDL and I-Plan development. These research and development needs may be generally considered to be motivated by the need to quantify and reduce uncertainties in the measurement, identification and modeling of bacterial contaminants.

In previous sections, the diversity of bacteria sources within watersheds and the complexity of their proliferation and movement on the landscape and in receiving waters have been discussed. There are unavoidable inaccuracies in the depiction of the origin, fate and transport of environmental indicator bacteria within fate and transport models, and these represent common sources of uncertainties associated with the load allocation process of a TMDL and its subsequent I-Plan development. Broadly, uncertainties may be reduced by efforts along two parallel paths: (1) refinement of kinetic- and transport-type input parameters used in the preferred models to be applied in Texas and (2) reformulation of kinetic processes in these same models to better represent the present state of understanding of bacteria fate and transport. Laboratory and field studies in combination with model enhancements will be needed in these efforts to reduce uncertainties. BST methods can strongly support the TMDL process, and additional research and development in this arena is also anticipated to be important in reducing uncertainties and providing for improved tools and methods.

Finally, it is recommended that TCEQ and TSSWCB form a work group, in addition to the Task Force, whose focus would be to create a blueprint for a successful stakeholder process. Such a blueprint could be used by staff of both agencies statewide in TMDL, I-plan and watershed protection plan processes. This work group would address stakeholder group membership, attendance at meetings and communication to stakeholders. In addition, it would evaluate the inclusion of state and local agencies on stakeholder groups in order to ensure TMDL and other regulatory issues are addressed in a manner appropriate to the relevant authority.

The specific research and development needs reported herein were accumulated based on the collective expertise of Task Force members and Expert Advisors, recommendations from the Texas A&M Bacteria Roundtable Discussion of August 10, 2006, studies reported in Rifai et al. (2005), and an overview report on bacteria fate and transport modeling (Benham et al., 2006).

Characterization of Sources

Often a high level of uncertainty exists in the specification of bacteria sources within fate and transport models. Because of the numerous sources of fecal bacteria and the diversity of delivery mechanisms of the bacteria to receiving waters, a broad spectrum of research items will provide useful information.

- Studies to quantify species-specific bacteria production in feces and to measure the variability of this production. There are numerous mammalian and avian species (human, pet, livestock and non-domestic animals), all of which shed fecal bacteria. Within these proposed studies, focus is suggested on dominant and relevant species. While bacteria content of feces has been reported in literature for some species and has been summarized in some reports used in TMDL development, often this information has not been the focus of the reported research and therefore has not undergone thorough peer review. Further, some indications exist that fecal bacteria content may be related to latitude, elevation, diet and water source, which increases the anticipated variability of the data.
- Studies to quantify behavioral patterns of important mammalian and avian species, such as feral hogs. These studies would entail investigations for important species of the fraction of time spent in the water, preferential defecation locations (herding and flocking behavior), and other factors that impact location of feces deposition.

- Studies to improve methods of estimating animal densities in watersheds. Estimations of livestock and non-domestic animal densities in a watershed are often based on limited data and county-level data, and potentially there may be no existing data for some important sources of fecal bacteria (e.g., feral hogs, coyote, rodents and migratory birds). Improved methods are needed to optimize use of existing data to quantify source densities and to provide means of estimating pet, livestock, and non-domestic animals densities for species for which there is no or limited information. These improved methods could include integration of GIS land use and land cover with various types of census data, enhanced stakeholder involvement and detailed sanitary surveys, and other methods that optimize use of existing data and watershed specific resources and knowledge.
- Studies to improve characterization of bacteria loadings from WWTPs and sanitary sewer collection systems. WWTPs are required to disinfect their effluents using chlorination or other equivalent methods (e.g., ultraviolet radiation), and under conditions of proper operation bacteria loads are typically low from such facilities. However, under less than optimal conditions, WWTPs can directly discharge significant bacterial loads directly into receiving waters. Less than optimal conditions may occur because of wet weather, upsets in operating conditions, etc. Regrowth of bacteria relative to the completeness of disinfection is another area of focus worthy of more study. Regrowth and reactivation of bacteria after the disinfection process of WWTPs effluent appears to be a research topic of some concern within Texas and, in particular, Harris County where existing research is occurring on this subject in effluent dominated receiving streams. Quantification of fecal bacteria concentrations in the effluent of WWTPs will require sampling of facilities of various permitted capacities, different operational conditions and varying ages over a wide range of environmental and operational conditions. A related facet of bacteria loading is associated with sanitary sewer collection systems. Studies to quantify frequency of and conditions causing overflows (e.g., wet weather, grease and rags) from sanitary sewer systems and associated bacteria loadings can provide important information to models of urban areas.

- Studies to quantify failure rates of on-site sewage facilities (OSSFs). Failing OSSFs and even straight pipe discharges can be an important contribution of bacteria loading to some receiving waters. Local information at the county- and city-level will often be important in estimating failed OSSFs in a watershed. However, state- or regional-level statistical analyses relating failure rates to income level, education, age of communities, soil types, rainfall and physiographic region will provide additional support and defense of estimates regarding failure rates and bacteria loadings from OSSFs. As a starting point of these studies, a 2001 study funded by the Texas On-Site Wastewater Treatment Research Council (Reed, Stowe & Yanke, LLC, 2001) provides regional information on reasons for and magnitude of malfunctioning OSSFs.
- Studies to quantify bacteria (especially indicator bacteria such as *E. coli*) production/shedding from non-animal sources, such as mulch, gardens or other organic-rich environments.
- Studies to determine sources of the high concentration of indicator bacteria in rainfall runoff from a spectrum of land uses that might be anticipated to contain low concentrations of bacteria, (e.g., parking lots, streets, building roofs).
- Studies on pathogen sources and forms in stormwater. Research is needed on the sources of pathogenic bacteria in stormwater, the relationship of pathogenic bacteria to indicator bacteria in stormwater as compared to the relationship in such sources as human sewage and the human health significance of the pathogenic bacteria forms found in stormwater.
- Studies to better define indicators and disease risk for water bodies without focused areas of frequent swimming and contact recreation. The original EPA studies to identify indicator bacteria criteria to protect contact recreation use were conducted in lakes with designated swimming areas and nearby wastewater discharge points (EPA, 1986). Criteria development is needed for water bodies without focused or designated areas where swimming and contact recreation use are infrequent. Such water bodies would more likely involve recreational use with incidental contact during boating and wading activities.

Characterization of Kinetic Rates and Transport Mechanisms

Quantification of production, mobilization and movement of fecal bacteria from the landscape to receiving waters and the subsequent fate and transport of these bacteria in receiving waters is addressed by some comprehensive hydrologic/water-quality models as well as simpler *ad hoc* models (e.g., mass balance methods). In many instances, the scientific understanding of relevant processes concerning fate and transport on the landscape and in receiving waters is primitive, and in other instances, this scientific understanding exceeds the representation of those processes in existing models. Note that buildup (i.e., accumulation and proliferation) and mobilization of bacteria on the landscape will also be considered under this loose definition of fate and transport. Within this subsection, the focus will be upon possible studies to enhance the understanding of fate and transport processes, and within the next subsection, potential enhancements to hydrologic/water-quality models will be discussed. This artificial separation, however, should not be taken to mean that the empirical data collection and analyses designed to better understand physical, chemical and biological processes important to landscape and receiving water fate and transport of fecal bacteria can occur in the absence of interaction with model enhancement efforts. On the contrary, such interactions are encouraged and are necessary to the overall success of improving our TMDLs and I-Plans.

- Studies to quantify buildup and mobilization of fecal bacteria from the landscape. The release of fecal bacteria during rainfall-runoff events is a function of many processes antecedent to the event (e.g., rates and timing of manure and feces deposition, *in situ* die-off rates, growth, etc.) and activities during the event (e.g., rainfall duration and intensity and transport processes). Studies that increase understanding of the processes and factors determining bacteria buildup and mobilization and that provide quantification of those processes and factors are needed to enhance our understanding of mechanisms delivering bacteria to receiving waters. These studies can include different land uses (e.g., low-density residential and surface applied manure application fields, to name but two) and could also include investigations of important transport mechanisms such as surface mobilization and runoff and subsurface movements, including preferential pathways.

- Studies to identify dominant environmental factors that affect bacterial transport in landscapes (e.g., vegetative cover, soil type, temperature, etc.) and persistence and survival of bacteria in soil.
- Studies to quantify bacteria die-off phases in receiving waters. While bacteria die-off is generally assumed to follow Chick's law, experimental data indicate that fecal bacteria often do not follow this law and that die-off occurs in various phases. Further, die-off (and possibly regrowth) during these phases is further complicated by such factors as 1) whether the bacteria are planktonic, attached to suspended sediment, or re-suspended from bed sediments and 2) water temperature, sunlight intensity and levels of nutrients and suspended solids present. Further research to identify and define bacteria die-off phases and to mathematically describe die-off under a variety of conditions will improve our knowledge base on bacteria persistence in receiving waters. Instream regrowth of bacteria under various sediment, nutrient, occurrences of WTTP effluent and water temperature conditions is an additional important consideration under the broad category of bacteria die-off. Harris County is involved in a study on die-off and regrowth of bacteria from WWTP effluents, and any additional studies in this area should be coordinated with that ongoing study.
- Studies to identify dominant environmental factors that affect bacterial transport in streams (e.g., physical and chemical composition of stream waters [pH, total suspended solids, total dissolved solids, nutrients, etc.], temperature, etc.).
- Studies to provide better understanding of spatial and temporal distribution of instream bacteria conditions under various environmental conditions. The State's existing monitoring programs provide insufficient information to quantify spatial and temporal distributions of fecal bacteria at the time scales typically applicable in TMDLs. These time scales may in some instances be less than a day. Intensive spatial and temporal sampling of selected streams under various conditions (e.g.,

rainfall-runoff and dry conditions, high and low water temperatures) could enhance our basic understanding of bacteria issues within the state.

- Studies to quantify suspended bacteria in stream water column and deposited bacteria in stream sediments. Resuspension of bacteria from sediments to water column during peak flows and streambed erosion should be studied as well as, studies to improve understanding of sediment contributions to water-column bacteria levels. Settling of bacteria to sediments during periods of low turbulence and re-suspension of sediments and associated bacteria during conditions of high turbulence are recognized fate and transport processes. Studies are needed to better understand and quantify the interactions of the water column and sediments from the perspective of bacteria fate and transport dynamics in Texas streams and tidal systems.
- Determination of acceptable default inputs which can be used in model development and application. An initial set of inputs representing reasonable estimates of these processes needs to be proposed and agreed upon by the participating agencies. Initially these values should be taken from available literature and as time progresses may be changed to reflect recent research developments.

Enhancements to Bacteria Fate and Transport Models

Hydrologic/water quality models and some of the simpler models that partially incorporate mechanistic processes could benefit from improvements to their fate and transport processes.

- Enhancements to allow better representation of bacteria life cycle and processes. With support from the previously mentioned experimental studies on characterization of bacteria fate and transport, existing models can benefit from improvements and modifications in their representation of bacteria life cycles and processes.

- Enhancements to allow better representation of fate and transport processes. Again, with support from experimental studies, benefits to selected bacteria models would result from improvements in their representations of 1) sorption and bacteria release processes on the landscape and in receiving waters, 2) die-off and regrowth, 3) other fate and transport processes, and 4) effects of various environmental factors (e.g., temperature, light intensity, pH, etc.) on growth and die-off.

- Development of a spatially-explicit tool that will assess bacterial sources, distribute estimated loads to the land as a function of land use and source type, and generate bacterial load input parameters for watershed-scale simulation. This tool can build upon existing and under-development tools, such as SELECT, SPARROW, BLEST and BIT, among others previously mentioned in the Bacteria Fate and Transport Model section.

- Studies to improve linkages of BST and allocation modeling. A stand-alone spatially explicit load allocation tool's results can be validated with BST data or vice versa. Research is needed to determine benefits of linking BST and allocation modeling. At least two questions need to be addressed by these studies. Can BST and modeling be linked in a manner the benefits either TMDL load allocation or I-Plan development? If there were benefits from such linkage, how would that linkage occur?

Bacteria Source Tracking

Within the section on BST, a few areas of research and development were mentioned, and these are repeated below with some additional research items.

- Determine a reasonable expectation for the level of source identification by BST. For example, can BST methods reliably identify to the individual animal species level or is a coarser cut all that is reasonable (e.g., separation into categories of sewage, livestock and non-domestic animals)?

- Investigation and refinement of library-independent BST methods to assist in the TMDL process, and determine which library-independent BST method or methods are best suited for Texas TMDL development and implementation.
- Continue investigations into the most promising library-dependent BST methods, and continue research into promising combinations of such methods.
- Investigate the usefulness of a regional known-source library for BST library-dependent methods. Geographic and temporal stability of BST libraries is not well understood. Additional studies are needed to address these issues and to make library-dependent BST techniques better tools. These studies should build upon and not duplicate ongoing studies in Texas that are cross-validating the libraries generated in the Lake Waco study and the San Antonio watershed study in an attempt to explore issues of geographical and temporal stability of BST libraries, refine library isolate selection, and determine accuracy of water isolate identification.
- Define appropriate ambient water sampling protocol to provide desired statistical confidence with BST findings. For example, in some past studies, 10 to 12 monitoring events are conducted at each station; for each ambient water monitoring event five water samples are collected at a station with one to two minutes between collection of each sample; and two randomly selected bacteria isolates from each cultured sample are subsequently identified using BST methods (e.g., TIAER et al., 2005). Is this level of sampling adequate for the subsequent statistical characterization of sources and determination environmental conditions influencing source contributions (often wet versus dry weather conditions)?
- What is an appropriately sized watershed or sub-watershed for BST sampling design? Beyond what size drainage area do BST results tend to show a wide mix of contributions from all species in a library? Are there factors such as the degree of land development or anthropogenic activity that determine an appropriate drainage size to optimize source discrimination?

These listed items can be developed into a series of studies to advance BST methods and the utility of these methods for Texas bacteria TMDLs.

Determination of Effectiveness of Control Measures

Another research area directly supporting bacteria TMDL and I-Plan development entails determination of effectiveness of various control practices and best management practices to remove and reduce bacteria loadings and concentrations from sources. Success of an I-Plan and willingness of individuals and entities to adopt various control practices and best management practices may be greatly enhanced in the presence of scientifically conducted studies showing efficacy of various practices under a variety of conditions (e.g., rainfall patterns, landscape position, etc.).

- Studies to determine efficiency of agricultural best management practices. Prominent BMPs for bacteria load reduction from agriculture should be evaluated to determine their efficiencies under a variety of environmental conditions. Specifically, those conditions that exceed the ability of these measures to function should be identified.
- Studies to determine efficiency of urban control practices. Prominent control practices for achieving bacteria load reduction from urban and suburban areas should be evaluated to determine their efficiencies under a variety of environmental conditions. Specifically, those conditions that exceed the ability of these measures to function should be identified.

Quantification of Uncertainty and Communication of Risk

Because of the nature of the pollutant, bacteria TMDLs and I-Plans, while using best available information and applying accepted methods of determination, will contain uncertainties. Even if sources of error in field sampling, kinetics modeling and numerical implementation could be eliminated, there is a core uncertainty associated with the "noise" in the bacterial determination methodologies themselves, as indicated by imprecision in replicate measurements. The spectrum of those involved in bacteria TMDLs (including, to name a few, the regulated community, environmental regulatory agencies, engineers and scientists performing technical evaluations and those providing assistance to unregulated sources) are cognizant of the degree of uncertainty in bacteria TMDL development. Efforts to reduce this uncertainty and to provide heightened defensibility of the process are both worthy and necessary goals, and the research and development studies enumerated above will provide significant advances toward realization of those goals. However, the brutal reality is that over the near future uncertainties — that are sometimes quite large compared to other water-quality parameters — will exist in bacteria TMDL and I-Plan development. Hence, the need exists for one other potential area of research — quantification of uncertainty and the associated communication of risk resulting from the uncertainty associated with TMDLs and I-Plans.

- Studies to quantify uncertainty. A body of literature exists on uncertainty and how to incorporate uncertainty analysis, typically via Monte Carlo techniques, into environmental models. In fact, the latest version of SWAT contains a feature allowing the performance of uncertainty analysis. Some other models employed in TMDL load allocation development do not contain this feature. Knowledge of how to incorporate uncertainty into the TMDL and implementation process can be obtained from existing literature. That knowledge can be transferred to the unique characteristics of the Texas TMDL process for purposes of developing methods to allow quantification of uncertainty.

- Development of proper means to communicate the risks arising from uncertainties in the TMDL process. This communication can assist in overcoming roadblocks that can dampen stakeholder enthusiasm or become excuses for no action in reducing bacteria loadings. Again, a body of literature (e.g., Morgan and Henrion, 1990) and experience exists on risk communication that can be exploited for application to the Texas situation. Successful risk communication can assist in overcoming the uncertainties within bacteria TMDLs and I-Plans and assist in moving the process toward the desired outcome of restored and improved water quality. Areas of study could review lessons learned, examples in the United

States of successful TMDL implementation in spite of uncertainty, and identifying positive paths forward in areas of known difficulties in present and recent bacteria TMDLs that include uncertainty. Results could be implemented to enhance interactions with stakeholders with a focus on the development of best mechanisms of risk communication.

Prioritization of Research and Development Activities

The activities briefly described above are not exhaustive, but these activities do provide indications of major areas where research and development advancements can benefit TMDL and I-Plan development. Additionally, this listing of needs helps to inform the decision makers at the TCEQ and TSSWCB of the current state of the science and techniques. These needs encompass a breadth of activities that most certainly will exceed the resources available for the successful performance of all potential studies. Purposefully, within this section no attempt has been made to prioritize these research and development activities. The selected activities need to be focused to support management decisions, which provide a broad direction to the TMDL and I-Plan processes. For example, such broad direction could include which models are to be supported in the near term for TMDL development. Also, known technical needs can define and inform prioritization of research and development needs that will, over the next several years, improve the tools and methods available to TCEQ and TSSWCB for bacteria TMDL and I-Plan development. Review of existing literature will be an important first step in further defining some of the possible research and development activities enumerated above under several research headings: characterization of sources, characterization of kinetic rates and transport mechanisms, enhancements to bacteria fate and transport models, BST, determination of effectiveness of control measures, and quantification of uncertainty and risk communication.

Some Expert Advisory members voiced certain research preferences during the conference call process used to refine and develop this final report. Those research topics preferentially voiced by certain Expert Advisory members include the following: 1) the issue of regrowth of bacteria in WWTP effluents and in effluent dominated streams, 2) better quantification of species-specific bacteria production and loadings that used as input to many bacteria fate and transport models, 3) integration of fate and transport models and BST methods within the TMDL and I-Plan process, and 4) improved understanding of the accuracy and precision of BST methods. This list of preferred research topics is included within the more refined lists provided previously within this report section. It should be noted that these four research topics only reflect the views of certain Expert Advisory members and do not necessarily reflect the views of all Expert Advisory members and the Task Force members.

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Appendix 1: Bacteria TMDL Task Force Members and Expert Advisors

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Appendix 2: Models Used in Bacteria TMDLs as Described in EPA Publications

HSPF: Hydrological Simulation Program—Fortran

HSPF is a comprehensive watershed-scale model developed by EPA. The model uses continuous simulation of water balance and pollutant buildup and washoff processes to generate time series of runoff flow rates, as well as pollutant concentration at any given point in the watershed. Runoff from both urban and rural areas can be simulated using HSPF; however, simulation of CSOs is not possible. Because of the comprehensive nature of the model, data requirements for HSPF are extensive and using this model requires highly trained personnel (EPA 2002b).

SWMM: Storm Water Management Model

SWMM is a comprehensive watershed-scale model developed by EPA. It can be used to model several types of pollutants on either a continuous or storm event basis. Simulation of mixed land uses is possible using SWMM, but the model's capabilities are limited for rural areas. SWMM can simulate loadings from CSOs. The model requires both intensive data input and a special effort for validation and calibration. The output of the model is time series of flow, storage and contaminant concentrations at any point in the watershed (EPA 2002b).

STORM: Storage, Treatment, Overflow, Runoff Model

STORM is a watershed-loading model developed by the U.S. Army Corps of Engineers for continuous simulation of runoff quantity and quality. The model was primarily designed for modeling storm water runoff from urban areas, but it also can simulate combined sewer systems. It requires relatively moderate to high calibration and input data. The simulation output is hourly hydrographs and pollutographs (EPA 2002b).

CE-QUAL-RIV1: Hydrodynamic and Water Quality Model for Streams

CE-QUAL-RIV1 is a dynamic, one-dimensional model for rivers and estuaries consisting of two codes — one for hydraulic routing and another for dynamic water quality simulation. CE-QUAL-RIV1 allows simulation of unsteady flow of branched river systems. The input data requirements include the river geometry, boundary conditions, initial in-stream and inflow boundary water quality concentrations and meteorological data. The model predicts time-varying concentrations of water quality constituents (EPA 2002b).

Predicting the response of lakes and estuaries to pathogen loading requires an understanding of the hydrodynamic processes. Shallow lakes can be simulated as a simplified, completely mixed system with an inflow stream and an outflow stream. However, simulating deep lakes or estuaries with multiple inflows and outflows that are affected by tidal cycles is not a simple task. Pathogen concentration prediction is dominated by the processes of advection and dispersion, and these processes are affected by the tidal flow. The size of the lake or the estuary, the net freshwater flow, and wind conditions are some of the factors that determine the applicability of the models. The lake and estuary models are briefly described below (EPA 2002b).

WASP5: Water Quality Analysis Simulation Program

WASP5 is a general-purpose modeling system for assessing the fate and transport of pollutants in surface water. The model can be applied in one, two or three dimensions and can be linked to other hydrodynamic models. WASP5 simulates the time-varying processes of advection and dispersion while considering point and nonpoint source loadings and boundary exchange. The water body to be simulated is divided into a series of completely mixed segments, and the loads, boundary concentrations, and initial concentrations must be specified for each state variable (EPA 2002b).

CE-QUAL-ICM: A Three-Dimensional Time-Variable Integrated-Compartment Eutrophication Model

CE-QUAL-ICM is a dynamic water quality model that can be applied to most water bodies in one, two or three dimensions. The model can be coupled with three-dimensional hydrodynamic and benthic-sediment model components.

CE-QUAL-ICM predicts time-varying concentrations of water quality constituents. The input requirements for the model include 140 parameters to specify the kinetic interactions, initial and boundary conditions, and geometric data to define the water body to be simulated. Model use might require significant expertise in aquatic biology and chemistry (EPA 2002b).

EFDC: Environmental Fluid Dynamics Computer Code

EFDC is a general three-dimensional hydrodynamic model developed by Hamrick (1992). EFDC is applicable to rivers, lakes, reservoirs, estuaries, wetlands and coastal regions where complex water circulation, mixing and transport conditions are present. EFDC must be linked to a water quality model to predict the receiving water quality conditions. HEM-3D is a three-dimensional hydrodynamic eutrophication model that was developed by integrating EFDC with a water quality model. Considerable technical expertise in hydrodynamics and eutrophication processes is required to use the EFDC model (EPA 2002b).

CE-QUAL-W2: A Two-Dimensional, Laterally Averaged Hydrodynamic and Water Quality Model

CE-QUAL-W2 is a hydrodynamic water quality model that can be applied to most water bodies in one dimension or laterally averaged in two dimensions. The model is suited for simulating long, narrow water bodies like reservoirs and long estuaries, where stratification might occur. The model application is flexible because the constituents are arranged in four levels of complexity. Also, the water quality and hydrodynamic routines are directly coupled, allowing for more frequent updating of the water quality routines. This feature can reduce the computational burden for complex systems. The input requirements for CE-QUAL-W2 include geometric data to define the water body, specific initial boundary conditions and specification of approximately 60 coefficients for the simulation of water quality (EPA 2002b).

QUAL2E: The Enhanced Stream Water Quality Model

QUAL2E is a steady-state receiving water model. The basic equation used in QUAL2E is the one-dimensional advective-dispersive mass transport equation. Although the model assumes a steady-state flow, it allows simulation of diurnal variations in meteorological inputs. The input requirements of QUAL2E include the stream reach physical representation and the chemical and biological properties for each reach (EPA 2002b).

TPM: Tidal Prism Model

TPM is a steady-state receiving water quality model applicable only to small coastal basins. In such locations, the tidal cycles dominate the mixing and transport of pollutants. The model assumes that the tide rises and falls simultaneously throughout the water body and that the system is in hydrodynamic equilibrium. Two types of input data are required to run TPM. The geometric data that define the system being simulated are the returning ratio, initial concentration and boundary conditions. The physical data required are the water temperature, reaction rate, point and nonpoint sources and initial boundary conditions for water quality parameters modeled (EPA 2002b).

BASINS: Better Assessment Science Integrating Point and Nonpoint Sources

BASINS system Version 2.0, with the Nonpoint Source Model (NPSM), can be used to predict the significance of fecal coliform sources and fecal coliform levels watersheds. BASINS is a multipurpose environmental analysis system for use in performing watershed and water quality-based studies. A geographic information system (GIS) provides the integrating framework for BASINS and allows for the display and analysis of a wide variety of landscape information (e.g., land uses, monitoring stations, point source discharges). The NPSM model within BASINS simulates nonpoint source runoff from selected watersheds, as well as the transport and flow of the pollutants through stream reaches. Through calibration of model parameters and representation of watershed sources, the transport and delivery of bacteria to watershed streams and the resulting in-stream response and concentrations were simulated (EPA 2002a).

Models Used in Bacteria Source Tracking as Described in EPA Publications References

EPA (Environmental Protection Agency). 2002a. *Protocols for Developing Pathogen TMDLs*. EPA 841-R-00-002.

EPA (Environmental Protection Agency). 2002b. *National Beach Guidance and Required Performance Criteria for Grants*. June 2002.

Appendix 3: EPA Bacteria TMDL Guidelines

This section provides an overview of several EPA guidance documents related to the use of models and BST to develop bacteria TMDLs. Components of a TMDL include (1) Problem Statement, (2) Numeric Targets, (3) Source Assessment, (4) Linkage Analysis, (5) Allocations and (6) Monitoring/Evaluation Plan (for phased TMDLs). Because BST and modeling are primarily used to assist with source assessment, linkage analysis and allocations, this chapter will focus primarily on these components of the TMDL (EPA 2002a).

Overall, EPA allows a great deal of flexibility in bacteria TMDL development as long as the method selected adequately identifies the load reductions or other actions needed to restore the designated uses of the water body in question. There are trade-offs associated with using either simple or detailed approaches. These trade-offs, along with site-specific factors, should always be taken into account and an appropriate balance struck between cost and time issues and the benefits of additional analyses (EPA 2002a).

Source Assessment

Source Assessment involves characterizing the type, magnitude and location of pollutant sources of fecal indicator loading. Source assessments also consider the conditions under which a particular source may have the most influence. For example, nonpoint sources typically predominate during high flow events while point sources predominate under low flows. For this reason, data collection efforts to support source assessment must focus on specific conditions. Monitoring data should be used to estimate the magnitude of loads from the major sources when available. In the absence of such data, a combination of literature values, best professional judgment, BST and empirical techniques/models is necessary. In general, EPA (2002a) recommends the use of the simplest approach that provides meaningful predictions.

EPA (2002a) encourages starting with the assumption that models are not required. If it is determined that models are required, then the following factors should be considered:

- Availability of data and/or funds to support data collection
- Availability of staff
- Familiarity of staff with potential models or other analytical tools
- Level of accuracy required

Depending on the complexity of the sources in the watershed, load estimation might be as simple as conducting a literature search or as complex as using a combination of long-term monitoring and modeling. Analysis of pollutant waste loads from point sources are generally recommended to be based on the effluent monitoring required for the National Pollutant Discharge Elimination System (NPDES) permit or based upon the permit's effluent limitations (EPA 2002a). However, many NPDES (and TPDES permits in Texas) require monitoring of chlorine residual to verify the effectiveness of chlorination but do not include either report or effluent limits for bacteria.

Nonpoint source loads are typically separated into urban and rural categories since runoff processes differ between these environments. Pathogen loads in urban stormwater can be estimated using a variety of techniques, ranging in complexity from simple loading rate assumptions and constant concentration estimates, to statistical estimates, to highly complex computer simulation (EPA 2002a). Examples of techniques for estimating pathogen loads in urban storm water include the FecaLOAD model, constant concentration estimates, statistical or regression approaches and stormwater models, such as SWMM and HSPF.

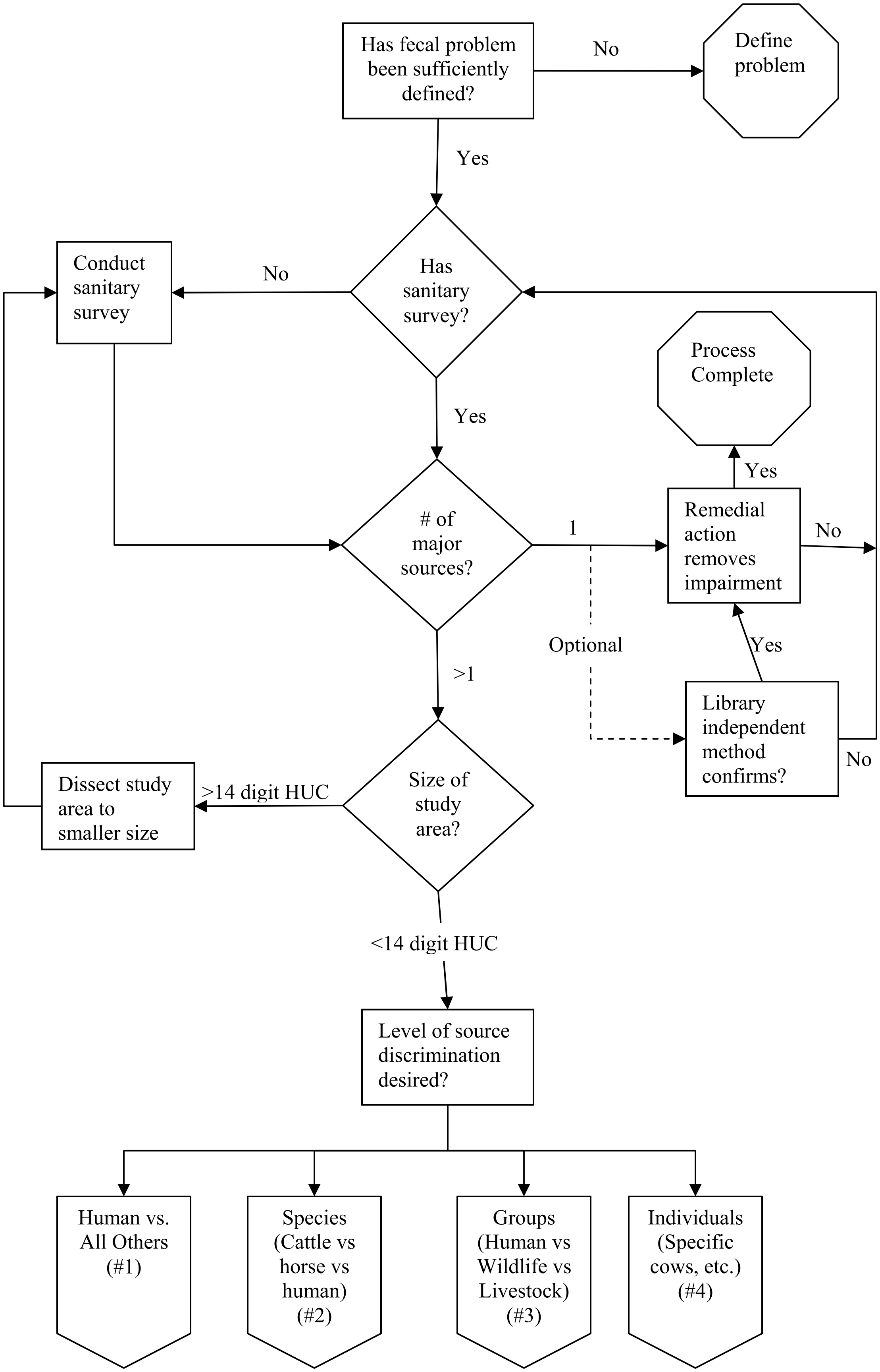
Rural nonpoint source loads may also be estimated using a variety of techniques, ranging from simple loading function estimates to use of complex simulation models. Techniques, such as the loading function approach, site-specific analysis, estimates of time series of loading and detailed models, such as AGNPS (Agricultural Nonpoint Source), may be used (EPA 2002a). Models are discussed in greater depth in the Linkage Analysis section.

DNA fingerprinting may also provide information for Source Assessments (EPA 2002a). There are many BST methods available and more are under development. Overall, molecular BST methods may offer the most precise identification of specific types of sources, but are limited by high costs and detailed, time-consuming procedures (EPA 2002c). Costs vary however, based on:

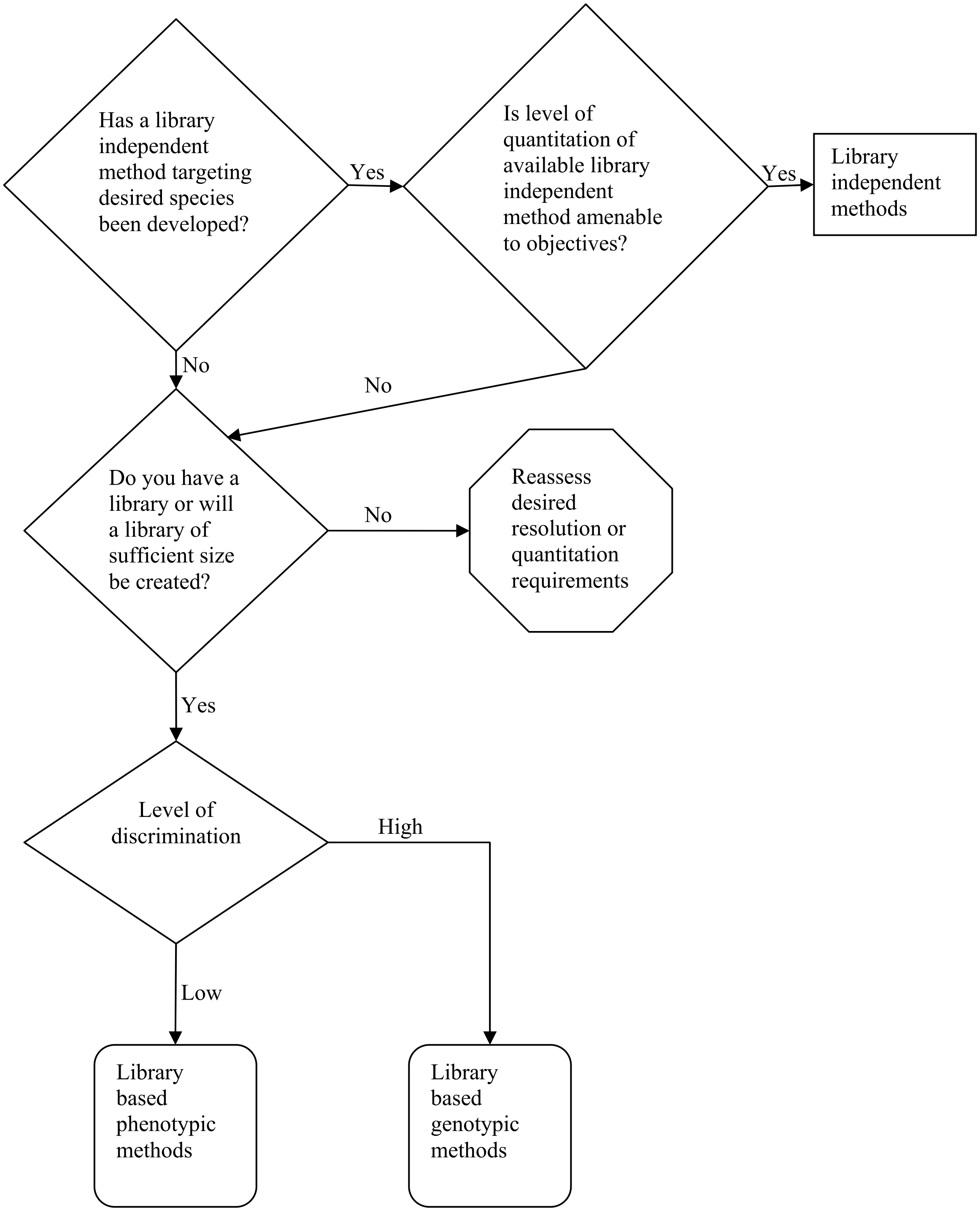
- Analytical method used
- Size of the database needed
- Number of environmental isolates analyzed
- Level of accuracy needed
- Number of subwatersheds and geographical size of the area under study

Comparison studies have shown that no single method is clearly superior to the others. Thus, the decision on which method to use depends on the unique set of circumstances associated with the area in question, the results of sanitary surveys, and budgetary and time constraints. A decision tree was created by EPA to assist in deciding whether BST methods are necessary to determine the sources of fecal pollution in a particular watershed and, if so, which group of methods might be most appropriate (EPA 2005). The decision tree included on the next four pages consists of five steps:

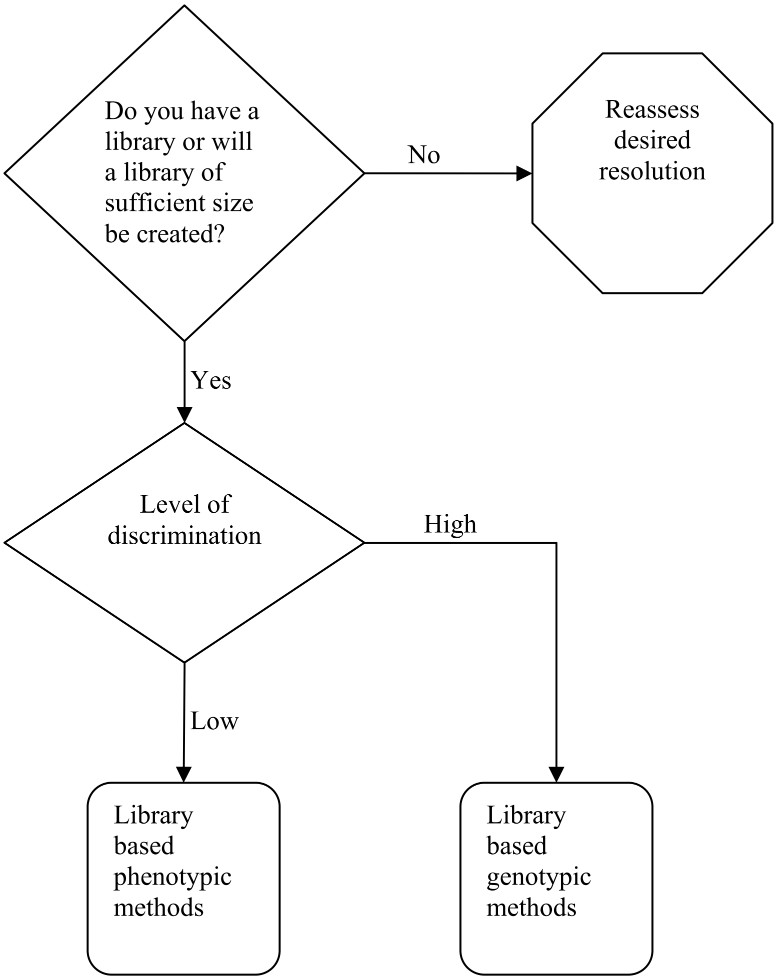
- Adequately defining the problem
- Conducting a sanitary survey
- Determining the potential number of major sources
- Ensuring the watershed/study area is of manageable size
- Determining the desired level of discrimination


Has fecal problem been sufficiently defined?
No
Define problem
Yes
Has sanitary survey?
No
Conduct sanitary survey
Yes
Process Complete
Yes
# of major sources?
1
Remedial action removes impairment
No
Optional
Yes
Library independent method confirms?
No
>1
Size of study area?
>14 digit HUC
Dissect study area to smaller size
<14 digit HUC
Level of source discrimination desired?
Human vs. All Others (#1)
Species (Cattle vs horse vs human) (#2)
Groups (Human vs Wildlife vs Livestock) (#3)
Individuals (Specific cows, etc.) (#4)

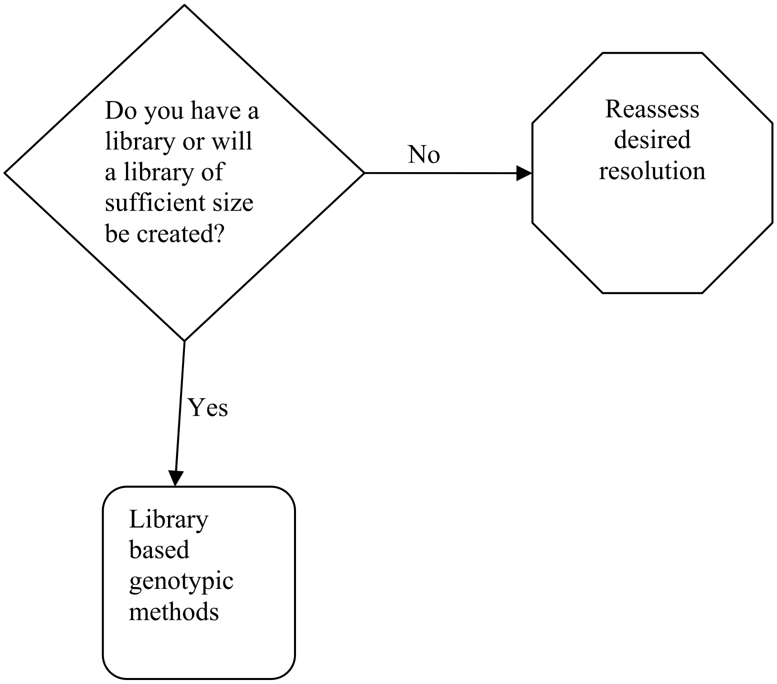
Human only #1 and Species Specificity #2 (EPA 2005)



Define by Groups #3 (EPA 2005)



Define to specific sources by type and location #4 (EPA 2005)



EPA (2003) has identified three analytical methods appropriate for calculating loads and linking water quality targets and sources:

- Empirical Approaches – When sufficient observations are available, existing data can be used to determine linkage between sources and water quality targets (e.g., regression approach).
- Simple Approaches – When permitted sources are sole source of bacteria, simple dilution calculations and/or compliance monitoring are adequate.
- Detailed Modeling – When sources of bacteria are complex, a water quality modeling approach (e.g. dynamic or steady-state modeling) is typically used. When detailed modeling is used, different types of models are required for accurate simulation for rivers and streams as compared to lakes and estuaries because the response is specific to the water body.

Steady-state modeling uses constant inputs for effluent flow and concentration, receiving water flow and meteorological conditions and is generally used where insufficient data exists for developing a dynamic model. Steady-state modeling provides very conservative results when applied to wet weather sources. If a state elects to use a steady state model, EPA recommends a dual design approach (e.g., load duration curve) where the loadings for intermittent or episodic sources are calculated using a flow duration approach and the loadings for continuous sources are calculated based on a low flow statistic (EPA 2003).

Dynamic modeling considers time-dependent variation of inputs and applies to the entire record of flows and loadings. In certain situations, EPA (2003) recommends the use of dynamic modeling to calculate loads. The three dynamic modeling techniques recommended are:

- Continuous simulation
- Monte Carlo simulation
- Log-normal probability modeling

Specific models recommended by EPA can be divided into two categories — watershed loading models and pathogen concentration prediction models. Loading models provide estimates of either the total pollutant loading or a time series loadings. The key watershed loading models suited for pathogens include HSPF, SWMM and STORM (EPA 2002b). These are briefly described in Appendix 3 and the previous section about models.

Prediction of pathogen concentration in rivers and streams is dominated by advection and dispersion processes and bacteria die-off. One-, two- and three-dimensional models have been developed to describe these processes. Water body type and data availability are the two most important factors that determine model applicability. For most small and shallow rivers, one-dimensional models are sufficient. However, for large and deep rivers and streams, two- or three-dimensional models that integrate the hydrodynamics of the system should be used (EPA 2002b). The river and stream models are briefly described in Appendix 3 and include the following:

- HSPF: Hydrological Simulation Program–FORTRAN
- CE-QUAL-RIV1: Hydrodynamic and Water Quality Model for Streams
- WASP5: Water Quality Analysis Simulation Program
- CE-QUAL-ICM: A Three-Dimensional Time-Variable Integrated-Compartment Eutrophication Model
- EFDC: Environmental Fluid Dynamics Computer Code
- CE-QUAL-W2: A Two-Dimensional, Laterally Averaged Hydrodynamic and Water Quality Model
- QUAL2E: The Enhanced Stream Water Quality Model
- TPM: Tidal Prism Model

In closing, EPA (2002a) recommends that when developing linkages between water quality targets and sources, states should:

- Use all available and relevant data (specifically monitoring data for associating water body responses with flow and loading conditions).
- Perform a scoping analysis using empirical analysis and/or steady-state modeling to review and analyze existing data prior to any complex modeling. The scoping

analysis should include identifying targets, quantifying sources, locating critical points, identifying critical conditions, and evaluating the need for more complex analysis.

- Use the simplest technique that adequately addresses all relevant factors when selecting a technique to establish a relationship between sources and water quality response.

EPA Bacteria TMDL Guidelines References

EPA (Environmental Protection Agency). 2002a. Protocols for Developing Pathogen TMDLs. EPA 841-R-00-002.

EPA (Environmental Protection Agency). 2002b. National Beach Guidance and Required Performance Criteria for Grants. June 2002.

EPA (Environmental Protection Agency). 2002c. Wastewater Technology Fact Sheet – Bacterial Source Tracking. EPA 832-F-02-010.

EPA (Environmental Protection Agency). 2003. Implementation Guidance for Ambient Water Quality Criteria for Bacteria. DRAFT Document.

EPA (Environmental Protection Agency). 2005. Microbial Source Tracking Guide Document. EPA/600-R-05-064.

Appendix 4: State Approaches to Bacteria TMDLs

This section provides a brief overview of approaches other states are using to develop TMDLs for bacteria and related issues. EPA has allowed much flexibility in developing pathogen TMDLs, as outlined in the agency's 2002 publication "Protocols for Developing Pathogen TMDLs" and 2003 DRAFT publication "Implementation Guidance for Ambient Water Quality Criteria for Bacteria." As a result, states have taken a variety of approaches to developing bacteria TMDLs. A large number of bacteria TMDLs have been approved by EPA since 1996 (Table 1). Most of these have been approved in states in which EPA is under court order or agreed consent decree to establish TMDLs.

Table 1. EPA Approved Pathogen TMDLs in Regions 3, 4, 6 and 7.

EPA Region	**State**	**EPA Approved TMDLs**						**Court Order**	**Litigation Dismissed**
		FC	**Pathogen**	**Bacteria**	**Fecal**	**TC**	***E. coli***		
3	Delaware			25				Yes	No
3	DC	22	9					Yes	No
3	Maryland	57	1					No	Yes
3	Pennsylvania	1	100					Yes	No
3	Virginia	186	94		1			Yes	No
3	W. Virginia	196						Yes	No
4	Georgia	534						Yes	No
4	Florida	21			48	45		Yes	No
4	Kentucky	23						No	No
4	Alabama	26						Yes	No
4	Mississippi	172						Yes	No
4	N. Carolina	38			1			No	Yes
4	Tennessee	62					191	Yes	No
4	S. Carolina	270						No	No
6	Arkansas	2						Yes	No
6	Louisiana	27						Yes	No
6	New Mexico	20						Yes	No
6	Oklahoma	0						No	Yes
6	Texas	0						No	No
7	Kansas	471						Yes	No
7	Nebraska	11					20	No	No
7	Missouri	3						Yes	No
7	Iowa		1					Yes	No

TMDLs that are prepared hurriedly to meet court-mandated deadlines may not be sufficiently specific or achieve adequate stakeholder acceptance to support development of comprehensive I-plans, particularly where multiple sources and types of sources are involved. Accordingly, the approval of a large number of bacteria TMDLs does not necessarily represent a significant improvement in water quality.

A brief overview of the TMDL methods used by states in EPA Regions 4 and 6, along with a few examples from select states in other regions is presented here. No examples were found of any state that has successfully improved water quality by implementing a bacterial TMDL. EPA Region 4 was initially targeted by this survey because environmental conditions (e.g. climate, rainfall, temperature) are most like the eastern portion of Texas where a majority of the 303(d) listings occur. This was later expanded to other regions. Much of the information for this summary was acquired from EPA's TMDL Web site at http://www.epa.gov/owow/tmdl/ and the Web sites of the individual states referenced.

EPA Region 6

In EPA Region 6, a total of 49 fecal coliform TMDLs are reported to have been approved since January 1, 1996. The load duration curve model was the primary model used to develop the approved TMDLs to date. The only exceptions are the two TMDLs developed in Arkansas, which used empirical methods.

Although no bacteria TMDLs are currently approved in Texas, a number of bacteria TMDLs and watershed protection plans are under way. Texas has taken the approach of spending more time in developing TMDLs that are designed to achieve stakeholder buy-in and result in meaningful implementation of water quality improvements. Texas has primarily used the HSPF and load duration curve models for a majority of the TMDLs under development to date (Table 2).

Table 2. Bacteria TMDLs Under Development in Texas.

Project	**HSPF**	**Load Duration**	**Other Models**	**Bacteria Source Tracking Method**
Upper San Antonio River	❶			ERIC-PCR and RiboPrinting
Leon River	❶			ERIC-PCR and RiboPrinting
Peach Creek	❶			ERIC-PCR and RiboPrinting
Adams and Cow Bayous	❶		RMA2/ACE	No BST
White Oak and Buffalo Bayous	❶			ARA and CSU
Lower San Antonio River		❶		ERIC-PCR and RiboPrinting
Atascosa River		❶		No BST
Elm and Sandies Creeks		❶		No BST
Upper Trinity River		❶		Ribotyping (Institute for Environmental Health, Inc., Seattle, WA)
Guadalupe River above Canyon Lake		❶		Ribotyping (Source Molecular Corporation, Inc., Miami, FL)
Upper Oyster Creek		❶		Ribotyping (Institute for Environmental Health, Inc., Seattle, WA)
Copano Bay and Mission and Aransas Rivers			ArcHydro\Monte Carlo Simulation	ARP and PFGE
Oso Bay and Oso Creek			ArcHydro\SWAT	No BST
Gilleland Creek		❶		No BST
Clear Creek		❶		
Metropolitan Houston (Brays, Greens, Halls and other Bayous)	❶			ARA and CSU
WPP – Lake Granbury				
WPP – Buck Creek			TBD	*E. faecium*, ERIC-PCR, RP
WPP – Bastrop Bayou				
WPP – Plum Creek		❶	SELECT, SPARROW, SWAT	No BST

Unlike other states in Region 6, Texas has supplemented the models utilizing BST. The primary BST methods that have been used include:

- ERIC-PCR conducted at TAES – El Paso
- RiboPrinting conducted at TAES – El Paso
- Antibiotic Resistance Analysis (ARA) conducted at the University of Houston
- Carbon Source Utilization (CSU) conducted at the University of Houston
- Ribotyping conducted at Institute for Environmental Health, Inc., Seattle, WA
- Ribotyping conducted at Source Molecular Corporation, Inc in Miami, Florida
- Antibiotic Resistance Profiling (ARP) conducted at Texas A&M University – Corpus Christi
- Pulse Field Gel Electrophoresis (PFGE) conducted at Texas A&M University-Corpus Christi and Texas A&M University – College Station

EPA Region 4

A total of 1,146 fecal coliform, 191 *E. coli*, 49 fecal and 45 total coliform TMDLs are reported to have been approved in EPA Region 4 since January 1, 1996. As in Region 3, litigation has driven much of the TMDL development. Only Kentucky and South Carolina have escaped litigation.

Georgia has led the way in TMDL approval. EPA Region 4 completed a number of these (e.g., Chickasawatchee Creek) using the BASINS model (HSPF) for both source analysis and for linking sources to indicators. LDCs and the equivalent site approach (as described below) have also been used extensively in Georgia. Georgia has not explicitly published a guidance document describing its methodology for developing bacteria TMDLs; however, their “Analytical Approach” is outlined in TMDLs, such as the “TMDL Evaluation for the Chattahoochee River Basin (Fecal coliform)” which can be found at: www.gadnr.org/epd/Files_PDF/techguide/wpb/TMDL/Chattahoochee/chatt_fc_tmdl.pdf. For those segments in which sufficient water quality data was available to calculate at least one 30-day geometric mean that was above the regulatory standard, the load duration curve approach was used. The method involves comparing the “current” critical load to summer and winter seasonal TMDL curves. For listed segments that do not have sufficient data to calculate the 30-day geometric mean fecal coliform concentrations, Georgia used an equivalent site approach to estimate the "current" and TMDL loads. This approach involves calculating loads based on the relationship of the stream segments that lack sufficient data to equivalent site(s) that have data. This method provides estimates that can be refined as additional data are collected. The WLA loads are calculated based on the permitted or design flows and average monthly permitted fecal coliform concentrations or a fecal coliform concentration of 200 counts/ 100 mL as a 30-day geometric mean. The LA is calculated as the remaining portion of the TMDL load available after allocating the WLA and the MOS.

The Florida Department of Environmental Protection has developed and published their methodology in a document titled "TMDL Protocol" in June 2006. Source identification in Florida begins with evaluating existing data and developing GIS layers to map probable sources. If the sources cannot be determined with existing data and field inspections, then simple and inexpensive chemical and biological tracers are used for identifying sources during dry and wet weather conditions. If the simple methods do not provide the level of source identification needed, then more complex and expensive BST methods are used. Modeling tools are then used to evaluate flows and loads, define allowable loads, and evaluate BMPs. No watershed models are specifically identified for developing bacteria TMDLs; however, a number of receiving water models are identified (e.g. AESOP, CE-QUAL-R1, CE-QUAL-RIV1, EFDC, EPDRiv1, HEC-5Q, HSPF-RCHRES, SWMM, TWQM, and WASP). A document such as this would be very beneficial in Texas: (http://www.dep.state.fl.us/water/tmdl/docs/TMDL_Protocol.pdf).

Kentucky is one of only two states in EPA Region 4 not under litigation or consent decree to complete TMDLs. Like Georgia, Kentucky has not published specific guidance on development of TMDLs; however, a review of its approved TMDLs shows that, mass balance and load duration curves have been used to develop a large number of their bacteria TMDLs. Their approach to using LDCs is typically outlined under the "Data Analysis" section of their TMDLs, such as the Brush Creek and Crooked Creek TMDL:

http://www.water.ky.gov/NR/rdonlyres/B2EE6B7D-A658-4FA6-A0BA-67C10EB77369/0/TMDLBrush_Crooked.pdf
In this TMDL, where a LDC was used, the allowable loading curves was divided into five zones representing high flows (0-10%), moist conditions (10-40%), median or mid-range flows (40-60%), dry conditions (60-90%), and low flows (90-100%). If more than five sample points plot above the allowable load line, a trendline can be drawn through the data violations for predicting the load at other duration intervals and the correlation factor (r^2) determined. If insufficient numbers of samples are available or r^2 is not high, then no line is drawn. Existing loads are expressed as a range based on the zones where the violations occur (e.g. median flow, moist conditions, etc.). When multiple violations occur within a zone, the existing load is represented as 90th percentile value. The percent reduction required to meet the criterion is calculated based on the 90th percentile of coliform concentrations collected during the recreation season that violate the fecal coliform target and calculated as follows:

Percent Reduction (%) = (existing concentration – target) / existing concentration x 100

Alabama, like most other states, has not published a protocol for developing bacteria TMDLs. A review of approved TMDLs in Alabama on EPA's TMDL website reveals that a variety of approaches have been used including:

- Empirical models
- Loading Simulation Program in C++ (LSPC), Environmental Fluid Dynamics Code (EFDC), Water Quality Analysis Simulation Program (WASP)
- BASINS Watershed Characterization System (WCS) and Nonpoint Source Model (a modified version of HSPF)
- Mass balance
- Load duration curves (LDCs)

A review of approved TMDLs in Mississippi reveals that state has primarily utilized empirical linear regression models, BASINS NPSM, and mass balance. The BASINS NPS Model (NPSM), a modified version of HSPF, was used in the Pearl River TMDL, (http://www.deq.state.ms.us/MDEQ.nsf/pdf/TWB_PearlRivMarionDc00/$File/PearlRBPearlRiv(Marion)Dc00.pdf?OpenElement) for estimating current conditions. The key reason for using BASINS as the modeling framework was its ability to integrate both point and nonpoint sources in the simulation, as well as its ability to assess instream water quality response.

North Carolina has used a number of models including BASINS HSPF, LDCs and Watershed Analysis Risk Framework (WARMF). Load duration curves are based on the cumulative frequency distribution of flow conditions in the watershed. Allowable loads are average loads over the recurrence interval between the 95th and 10th percentile flow record (excludes extreme drought (>95th percentile) and floods (<10th percentile). Percent reductions are expressed as the average value between existing loads (typically calculated using an equation to fit a curve through actual water quality violations) and the allowable load at each percent flow exceeded.

Tennessee utilizes a variety of models including the BASINS Watershed Characterization System and NPS Model (NPSM); Loading Simulation Program in C++ (LSPC) / Hydrologic Simulation Program –FORTRAN (HSPF) / Watershed Characterization System (WCS) model combination, LDCs and mass balance.

South Carolina has primarily used LDCs. In limited circumstances, they have also used empirical methods, mass balance or the BASINS/HSPF/WSC combo. A “TMDL Talk” on TMDLS.NET titled *Watershed Characterization & Bacteria TMDL’s: South Carolina’s Approach* may indicate greater use of BASINS/HSPF/WSC in coming years. The use of the Watershed Characterization System (WSC) ensures adequate consideration of the wide array of sources and is a key component of the technical approach toward building bacteria TMDLs and describing allocation options. In evaluating pollutant sources, loads are characterized using the best available information (e.g. monitoring data, GIS data layers, literature values and local knowledge). Pollutant sources are then linked to water quality targets using analytical approaches including WCS and the Nonpoint source Model (NPSM), a modified version of HSPF. Estimates of loading rates are generated by fecal coliform spreadsheet tools included with WCS. These loading rate estimates are then used by NPSM to simulate the resulting water quality response. Allocation for point sources considers discharge-monitoring information. NPS allocations for significant categories are identified at key points in the watershed from the model analyses. This approach was used for the Rocky Creek TMDL and others.

Other States

Connecticut and Delaware use the Cumulative Frequency Distribution Function Method, developed by the Connecticut Department of Environmental Protection, to develop TMDLs. The reduction in bacteria density from current levels needed to achieve compliance with state water quality standards is quantified by calculating the difference between the cumulative relative frequency of the sample data set (a minimum of 21 sampling dates during the recreational season) and the criteria adopted to support recreational use. Adopted water quality criteria for *E. coli* are represented by a statistical distribution of the geometric mean 126 and log standard deviation 0.4 for purposes of the TMDL calculations. TMDLs developed using this approach are expressed as the average percentage reduction from current conditions required to achieve consistency with criteria. The procedure partitions the TMDL into wet and dry weather allocations by quantifying the contribution of ambient monitoring data collected during periods of high stormwater influence and minimal stormwater influence to the current condition.

In EPA Region 7, a total of 485 fecal coliform, 20 *E. coli* and 1 pathogen TMDLs are reported to have been approved since October 1, 1995. Development in Kansas, Missouri, and Iowa has been driven by court orders. Much like EPA Region 6, LDCs appear to be the method of choice for developing bacteria TMDLs. Bacteria TMDLs approved in Kansas, Missouri and Nebraska primarily used LDCs. Kansas has lead the way in the use of LDCs. Kansas TMDL Curve Methodology can be found at the following website: (http://www.kdheks.gov/tmdl/basic.htm#data).

Use of LDCs in Nebraska is described in the document entitled "Nebraska's Approach for Developing TMDLs for Streams Using the Load Duration Curve Methodology." Only one pathogen TMDL (*E. coli)* has been approved in Iowa. Iowa used the Soil and Water Assessment Tool (SWAT) model to estimate daily flow into Beeds Lake. The SWAT flow estimates were then used to create a load duration curve. Use of EPA's bacterial indicator tool was used to identify the significance of bacteria sources in the watershed.

Indiana also uses LDCs and provides very good "Duration Curve Information" on their website (http://www.in.gov/idem/programs/water/tmdl/documents.html) and includes helpful tutorials, spreadsheets and publications on developing LDCs.

Nevada Division of Environmental Protection uses Load Duration Curve Methodology for Assessment and TMDL Development and has developed guidance on their website (http://www.ndep.nv.gov/bwqp/loadcurv.pdf) for developing LDCs.

New Jersey's policy is published in a fact sheet titled "Fecal Coliform TMDLs" (http://www.nj.gov/dep/watershedmgt/DOCS/tmdlfactsheet2.pdf). Nonpoint sources and stormwater point sources were identified as the primary contributors to all listed streams while Publicly Owned Treatment Works (POTWs) were considered insignificant and not allocated any loading reductions. The percent reduction was calculated empirically; however, when data was available, LDCs were used. Sources are identified using river assessments, visual surveys, stakeholder input and aerial photography.

New York used a statistical rollback method to estimate reductions needed and the Watershed Treatment Model (WTM) for characterizing the water bodies. The method for determining the geomean rollback factor follows:

$$F_{\text{rollback}} = (\text{Observed geomean} - \text{water quality standard})/(\text{Observed geomean})$$

The same method is applied for the 90th percentile values and standards:

$$F_{\text{rollback}} = (\text{Observed } 90^{\text{th}} \text{ percentile} - \text{water quality standard})/(\text{Observed } 90^{\text{th}} \text{ percentile})$$

The most restrictive of the two (i.e., the greatest percent reduction required) is chosen as the target reduction. More information on the WTM is included in section 6 of the "Final Report for Peconic Bay TMDL" (http://www.dec.state.ny.us/website/dow/pecpart56.pdf).

Virginia's approach is outlined through a series of Guidance Memos. "HSPF Model Calibration and Verification for Bacteria TMDLs" is outlined in Guidance Memo No. 03-

2012 (http://www.deq.virginia.gov/waterguidance/pdf/032012.pdf). Guidance Memo No. 03-2015 (http://www.deq.virginia.gov/waterguidance/pdf/032015.pdf) describes the "Method for Representing WLAs in Bacteria TMDLs". These memos were released to achieve greater consistency in their TMDL development. Even though the state is under court order, it is similar to Texas in many respects. Virginia develops bacteria TMDLs primarily using either LDCs or the HSPF model (or a modified version – NPSM); however, in a number of TMDLs, BST has been utilized in conjunction with simplified modeling approaches. One such example is the Little Wicomico River Watershed TMDL and Coan River Watershed TMDL, where Virginia DEQ utilized its point source inventory, a shoreline survey, and antibiotic resistance analysis to determine the potential sources of bacteria and quantify source loadings from humans, livestock and non-domestic animals. In addition, a simplified modeling approach (Tidal Volumetric Model) was used. The BST data was used to determine the relative sources of fecal coliform violations and ambient water quality data used to determine the load reductions needed to attain the applicable criteria. The most recent 30 months of data coinciding with the end of the TMDL study were reviewed to determine the loading to the water body. The geometric mean loading is based on the most recent 30-month geometric mean of fecal coliform. The load is also quantified for the 90th percentile of the 30-month grouping.

The geometric mean load is determined by multiplying the geometric mean concentration based on the most recent 30-month period of record by the volume of the water. The acceptable load is then determined by multiplying the geometric mean criteria by the volume of the water. The load reductions needed for the attainment of the geometric mean are then determined by subtracting the acceptable load from the geometric mean load.

Example: (Geometric Mean Value MPN/100ml) x (volume) = Existing Load
(Criteria Value 14 MPN/100ml) x (volume) = Allowable Load
Existing Load – Allowable Load = Load Reduction

The 90th percentile load is determined by multiplying the 90th percentile concentration, based on the most appropriate 30-month period of record, by the volume of the water. The acceptable load is determined by multiplying the 90th percentile criteria by the volume of the water. The load reductions needed for the attainment of the 90th percentile criteria are determined by subtracting the acceptable load from the 90th percentile load. The more stringent reductions between the two methods (i.e. 90th percentile load or geometric mean load) are used for the TMDL. The more stringent method is combined with the results of the BST to allocate source contributions and establish load reduction targets among the various contributing sources.

The BST data determines the percent loading for each of the major source categories and is used to determine where load reductions are needed. Since one BST sample per month is collected for a period of one year for each TMDL, the percent loading per source is averaged over the 12-month period if there are no seasonal differences between sources. The percent loading by source is multiplied by the more stringent method (i.e. 90th percentile load or geometric mean load) to determine the load by source. The percent reduction needed to attain the water quality standard or criteria are allocated to each source category.

Washington primarily uses LDCs for calculating bacteria TMDLs. To identify nonpoint sources of bacteria, a yearlong (minimum) water quality study of possible source areas is conducted. Once the locations of the bacterial sources are narrowed down, the state works with local interests to identify sources of pollution. Two methods that can be used to identify bacteria sources: (1) pinpointing the location of the source and (2) identifying the types of sources contributing to the problem. One of the most economical methods pinpointing the locations of sources is to conduct intensive upstream-downstream water quality monitoring, including flow measurements, to identify specific stream reaches, land uses or tributaries that are a problem. Dye testing can also be used for pinpointing the locations of sources. BST can be used to determine the types of sources. Most BST techniques are quite costly; thus, it is important to pick the appropriate method and time to use BST. BST does not tell you how much each source contributes to bacterial contamination, only the different kinds of sources. In addition, it is possible that not all source types will be identified or, with some techniques, that sources will be misidentified. Washington State Department of Ecology's Fact Sheet "Focus on Bacterial Source Tracking" provides an overview of their approach for identifying sources and using BST (http://www.ecy.wa.gov/pubs/0310059.pdf).

Other states using BST for TMDLs include New Hampshire and Maryland. Ribotyping has been used in New Hampshire to determine sources of bacteria for TMDLs. Maryland is using Antibiotic Resistance Analysis (ARA) BST methodology to determine the relative contribution of bacteria from various categories.

EPA Bacteria TMDL Guidelines References

EPA (Environmental Protection Agency). 2002. Protocols for Developing Pathogen TMDLs. EPA 841-R-00-002.

EPA (Environmental Protection Agency). 2003. Implementation Guidance for Ambient Water Quality Criteria for Bacteria. DRAFT Document.

EPA (Environmental Protection Agency). 2006. Total Maximum Daily Loads. http://www.epa.gov/owow/tmdl/

FDEP (Florida Department of Environmental Protection). 2006. TMDL Protocol. Task Assignment 003.03/05-003. Version 6.0.

TMDLs.NET. 2006. America's Clean Water Foundation and Association of State and Interstate Water Pollution Control Administrators.

Appendix 5: Comments from Expert Advisory Group

The Bacteria TMDL Task Force solicited feedback from the Expert Advisory Group on the contents of the Task Force Report Drafts One and Two. Those drafts, as well as the Expert Advisory Group's comments and recommendations have been posted on the Texas Water Resources Institute's Web site at http://twri.tamu.edu/bacteriatmdl

Most comments and recommendations have also been collected in Appendix 5 of Draft Three of the Task Force Report.

Comments from TCEQ and TSSWCB staff were submitted as Track Changes within Drafts One and Two of the Task Force Report. They can be viewed on the Web site.

Texas Parks and Wildlife Department's Role in the Bacterial TMDL Process

October 20, 2006

Texas Parks and Wildlife Department ("the Department") is the state agency with primary responsibility for protecting the state's fish and wildlife resources (Parks and Wildlife Code §12.0011(a)). Further, the Department is tasked with providing information on fish and wildlife resources to entities that make decisions affecting those resources (Parks and Wildlife Code §12.0011(b)(3)).

Texas Parks and Wildlife Department has purview over the wild animals, wild birds, and aquatic animal life of the state (Parks and Wildlife Code §61.005). The Department's authority extends, through the definition of "wildlife," to any wild mammal, animal, wild bird, or any part, product, egg, or offspring, of any of these, dead or alive (Parks and Wildlife Code §68.001).

The Department's authority is limited to indigenous species through the definition of "wild.” Exotic livestock is specifically excluded. "Wild," when used in reference to an animal, means a species, including each individual of a species that normally lives in a state of nature and is not ordinarily domesticated. This definition does not include exotic livestock defined by Section 161.001(a)(4), Agriculture Code (Parks and Wildlife Code §1.101). The Agriculture Code defines "exotic livestock" as grass-eating or plant-eating, single-hooved or cloven-hooved mammals that are not indigenous to this state and are known as ungulates, including animals from the swine, horse, tapir, rhinoceros, elephant, deer, and antelope families (Agriculture Code §161.001(a)(4)). Thus, certain species, such as feral swine, axis deer, and sika deer, do not fall within the scope of the Department's authority to protect or manage.

The Department recognizes that water is the basis for a significant recreational resource in Texas that includes boating, fishing, swimming, sailing, diving, bird watching and paddle sports (Texas Parks and Wildlife Department, Land and Water Conservation and

(TPWD’s comments continued)

Recreation Plan, Recreation Priorities on Texas Waters, pg. 64). As such, the Department has established as one of its major goals to maintain or improve water quality and quantity to support the needs of fish, wildlife and recreation (Texas Parks and Wildlife Department, Land and Water Conservation and Recreation Plan, Goal 7, pg. 75). The Department recognizes that the Texas Commission on Environmental Quality ("the Commission") is the state agency with primary responsibility for protecting water quality (Water Code §26.011). The Department supports the Commission's efforts to improve and restore water quality through the Total Maximum Daily Load (TMDL) process. Within the scope of its authority, as outlined above, the Department is committed to assisting the Commission and the Texas State Soil and Water Conservation Board ("the Board") in their efforts to restore full use of water bodies for which the contact recreation use is impaired.

Specific Comments

1. "Begin with the end in mind.” In order to assist in restoring impaired water bodies, it is important to develop data that are useful to the stakeholders who will ultimately implement the recommended best management practices. This may mean different things to different stakeholders.

2. One of the tools available to the Department is to assist private landowners in developing habitat management plans. These plans contain a comprehensive treatment of past and existing management and habitat conditions, existing wildlife species to be managed, list of landowner goals, and management recommendations that detail how to achieve those goals on a specific parcel. In order to develop such plans, there is a need to have species-specific information about contributions to bacterial loads. At present, the TMDL process does not provide the information the Department would need.

3. The approach currently taken in bacterial source tracking (BST) studies needs

(TPWD's comments continued)

refinement. Overall, the library needs to be extended to include more taxa with rigorously collected samples with adequate replication for each species.

a) Field sampling methods need to be improved. We understand that at least some samples have been collected from deposited fecal matter. This provides opportunity for contamination. The Department would recommend killing and gutting specimens to avoid the potential for contamination.

b) It is not clear that the BST library sampling is adequate from a statistical design perspective. We believe that the library lacks adequate replication. With the information available to us now about bacterial strains and promiscuity, we would recommend that ten or more samples be collected for each species, e.g. ten samples of great blue herons, ten samples of American egrets, etc.

c) In developing the library, it is important to have a sense of the species in each watershed that may be contributing the largest bacterial load to the water body. In general, one would expect these to be the species that spend time on or near the water. These are not necessarily the largest species in the watershed, nor would they necessarily be the species with the greatest biomass in the watershed.

City of Waco/Baylor University Comments

November 13th, 2006

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General Comments on the Formation of the Bacterial TMDL Task Force Commissioned by TCEQ and the TSSWCB

1. The main task force membership does not fairly represent municipal stakeholders around the state in that it does not include a municipal representative from a city or cities that would typically be impacted by the future bacterial TMDL guidelines. These municipalities, water boards, and water authority groups will be financially responsible for implementing the TMDL assessments and implementations, yet are not represented on the task force. Representation for these entities in the Expert Advisor group to the Task Force is not sufficient in that comments from the Expert Advisor group are currently considered but not required to be included in the document. It is recommended that a municipal representative be added to the main Task Force.

2. The task force does unfairly represent professionals who have represented or worked for industries that have polluted Texas waterways in the past. The majority of scientists and advisors in the primary task force have been publicly involved in research or investigations paid for by representatives of private industries. For example, several of the task force representatives recently

(City of Waco/Baylor University Comments continued)

completed a (BST) project financed by the Texas Farm Bureau. It is critical to the integrity of this process that the actual and perceived fairness and objectivity that there is input from a Task Force that fairly represents ALL of the major stakeholders. To foster this objectivity, it is recommended that input be solicited from other nationally recognized BST scientists in addition to the current task force members.

3. It is requested that all of the main task force members fully disclose and describe to the Expert Advisor Group and to the public any current or previous business, research, or consulting activities, or holdings or financial interests that might be related to this process so that any potential conflicts of interest may be identified.

General Comments on the First Draft of the Bacterial TMDL Task Force Report

1. Recommendations and decisions regarding what methods to recommend for use in developing bacterial TMDL guidelines should be made on the basis of objective scientific data, water quality reports, and economic data available from recent studies both within the state of Texas and around the nation. This does not necessarily mean that years of additional research are required before a method can be recommended. A number of studies have been published in scientific, peer-reviewed journals and reports from state or federal agencies that provide insight into the methods that are currently available. All possible modeling and BST methods that have been published in scientific journals or used in other states should be thoroughly considered for their potential application in Texas. In addition, the TMDL Task Force Report should be expanded to include input from other nationally known BST scientists that provides an objective overview of the benefits and limitations of these methods and references appropriate scientific data and federal reports.

(City of Waco/Baylor University Comments continued)

2. It is not sufficient to recommend a method simply because it has been used in Texas previously. In addition, it is also not sufficient to include a partial list of methods that have been used by a few scientists within the state. Currently, there are only a few dozen scientists that conduct BST research in the nation, and there are only a handful in the state of Texas. These Texas researchers include Drs. George Di Giovanni, Joanna Mott, Rene Massengale, and Suresh Pillai among a few others. Therefore, although evidence from current and previous Texas studies should be considered, this cannot be the sole basis for method recommendations.
3. In considering recent BST studies both from within the state of Texas and around the nation, it is also important to take into consideration the limitations of these studies, both scientific and financial.

Comments on the Bacterial Source Tracking Section of Draft #1

1. This is a good start to the draft BST section for the Task Force report. I compliment Drs. Di Giovanni and Mott for their initial review and assessment of the BST information available and their summary of the work that has been completed in Texas in the past.
2. The list of methods reviewed as potential TMDL BST methods is incomplete in that it does not include studies from BST scientists in the state or around the nation other than Drs. Di Giovanni and Mott. As stated in the earlier section, all major methods should be objectively reviewed for their potential benefits and limitations and applicability as a TMDL assessment method. The current list is incomplete. Other methods may also be appropriate for consideration including repPCR, routine ARA, and carbon-utilization profiling. A list of recent BST studies utilized in other watersheds can be provided upon request.

(City of Waco/Baylor University Comments continued)

3. A discussion of the general benefits and limitations of bacterial source tracking studies should be included in the document. This additional section should address library-based methods versus library-independent methods, library representativeness, library size, sample site selection, source category selection, and the statistical methods used to evaluate the library and analysis. This section should list scientific evidence that illustrates these benefits and limitations of the BST methods.

4. A general section describing BST should be included that explains the basic concepts of creating a known-source library, average rates of correct classification (ARCC) values, positive-predictive values (PPV), negative-predictive values (NPV), and other concepts and statistics. This will ensure that lay persons and non-technical reviewers and readers will be able to read and understand the content of the report. This is important if all stakeholders are to be provided with equal access to the TMDL development process and understanding of that process.

5. Ribotyping is a method that has shown good results in past BST studies; however, it does require technicians with more training despite its automation. Highly trained technicians are required for set-up, operation, troubleshooting and maintenance of the equipment. This method is significantly cost prohibitive and is the most costly method proposed in the document. The riboprinter is approximately $125,000-$150,000 and the reagent cost per assay is $40-65 depending on the quantities used. It is surprising that this method is promoted so strongly by the task force members over other much less expensive methods such as repPCR, PFGE, or ARA. Riboprinting may be feasible for larger water labs, but certainly not for small labs or municipalities with limited staffing and resources.

(City of Waco/Baylor University Comments continued)

6. RepPCR has been cited in the scientific literature several times as a cost-efficient, sensitive method of analyzing *E. coli* and Enterococci. It does require additional training of lab personnel but is actually less labor-intensive than ribotyping. In addition, repPCR produces 25-30 DNA bands in a DNA gel compared to the 10-15 bands produced by ribotyping, therefore increasing the sensitivity of repPCR over ribotyping. A separate method, ERIC-PCR, is listed in the document; however, it is listed as labor-intensive and its benefits are not adequately highlighted. This method has been used for genetic analysis of large numbers of isolates with reasonable discrimination; however, it is not clear as to the target DNA actually being amplified with this primer set in *E. coli*. It is recommended that the alternative repPCR of *E. coli* isolates using the BOX A1 primer set be added to the list of possible methods in the report based on recently published studies by Carson et al. 2003 (AEM 2003 69:1836) and on a project currently being completed by Dr. Massengale in the North Bosque watershed.

7. Several nationally published studies have estimated the minimum library size for known source samples. These studies should be listed and an appropriate minimum library size suggested. A list of these publications can be provided.

8. Targeted BST that focuses on collecting water samples in an area of known contamination or higher bacterial levels can improve BST sample design as recommended by Peter Hartel (J Environ Qual 2003). This should be added to the document.

9. Input from a modeling expert should be included regarding the minimum number of water sampling sites that should be included in assessment and a method for how to select the minimum number of water sampling sites. Inadequate sample site selection and numbers can limit the significance of TMDL assessments or any watershed study. We want to ensure that future TMDL assessments pinpoint sources of contamination as accurately as possible; thus, selection of a sufficient

number of sampling sites in appropriately selected locations will be necessary. It will also be necessary to include guidance in the Task Force Report regarding how to determine the number and location of these sites in a given watershed.

10. A discussion should be included pertaining to the selection of source categories for TMDL assessments. That discussion should review the types of animal categories to be included in a source library, how these categories should be selected, and how many samples should be isolated. Libraries consist of bacterial isolates from known source categories of fecal contamination. Previous research projects have included libraries that compared individual and combined animal categories with varying success. For example, a more detailed library may compare *cattle vs. human vs. wildlife vs. poultry vs. horse* while a more general library may compare *human vs. nonhuman*. Different goals for BST should be identified and then an appropriate plan developed for library category selection and creation. This point was also brought up in the public comments submitted by Texas Parks and Wildlife (Draft Appendix 5).
11. A recommendation to limit clonal isolates by appropriate sample collection and bacterial strain isolation. In addition, previous research has shown that selection of a few isolates (2-5 *E. coli*) from each fecal sample limits the probability of obtaining clonal isolates in the library. Clonal isolates artificially inflate the average rates of correct classification and representativeness measurements of a library and should not be included.

Parsons Comments

November 9, 2006

Comments on TX Bacteria TMDL Task Force Report (October 30, 2006 Draft)

Suggest the document be revised from a discussion report to an issue driven and recommendations oriented format. For example various issues identified in current TX TMDLs could be discussed.

The Task Force should consider developing Recommendations/Positions on key components of a TMDL required by USEPA which are: water quality target; Pollutant Source Identification; linkage between pollutant sources and receiving waters; WLA; LA; MOS; seasonal variability; and public comment.

Water Quality Target:

- Note in the document that the task force will **not** address water quality standards issues as directed by TCEQ. All Task Force recommendations will be based on the premise that the current Texas designated uses (Contact Recreation and Shellfish Harvesting) and corresponding numeric water quality criteria (*E. coli*, Enterococcus, fecal coliform) are valid.
- Task Force should consider and take a position on the concept that adopted TMDLs can be modified in the future if the water quality target is modified through the WQS triennial review process or a water body specific UAA is approved. The Task Force should recommend that TCEQ and TSSWCB establish policies and procedures for modifying WLAs and LAs in approved TMDLs. (see USEPA Memo dated August 2, 2006)

Pollutant Source Identification

- Task Force should agree on the complete list of possible bacteria sources that should be verified and discussed in a TMDL and recommend subcategories under point and nonpoint sources.

  For Example:
  Point sources – WWTP (major, minor), SSOs, CAFO facilities and lagoons, TPDES Phase I and Phase II Stormwater jurisdictions, wastewater collection systems? illicit discharges?
  Nonpoint sources – septic systems, sediment resuspension/bacteria regrowth, wildlife, exotic wildlife species, livestock, domestic pets, marinas, illicit discharges, compost sites, etc.

- It would be useful for the Task Force to also identify a list of data gaps corresponding to each of the point and nonpoint source subcategories and make recommendations on how to move forward with TMDL development despite these gaps and identify action items to address these gaps in the future. Stakeholders must understand that these data gaps create uncertainty which will be costly to reduce and they must also understand that data gaps create the need for assumptions which ultimately serve as the basis for the required Margin of Safety.

- Task Force should make recommendations on Bacteria Source Tracking in this section since this type of data will greatly enhance the scientific basis and provide more specificity to the Pollutant Source Identification portion of the TMDL.

Linkages between pollutant sources and receiving waters
This corresponds strongly to the Bacteria Fate and Transport Models section of the Task Force's First Draft Report.

- The Task Force could consider developing a short list of criteria or a decision tree tool to assist stakeholders, TCEQ and TSSWCB in selecting when to use a dynamic model or a simplistic model approach.
- The TCEQ and TSSWCB need a deliverable from the Task Force that provides them with a set of recommendations that address specific stakeholder issues and concerns (to date and anticipated) with both complex and simplistic modeling approaches. This exercise should also consider issues associated with modeling to support TMDLs on tidal streams and shellfish waters not supporting designated uses. This section could be organized in the following manner.

Example
Dynamic Modeling Approach (HSPF Model, SWAT)
Stakeholder Issue #1: Stakeholders disagree with the fecal production rates used for livestock and the county-wide census data used as inputs for the model.
Technical Response, Rebuttal, and Recommendation:
Stipulate recommendations that directly address each issue – aim the recommendations at how to move forward with TMDL development despite uncertainty.
Future Action Items: Longer term action items aimed at reducing uncertainty that would typically happen outside of the TMDL process.

Other issues needing to be address that have been expressed **include but are not limited to**:

Stakeholder Issue #2: Stakeholders question the assumption that conventional treatment of wastewater results in the discharge of little to no bacteria loads in the effluent from minor and major WWTPs.

Stakeholder Issue #3: Models have difficulty estimating bacteria loads from sediment resuspension and regrowth.

Stakeholder Issue #4: Are the assumptions made about fecal loading from direct deposition sources (wildlife, pets with access to water) appropriate?

(Parsons Comments continued)

> Stakeholder Issue #5: Are the percent failure rates used for septic systems and the corresponding transport of bacteria load from septic systems to receiving streams acceptable?
>
> *Stakeholder Issue #6:* What modeling approach is appropriate/best suited for developing TMDLs for Shellfish Waters

Simplistic Modeling Approach (Load Duration Curve)

Stakeholder Issue #1: Stakeholders do not see the benefit of using a tool that cannot simulate pollutant loading and transport.
Technical Response, Rebuttal, and Recommendation:
Stipulate recommendations that directly address each issue – aim the recommendations at how to move forward with TMDL development despite uncertainty.
Future Action Items: Longer term action items that would typically happen outside of the TMDL process.

Stakeholder Issue #2: Given limited flow data for streams throughout TX and that flow data is one of two key variables in LDCs, what is the most reliable (acceptable to the stakeholders) method for estimating stream flow on ungaged streams.
Technical Response, Rebuttal, and Recommendation:
Stipulate recommendations that directly address each issue – aim the recommendations at how to move forward with TMDL development despite uncertainty.
Future Action Items: Longer term action items that would typically happen outside of the TMDL process.

TMDL Calculations – WLA, LA, MOS

- Task Force should concur on the complete list of categories that should be included in the WLA and LA and how the numbers should be expressed (e.g., daily loads, monthly, percent reduction goal, combination).
- Task Force should concur on the use of an implicit MOS for bacteria TMDLs or establish a detailed rationale for utilizing an explicit MOS. Task Force should list and explain examples that would qualify as part of an implicit MOS.

Public Comment

- Task Force should summarize stakeholder concerns about the current TCEQ and TSSWCB stakeholder participation process.
- Task Force could make recommendations on how to improve stakeholder understanding of a key hurdle in most TMDLs – data limitations that create uncertainty.

Bacteria Source Tracking

- The table in the draft report is a very good informational matrix.

(Parsons Comments continued)

- The Task Force needs to make a recommendation that more BST should be done to support TMDL development projects in the future around the state.
- Rather than describe the different methods, the report should summarize in bullets the lessons learned from the 5 different BST projects done in TX.
- The Task Force should summarize a consensus recommendation that the TCEQ and TSSWCB should support the use of two methods on all future BST projects – ERIC-PCR and Riboprinting (with at least 2 enzymes).
- The Task Force should make recommendations on what is an acceptable confidence level for the Rate of Correct Classification and a rationale for whether or not the existing known source library is of sufficient size to maintain the RCC for BST projects throughout TX.

Recommended Decision-Making Process for Texas TMDL and Implementation Plan Development

- Task Force could make recommendations to TCEQ and TSSWCB that a policy and corresponding procedures should be established and disseminated on when TMDL implementation plans or Watershed Protection Plans should be initiated (e.g. once a TMDL has been issued for public comment, once a TMDL has been adopted by the TCEQ and TSSWCB, other?). The Task Force could consider developing a recommendation on whether a WPP can be developed in lieu of a TMDL.
- Task Force should try to clarify the current understanding or misunderstandings of the differences between a TMDL Implementation Plan and a WPP. While both are aimed at restoring beneficial uses by achieving pollutant reductions, they have different components and are typically executed differently. For example, a TMDL implementation plan is typically pollutant specific and to date have been prepared by TCEQ or TSSWCB. A WPP can and probably should address more than TMDL pollutants in a 303(d) listed watershed and can addresses a larger watershed area. A WPP can incorporate both restoration and protection objectives and can be initiated by TCEQ, TSSWCB, or any other organization.

Research and Development Needs

- Some of these Task Force recommendations would be derived from the Future Action Items identified above in response to stakeholder concerns or criticisms.

TEXAS DEPARTMENT OF TRANSPORTATION – HOUSTON DISTRICT
Comments on the Bacterial Total Maximum Daily Load Task Force Report First Draft, October 30, 2006

Comments Submitted November 13, 2006

Introduction

The Houston District of the Texas Department of Transportation (the District) operates over 3,000 miles[1] of roadway in the Houston metropolitan area. Various surface water bodies in the District's jurisdiction currently are listed as impaired because their contact recreational uses have been found by the Texas Commission on Environmental Quality (TCEQ) to be impaired. This has triggered a number of bacteria Total Maximum Daily Load (TMDL) studies in the region. Since the District is among the many entities that discharge stormwater into regional surface water bodies, and since urban stormwater frequently contains elevated bacteria levels, the District is very interested in the deliberations and findings of the Bacterial TMDL Task Force (Task Force). We appreciate the opportunity to provide comments and to assist the Task Force in its work.

General Comments

1. **Incorporate Discussion of Adaptive Management, Phased TMDLs, and Phased Implementation:** We believe that the Task Force should include an up-to-date discussion and consideration of the most recent guidance from EPA regarding options for developing phased TMDL's , the use of adaptive management, and phased implementation. We urge the Task Force to consider and incorporate elements from the August 2, 2006 EPA memorandum from Benita Best-Wong to all EPA regions[2] so that these concepts can be included.

2. **Incorporate Discussion of Wet Weather Concentrations and Loads:** Urban stormwater frequently can contain elevated bacteria concentrations and loads, however, the impact of these episodic events on attainment of contact recreational uses is not clear and certainly, no consensus on how to deal with wet weather has emerged. Approaches to consider stormwater loads during TMDL development and implementation planning are similarly not straightforward. We urge the Task Force to consider the November 22, 2002 EPA memorandum from Robert Wayland to all EPA regions[3] so that wet weather issues can be addressed.

3. **Problem Identification is Required:** The District believes that the Task Force should attempt to define the existing problems with and limitations to the TMDL process, as implemented in Texas, prior to suggesting or recommending new research and development approaches. For example, if bacteria fate and transport models are, in fact, adequate for TMDL development and implementation plan decision-making, then new models might not be required. We are not sure how a new model that might be marginally better in simulation accuracy or a new source identification method that might be slightly better in source identification will substantially improve the Texas TMDL program. We suggest that the problems may not lie in the tools available but rather the regulatory objectives to which the existing tools are being applied.

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[1] See http://www.dot.state.tx.us/hou/

[2] See http://www.epa.gov/owow/tmdl/tmdl_clarification_letter.html

[3] See http://www.epa.gov/npdes/pubs/final-wwtmdl.pdf

(TxDOT – Houston District comments continued)

Bacteria Fate and Transport Models

1. **Higher Level of Detail Required:** The evaluation of models and source identification tools appears to be a reasonably complete description of the available tools, but provides only a very superficial evaluation of their utility to the task at hand. This is perfectly understandable for a first draft, and is not intended as criticism of the draft, however, the District urges the Task Force to include more details about fate and transport models and their selection for various Texas waterbodies. For example, an estuarine environment would certainly require a different model than a recreational lake or an urban stream.
2. **Model Selection Challenges:** On page 2, it is mentioned that model selection is a challenging problem "due to the numerous water quality models that are available", but it should be added that the characteristics of each watercourse and the nature of the pollutant loads also drive the decision.
3. **Load Duration Curve:** The disadvantages of this method are not completely described. Other disadvantages include (a) The inability of managers to assess water quality responses for varying implementation or load reduction scenarios. (b) Older observed data may skew the TMDL towards sources that are no longer relevant due to changes in the watershed and the LDC only applies to points in the stream at which samples were taken. (c) The TMDL duration and frequency targets cannot be directly compared to the LDC.
4. **SWAT:** The model is not well explained, therefore, we feel that additional information should be provided. For example, what are the required data? What is the model development and set-up time? Does the model account for re-suspension from the bed stream and from deposition sources? What are the disadvantages and advantages of this model?
5. **SWMM:** Information about required data, model development and set-up time should be provided.
6. **WASP:** More information should be provided concerning data requirements, model development and set-up time, and advantages and disadvantages of model usage.
7. **Include Discussion of STORM and TPM:** Appendix 1 states that the EPA includes STORM and TPM as suitable models for pathogens. Why are STORM and TPM not described in this section? They were not evaluated by Ward and Benaman (1999), so they were not ruled out by that study.

Bacteria Source Tracking

1. **Bacteria Source Tracking is Not a Silver Bullet:** Information should be provided about the advantages and disadvantages of BST in general. Disadvantages include their propensity to be subject to false positives and negatives, the possibility of the EC population changing when exposed to environmental conditions, the possibility of the EC genetic sequence changing over time, questions about the stability of a host-based EC library, and the lack of a standard algorithm used for pattern matching. Also, the advantage of the ability of a BST method to distinguish between individual species is debatable. BST methods that distinguish between categories, i.e., humans, livestock, wildlife will most likely provide the necessary information to reduce the appropriate loadings.

BST Methods Should be Evaluated More Evenhandedly: There are three genotypic tools (ERIC-PCR, Ribotyping, and PFGE) described in detail, yet only one ARA tool (KB-ARA) is sufficiently described. There is no discussion why only one ARA tool is presented. More discussion is needed as to why EPIC-PCR, Ribotyping, and PFGE were chosen for comparison. Why are they "versatile and feasible"?

2. **Expand Discussion of KB-ARA:** What are the advantages of the KB-ARA method over other ARA methods?

Recommended Decision-Making Process for Texas TMDL and Implementation Plan Development

1. **Examine Other State Programs First:** Appendix 2 notes that Texas has not finalized any TMDLs since January 1996. Prior to developing decision-making recommendations for Texas, the District urges the Task Force to closely examine decision-making in other states and to more fully understand the policy and procedural differences among Region 6 states that has led to the striking differences in TMDL approval rates.

2. **Consider Technical and Regulatory Requirements as well as Stakeholder Acceptance:** We urge the Task Force to not just consider technical and regulatory requirements for both TMDL and implementation plan development, but also stakeholder acceptance. Since stakeholder rate payers may be faced with paying extremely large implementation costs in efforts to achieve TMDL load reductions, if meaningful stakeholder involvement and buy-in is not secured, administrative appeals and litigation could result, further delaying TMDL and implementation plan adoption in Texas.

3. **Research and Development Needs**

1. **Consider National Guidance and Recommendations First:** The EPA and the National Academy of Sciences have both produced significant publications identifying research needs. The District urges the Task Force to consider these publications when identifying research needs for Texas. These publications include Reckhow, Donigian, et. al., 2001;[4] Shoemaker, Dai, and Koenig, 2006;[5] and EPA, July 2002.[6] While these references don't explicitly and directly address <u>bacteria</u> TMDL issues, they do include important findings regarding the process, policy issues, scientific rigor, and equity issues that impact bacteria TMDL development and implementation.

Appendix 1: EPA Bacteria TMDL Guidelines

1. **Source Assessment:** The draft report suggests using point source effluent monitoring data. This would be fine for discharge permits that require compliance monitoring for bacteria, however, most municipal wastewater treatment plants are not required to monitor for bacteria under the assumption that chlorine residual is an adequate indicator of adequate disinfection process operation. A recent study conducted by Harris County on behalf of the Stormwater Joint Task Force[7] suggests that this may significantly underestimate the bacteria load from wastewater point sources. While the controls necessary to address elevated bacteria loads from WWTP's are available and are straightforward to implement, failure to identify WWTP's as a significant load will

Linkage Analysis: On page 27 pathogen concentrations in streams are said to be dominated by advection, dispersion, and die-off. We believe that re-growth and bed re-suspension are

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[4] See http://www.nap.edu/catalog/10146.html#orgs
[5] See http://www.epa.gov/ORD/NRMRL/pubs/600r05149/600r05149.pdf
[6] See http://www.epa.gov/ORD/NRMRL/pubs/600r05149/600r05149.pdf
[7] The JTF includes the City of Houston, Harris County Flood Control District, Harris County, and the Houston District of TxDOT.

also significant factors, especially in shallow and narrow waterways. We believe that these processes far exceed the impact of dispersion on instream bacteria concentrations.

Appendix 2: State Approaches to Bacterial TMDL Development

1. **Investigate State to State Disparity in TMDL Adoption:** In the review of work in other EPA regions it is noted that Texas has yet to produce an approved bacteria TMDL while other states in Region 6 have been more successful and states in other regions have been quite prolific in the production of TMDL documents. We believe that a full understanding of the reasons for the disparity would be a very useful product for the Task Force to generate.
2. **Interview State TMDL Coordinators:** The appendix indicates a lack of information on state website. If a state website does not include adequate information on TMDL and implementation plan development, we suggest the Task Force interview state TMDL coordinators or project managers to obtain key information about approaches and methods.

Texas Parks and Wildlife Department Comments

November 13, 2006

Texas Parks and Wildlife Department appreciates the opportunity to comment on the Bacterial TMDL Task Force Report, First Draft dated October 30, 2006.

Overall, the first draft is not what had been anticipated, given the scope of work of the task force as delineated in your email of October 17, 2006 to the Task Force expert advisers:

1. Review EPA TMDL guidelines and approaches taken by selected states to TMDL and implementation plan development.
2. Evaluate scientific tools, including microbial fate and transport modeling, microbial source tracking, and others.
3. Suggest alternative approaches to TMDL development, emphasizing scientific quality, timeliness, and cost effectiveness.
4. Suggest alternative approaches to TMDL implementation plan and watershed protection plan development, emphasizing scientific quality, timeliness, and cost effectiveness.
5. Develop a 3- to 5-year science roadmap to guide and improve our understanding of microbial fate and movement in Texas environments.

We recognize that two sections of the document are not yet available. That, of and by itself, makes it difficult to comment, as the information that is presented lacks context. However, we find the discussion in the sections that are available, Bacteria Fate and Transport Models and Bacteria Source Tracking, to focus on what has already been done in Texas rather a comprehensive review, critique and comparison of tools that are available. As such, we wonder if item 2 above, "evaluate scientific tools" has actually been addressed.

Given that this is a preliminary draft, we offer only the following
general comments.

1. The issue of data quality is not addressed anywhere in the document. We believe that data quality should be a major discussion point. The selection of non-biased sampling locations and the use of methodologies providing proven, accurate, reproducible data results are requirements for any meaningful TMDL modeling effort. We are concerned that the use of source tracking is one of the least accurate such methods. The BST authors seem to acknowledge this themselves on pg. 15, where they note efforts to "explore issues of geographical and temporal stability of BST libraries, refine library isolate selection, and determine accuracy of water isolate identification."
2. Numerical estimates of uncertainty, reliability, reproducibility, and sensitivity are not presented in either the modeling or BST sections. The BST section makes some effort in this regard, but we find the characterization of "high," "moderate," etc. not to be

helpful without the anchor of some numeric analysis. Further, it would be helpful to present information for BST regarding the tendency for false positives (or negatives).

3. In the modeling section, we found it helpful that a specific example was presented for BLEST. We note however, that the use of this tool for Buffalo and White Oak Bayous was presented as if it was beneficial use. A discussion on the limitations of this method should also be included. We are particularly interested in reliability of the calculations.

4. The BST section provides some discussion of and comparison between techniques, but does not provide the information necessary to determine if BST has the potential to be useful in bacterial TMDLs in Texas. We felt the section lacked a clear, detailed discussion of both the sampling requirements and problems with the method, such as selecting unbiased sample locations, fecal library issues with variable media, cross contamination, geographical variations, etc.; and the large variation in analytical data which necessitates a high number of samples to show statistically valid results.

5. In the BST section, the authors note on pg. 14 that the use of a three-way split of pollution sources into domestic sewage, livestock and wildlife source classes would likely be more scientifically justified. In this context, what does "scientifically justified" mean?

We note that such general classification would not be meaningful or useful for Texas Parks and Wildlife Department in any efforts to manage wildlife or its habitat.

6. In the BST section on pg. 14, please correct and clarify the sentence that reads "Library-independent methods .... than library-independent methods." We suspect that one of these should read "library-dependent, but we aren't sure which one. Could the authors provide more discussion or examples of library-independent methods?

7. Editorially, we note that the BST section is not consistent in its use of language. In some places BST is used, while other paragraphs use MST. Some paragraphs refer to "this study."

8. Appendix 2 presents information on bacterial TMDL development in other states. Much information is presented, but it is difficult to interpret. It would be helpful to provide a context for the discussion, such as consideration of which TMDLs have been implemented successfully and resulted in actual water quality improvements. It would seem that successful examples would be most important to Texas. Alternatively, it would be helpful if other states have critiqued the various available techniques and to understand their decision-making process.

Respectfully submitted on behalf of Texas Parks and Wildlife Department,

Dr. Patricia Radloff, Coastal Fisheries Division
Dr. David Sager, Inland Fisheries Division
Dr. Duane Schlitter, Wildlife Division

HARRIS COUNTY
PUBLIC INFRASTRUCTURE DEPARTMENT
10000 Northwest Frwy., Suite 108
Houston, Texas 77092
(713) 316-4877

November 15, 2006

C. Allan Jones, Ph. D., Director
Texas Water Resources Institute
1500 Research Parkway, Ste. 240
College Station, TX 77843-2118

SUBJECT: BTMDL Task Force Report – First Draft, October 30, 2006

Dear Dr. Jones:

Harris County appreciates the opportunity to comment on the referenced report. We applaud the efforts taken by you and the other members of the Task Force in guiding future work in the field of water quality. Transmitted herewith for consideration by the Task Force please find attached my comments on the First Draft of the Report.

If you need further information or have any questions regarding these comments, please call me at (713) 316-4877 or Alisa Max at (713) 290-3089.

Sincerely,

John Blount, P.E.
Deputy Director
Planning & Operations

Attachments: Comments on BTMDL Task Force Report

cc: Kevin Wagner – TWRI
Pat Smiley, P.E. – Harris County
Alisa S. Max, P.E. - Harris County
Trent Martin - Harris County
Joe Myers, P.E. - Harris County Flood Control District
Catherine Elliot - Harris County Flood Control District

John Blount, P.E. - Harris County

1. The section on Bacterial Source Tracking should be incorporated into a broader section that more rigorously addresses how to calculate loading into a selected model, with bacterial source tracking being one means of doing it. For areas in which sampling is done instead of, or in unison with, bacterial source tracking, discussion should be included to discuss how samples should be taken, and what level of reliability should be sought out for the sample results.
2. A section should be added to discuss the need for development of consistent methodologies for usage of each model, including acceptable methodologies for determining, calculating, and calibrating model inputs. This should also include what maximum acceptable deviations should be allowed during model calibration when compared to historical events. A handbook should be developed for each recommended model that details the recommended methods.
3. Guidelines should be given as to when data collected for other sources besides the TCEQ (and its consultants) could be used.
4. Guidelines should be given for consistent and defendable data collection methodologies. For example, the Buffalo/White Oak Bayou Bacteria TMDL project team determined a bacteria regrowth equation in WWTP effluent based on a small-scale experiment whose methodology was not explained. Harris County conducted a bacteria regrowth in WWTP effluent study which found much, much greater levels of regrowth. Similarly, recent studies by Harris County found that bacteria inputs from WWTPs are much greater than what the Buffalo/White Oak Bayou Bacteria TMDL project team earlier determined. Which is correct?
5. A recommendation should be presented that allows Stakeholders to participate in a detailed manner in bacteria TMDL development, not just being presented with the answers. Stakeholders with technical knowledge could be a real asset in assisting with the design of bacteria TMDL studies required.
6. Bacteria must not be viewed in a vacuum. If other influencing pollutants - such as nutrients, dissolved oxygen, or pH - are responsible for the growth, die-off, or longevity of bacteria, then those other pollutants need to be considered. This becomes especially important as the project moves into implementation.
7. A section should be allotted for the treatment of bacterial regrowth, resuspension, and other bacterial life history issues.
8. Guidelines should be given for consistent and defendable policy decisions so as not to unfairly influence scientific modeling. For example:
    a. In the Buffalo/White Oak Bayou Bacteria TMDL: Since illicit discharges are not allowable or permitted, contribution (allocation) from illicit discharges has been modeled as zero. This is in obvious contradiction to reality.
    b. Inputs from urban wildlife are sometimes allocated to background, but are sometimes not, since habitats for urban wildlife are the result of anthropomorphic disturbances.
    c. Older fecal coliform data is simply converted to *E. coli* at a ratio of 200:126. In reality, Harris County studies conclude that each stream (and

(Harris County comments continued)

likely each wastestream) has its own particular ratio, which must be sampled in order to be determined.

   d. When is the use of the geometric mean appropriate?

9. A recommendation should be included that the Bacteria TMDL team should use consistent terminology with the Permits teams, unless they specifically note otherwise.
10. Harris County is very pleased with the emphasis placed on a state-wide bacteria source tracking library and methodology. One comment related to BST - does BST differentiate between bacteria that is a product of regrowth in the external environmental versus bacteria that is from a discharge itself? These are two separate inputs into most models and spreadsheets, and the proposed implementation plan should be vastly different depending upon if the problem is based on regrowth versus direct pollutant loading.
11. It should be noted that recommended reductions should be within the realm of achievability (*i.e.*; within the rates of existing best available technology at the time of TMDL adoption), or else it should be recommended that a UAA or re-evaluation of other loadings should be performed prior to adoption of any TMDL. For example, it should not be assumed, as is the case with the Buffalo/White Oak Bayou Bacteria TMDL, that 100% reduction in bacteria can be achieved from any one point source loading unless realistic existing technologies can achieve that.
12. Similarly, policy should be developed to recommend that a TDML which finds that background levels exceed the desired standard should perform a UAA or re-evaluation of other loadings. Harris County conducted a study on an un-impacted stream and found that this stream could not meet primary contact recreation standard, despite its near-pristine condition. Big Creek in Fort Bend County, another un-impacted stream per TCEQ's own judgment, also cannot meet primary contact recreation stream standards.
13. As of the time of this comment, TCEQ has not released the BLEST model, which is being used for the Buffalo Bayou and White Oak Bayou Bacteria TMDLs. We request that the models discussed in the paper are available to the public. We request to be provided with a copy of the model.
14. An appendix should be developed to examine how different stream types influence how a TMDL and implementation plan is approached. For example, how to approach concrete flood control channels, effluent-dominated streams, rural streams, *etc.*
15. It would be helpful if Appendix 2 also included information related to what these approved TMDLs are doing for implementation, if there is any measure of success or failure being found with the implementation, if the stream is rural, urban or mixed, and if the stream appears to be effluent dominated.
16. Appendix 4: Please correct John Blount's affiliation on the expert advisor list. John is with Harris County.

LRCA Comments

November 13, 2006

1. Would it be prudent to discuss the fecal coliform versus *E. coli* question in the document? The Texas Surface Water Quality standard is now written for *E. coli* but most of the data collected has been fecal coliform.
2. Have any TMDLs been performed for pathogens in Texas? If so, which pathogens?
3. Appendix 3 is very similar to information found in a previous section. Could a similar table, to the one included for BST be included?
4. Is pollutant trading a possibility for bacteria TMDLs?
5. A summary of what was learned from EPA regions 3, 4 and 7 might be helpful.
6. The BST section that Drs. Mott and DiGiovanni wrote seems to be very comprehensive. Obviously, other sections have not been written yet.

Jerry Guajardo
Sr. Aquatic Scientist
Lower Colorado River Authority
(512) 473-3333 Extension 7633

Texas Department of Agriculture Comments

December 15, 2006

1. Stakeholder involvement should be a priority from the initial sampling phase. Having landowners willing to provide multiple sampling locations that are representative of the watershed or stream segment is preferable to limiting sampling to public access points such as bridges or relying on literature values. Stakeholders can provide insight that may not be apparent to someone from outside the watershed.

2 Acceptable uncertainty is adequately addressed at this point in the draft (pages 42-44). We need to make sure that the cost of this uncertainty is equally distributed amongst all potentially responsible parties, not just agriculture. Again, a different approach using tiers of water segments might be an option. First use the cheaper faster methods for all impaired watersheds, as this would be beneficial and cost effective. Move to higher tiers and the more complicated/expensive methods when there is too much uncertainty or difficulty.

3. We strongly believe that all point sources should be sampled at their outfall. Recent studies indicate that there are bacteria regrowth issues associated with current effluent disinfection systems. Actual sampling of the effluent as it enters the stream segment will provide hard numbers that can be used in the load assessment and can be used to show stakeholders that “real numbers” are being used instead of permit limits or literature values. As seen at recent bacteria TMDL stakeholder meetings, stakeholders are reluctant to accept assumptions when actual data can easily be collected.

4. We support the model and method matrix (toolbox approach, page 30) for options for particular TMDLs. Each water segment and stakeholder group needs to be assessed on a case by case basis for maximum success.

5. This draft adequately discusses the survivability question for *E.coli*. Some research needs to be done not on just the survivability of *E.coli*, but other major waterborne pathogens as well that may not survive as well or not as this indicator species, especially in estuarine or marine waters. We did not see this mentioned in the draft.

6. The ERIC-PCR/KB-ARA tandem methods (pg 27), especially using the KB method alone (ease of use and inexpensive) with very initial screening and the combined method for more defined work. Ultimately, the implementation plan needs to be based on the genotypic tests in which are more definitive. I also would think if a sound endeavor to use the PFGE method (pg 25) as CDC and the food industry use this a lot. The recent spinach and lettuce contaminations that have occurred indicates that it may be important in the future to relate TMDL info to possible epidemiological studies. We also heavily support using previously used methods in Texas to allow for comparisons across watersheds and prudent use of previous expenditures.

(TDA comments continued)

7. The research need to accurately calculate livestock and wildlife, stoking rates pg 36) and their distribution in a watershed should be emphasized.

December 15, 2006

Comments of Myron Hess on behalf of the National Wildlife Federation on Second Draft (Dec. 4, 2006) of Bacteria Total Maximum Daily Load Task Force Report

I provide these comments unencumbered by expert knowledge of the technical aspects of this issue. However, I hope that these comments might help provide some broader perspective that could be useful in developing a document that will be reasonably accessible and valuable to readers who are not technical experts.

Page 7, Discussion of Statistical and Mass Balance Bacteria Models. A number of previous comments by others have noted the need for consistent treatment of different modeling approaches in the text. The discussion likely would come across as more balanced and would be more accessible if, for each model, the discussion were divided into specific and consistent topic subheadings. The following subheadings might be considered:

What It Is
Data Requirements
Ease of Application
Value in Supporting Implementation
Examples of Previous Usage
Specific Strengths
Specific Limitations

Pages 12-13, Discussion of SELECT. It is unclear how this Methodology relates to Table 1. There isn't much information to allow a comparison with other methods.

Page 13, Discussion of SPARROW. It is unclear how this Methodology relates to Table 1. There isn't much information to allow a comparison with other methods.

Page 13, Discussion of Mass Balance Method. Add the acronym "(MB)" to match the reference in Table 1.

Pages 15-19, Discussion of Mechanistic Hydrologic/Water Quality Bacteria Models. The discussion would be much more accessible if, for each model, the discussion were divided into specific and consistent topic subheadings. In addition, use of consistent subheadings should help in ensuring a somewhat more balanced presentation of the various methods. The following subheadings might be considered:

What It Is
Data Requirements
Ease of Application
Value in Supporting Implementation
Examples of Previous Usage

(NWF comments continued)

Specific Strengths
Specific Limitations

Pages 18-19, Important Considerations for Bacteria Modeling. I think these are important summary points and a good addition to the document. It seems that their value would be strengthened by expanding on them somewhat. For example, the third and fourth bullet points note uncertainties about sediment settling and re-suspension processes and about bacterial regrowth and death, respectively. Is there something that can be done in the short-term to address these uncertainties? If not, how should these uncertainties affect the decision-making process, if at all? With respect to the last bullet point addressing uncertainty, it would be useful to provide some discussion of how this uncertainty should be considered in relation to the requirement in a TMDL for an adequate margin of safety.

Page 22, Table 2. The column regarding accuracy of source identification seems a bit ambiguous in the absence of some definition of the terms “moderate” and “high.” In particular, it would be helpful to have an explanation of how those terms relate to the range of “rates of correct classification” discussed on page 28. For example, it would be helpful to know if the accuracy characterizations in Table 2 refer to a three-way split, a seven-way split, or something else. It seems extremely important for this document to help inform expectations about what level of source discernment can realistically be expected for BST work. The discussion on page 28 provides useful information but it is not clear how it relates to some of the summary information, particularly the information in Table 2.

Page 30, Discussion of BST library. A more direct discussion of the geographical reach of an individual library would be helpful. It seems from the current discussion that there is an open issue of the extent to which a particular library can be relied upon outside of the watershed of collection. However, there is no clear statement as to the geographical extent to which use of a library should initially be limited absent a demonstration of validity outside of that initial area.

Page 33, Recommended Decision-Making Process for Texas TMDL and I-Plan Development.

Step 4, Load Duration Curves. The references to Step 2 in the discussion appear more properly to be references to Step 3.

Step 5, Bacteria Source Tracking. The reference to Step 2 in the discussion appears more properly to be a reference to Step 3.

Step 6, TMDL Development. It would be very helpful to have some elaboration on what is to be considered in determining whether “data is sufficient” for Step 6. Elaboration in this document on that issue could go a long ways in establishing realistic

(NWF comments continued)

expectations that could be very important in achieving buy-in from stakeholders down the road.

Step 7, **TMDL-IP Development.** It would be beneficial to have some discussion of the factors that should inform a decision about whether detailed simulation modeling studies are “needed.” This is the kind of information that could make a real difference on the ground. Also, it appears that the reference in the Step 7 discussion to flow data from “Step 2” should be a reference to Step 3.

Page 65, Appendix 4. It is extremely important to acknowledge that all TMDLs are not created equal in terms of their value in achieving actual water quality improvement. Texas has proceeded down a path of spending more time in developing TMDLs that are designed to achieve stakeholder buy-in and to result in meaningful implementation of water quality improvements. Many of the TMDLs developed in other states, particularly those driven by litigation, take a very different approach. In fairness, the discussion should acknowledge that more explicitly. For example, the following text could be added just before Table 1 on page 65: “TMDLs that are prepared hurriedly to meet court-mandated deadlines may not be sufficiently specific or achieve adequate stakeholder acceptance to support development of comprehensive implementation plans, particularly where multiple sources and types of sources are involved. Accordingly, the approval of a large number of bacteria TMDLs does not necessarily represent a significant improvement in water quality.”

As previous comments by others have indicated, it would be helpful, to the extent the information is reasonably available, to have an additional column in Table 1 of Appendix 4 that summarizes information about how many implementation plans have been developed and implemented in other states.

Texas Parks and Wildlife Department Comments

December 15, 2006

General Comments

This draft is much improved over the earlier drafts, particularly the modeling section. The bacteria source tracking section still does not provide quantified estimates of quality or accuracy, or sampling requirements, much less a comprehensive comparison of the methods. Methods used outside of Texas and by researchers other than the authors do not have sufficient information provided in the text or comparisons made with the methods discussed in the text. Considering that the purpose of this document is the evaluation of methods which will be used in a regulatory process requiring legally defensible data, the accuracy of the method results and sampling constraints are critical issues that must be addressed.

Providing general USEPA information in an appendix is not helpful. Comparisons of the methods need to be presented together to allow a more focused review rather than requiring the reader to dig out the information from other publications or appendices. We feel that it would be helpful to incorporate much of this information in the text.

While the modeling section of the report now at least acknowledges the importance of the data inputs being used (pages 18 and 19), we suggest that information be presented about the limitations of the different models and the reliability of the calculations.

If the readers are nonspecialists, after reading this document they are likely to be confused and uncertain of what any given model or BST method will reliably do. In addition to what is presented, can the material be summarized for the nonspecialist?

The term "wildlife" as used in this document is contrary to the regulatory definition of wildlife for the State of Texas. To eliminate confusion in this document and future TMDL studies, it is recommended that the term "wildlife" be deleted from this document and replaced with a more accurate term such as "non-domestic animals." At a minimum, the term "wildlife" should be clearly and openly defined for this document as including native wildlife, exotic animals and feral domestic animals such as feral hogs, ducks, cats, dogs, etc.

Acronyms need to be defined. A table of acronyms would be helpful.

Modeling Section

Table 1 – Bacteria modeling matrix – Runoff has not been included as a “LA Source.” Should “in-stream processes” be adjacent to “sediment transport?”

(TPWD comments continued)

Pg. 6 – The list of "dispersed (or nonpoint) sources" should include agricultural sources such as livestock, pastures and livestock holding facilities, as they may be major contributors.

Pg. 13 – For the SELECT tool, the text notes that, "The populations of agricultural animals, wildlife, and domestic pets will be calculated and distributed throughout the watershed according to appropriate land use." For the BLEST tool (pg. 14) the text notes that sources include wildlife and domesticated animals. We note that models are only as reliable as their input data and that estimation of the input parameters has been a source of concern for stakeholders. While research needs have been noted in a following section, can the modeling section provide a decision tool which identifies how to approach estimating input parameters with the data available today?

<u>BST Section</u>

Page 20 - The last sentence of the first paragraph notes that detailed discussion of topics related to quality control and quality assurance are "outside the scope of this report." It is suggested that this sentence be deleted and that information about quality control and quality assurance be included as part of the method evaluation.

As we understand it, the purpose of this report is to recommend methods and processes to be used in Texas TMDL regulatory efforts, which requires legally defensible data. As such, how can the authors ignore issues of quality control and quality assurance, since decisions on appropriate methods cannot be made without considering the validity of the results.

The authors seem to be presenting the methods as if they are already approved for use in the Texas regulatory process rather than fulfilling the task force's role of "<u>evaluating scientific tools</u>, including bacteria fate and transport modeling and bacterial source tracking (BST)" and "<u>suggesting alternative approaches</u> using bacteria modeling and BST for TMDL and I-Plan development, <u>emphasizing scientific quality</u>…" (from page 2 under Task Force charges, emphasis added.

In the last sentence of the second paragraph it is stated that bacterial source tracking has the advantage of direct regulatory significance. We feel that this statement is premature. Until the accuracy and quality of the results from this method are determined to be defensible in a legal (regulatory) context its significance cannot be measured. At this point, the information provided has not shown that the methods generate regulatory quality data.

The authors have declined to consider library size and representativeness. We disagree with this, as the construction and content of the library determines the accuracy of any library-dependent method. While internal accuracy can be measured by rates of correct classification, absolute accuracy cannot be determined without evaluation of the library.

(TPWD comments continued)

We recommend discussion of the shortcomings of library methods and feel that improvement of libraries is critical. This includes the need to expand the libraries with more species representatives, larger samples of individual species and samples with more geographic and temporal variation.

Page 22 (Table 2) - The table provides only qualitative information and does not provide any quantified comparisons. Definitions should be provided for the qualitative terms used (moderate, high, low, easy, etc.). The definitions should provide a numeric range of a quantified factor as a percentage (e.g., moderate = rate of correct classification of 50-75%). At a very minimum there should be text explaining the terms used. As it stands, it is not possible for a reader to understand the meaning of the table entries. Later in the document the authors consider a rate of correct classification of 60% as "relatively high" (page 28). Considering this is little better than the 50% expected in "flipping a coin," our confidence in these descriptive phrases instead of numerical values is minimal.

Page 23 - In the first paragraph the authors appear to imply that the libraries of isolates can be combined and used across the state in different studies by various researchers. There are obvious questions about the validity of combining libraries. Do isolation techniques vary between studies or are accepted, standard methods used for all libraries? It appears that there are no accepted standard methods (e.g., fecal material collection methods) to guarantee that all libraries are comparable or accurate. We wonder if it is scientifically valid to combine libraries from different studies and suggest that for libraries to be combined one must conduct an evaluation to determine that common methods and data quality exist. We recommend that a cautionary note be included in this document.

Pages 23-26 - In each of the method descriptions general, non-numeric terms are used to describe the ability of the method to resolve different closely related bacterial strains. As noted earlier for Table 2, these terms are not useful in making vital comparisons between the methods. As commented for Table 2 numerical ranges (e.g., 40-50%) or a numerical definition of the terms needs to be made to allow the reader to evaluate the methods.

Page 25 – In describing pulsed-field gel electrophoresis, the sentence, "While this allows higher confidence in the matches made, typically fewer environmental isolates are identified compared to other BST techniques," is used as a negative. Could the authors elaborate on this statement? Does it mean that fewer samples are analyzed or does it imply that pulsed-field gel electrophoresis has fewer false positives than other methods?

Page 26 - The Carbon Source Utilization method is not compared with the other methods. It was noted that this method was used in Texas and other states with at least some in conjunction with KB-ARA. The studies should be discussed and comparisons provided. The studies should also be cited.

(TPWD comments continued)

Page 27 – It would be helpful to provide a table illustrating the results from the Lake Waco and Belton Lake study and comparisons of the methods. This table should include information on the accuracy, blind controls, library quality, ability to identify water isolates, sample size, and statistical analyses results noted in the text. This information is vital in evaluating methods and should be shared.

The authors note percent congruence between some methods (we assume congruence means agreement). This should be clarified. This whole section should be expanded to provide the reader with more information on the comparisons and study parameters.

Page 28 – It is an improvement to the report that some mention of accuracy has been included. However, not enough information is provided. It would further improve the report to include an explanation of how rates of correct classification are determined. A table, (as requested for page 27) would be helpful. The accuracy values provided were 83%, 95%, 83%, 72%, 73%, 22 to 83%, 83%, and 60%. In general, we believe that field techniques that have accuracies below 80% should be used very cautiously as they may not hold up to critical review. Indeed, as noted before any accuracies near 50% are no better than flipping a coin.

The “rate of correct classification” analysis seems to address library internal accuracy. Has any work been done to determine absolute accuracy, rather than internal consistency? This is essentially a question of the accuracy of the library, particularly as relates to promiscuity of bacterial strains, statistical soundess, and sampling techniques. Stated another way: For a particular identification, from how many animals could the particular *E. coli* strain have come? How many of those animals are included in the library? Do we have adequate statistical replication to be certain? Could the strain have been introduced in a sample that was collected off the ground?

All that being said, we find it more defensible to use source tracking to identify a three-way split (domestic sewage, livestock, non-domestic animals) based on the limited information provided. However, source tracking for classes beyond this level (i.e., individual taxa) presently generates data that is suspect for regulatory actions and should not be proposed until the issues noted in these comments and the significant method development items noted in this report are addressed.

As a future goal, TPWD would support a separation of bacterial contributions into human, livestock, domesticated animals, native wildlife and exotic/feral wildlife. To be most helpful, even the native wildlife should be further separated into categories such as avian wildlife and mammalian wildlife. While it is desirable to have information down to taxa, with the present state of the science, it does not seem possible.

Page 29 - The statements in this section such as " no single BST method should be solely relied upon," "choosing the methods include the level of resolution needed," and "uncertainties regarding geographical stability of markers and the difficulty in

(TPWD comments continued)

interpreting results in relation to regulatory water quality standards and microbial risk" reinforce the difficulty in using BST techniques in a regulatory process. As noted above, we believe that BST should not presently be used beyond three-way splits until the method questions and problems are addressed and highly accurate standard techniques can be implemented for BST.

There is great detail in the report about library-dependent methods. Could more information be provided about how library-independent methods work? Is there potential to expand library-independent methods to other species, or are they inherently limited?

Page 30: The idea of combining BST libraries is again broached here. As commented earlier (page 23), only libraries using common accurate methodologies should be considered for combination and even in such situations the data need to be thoroughly examined for accuracy before such an action takes place. We agree that geographic and temporal stability need to be determined before such actions can be considered. These cautionary notes need to be more fully expressed in the text.

In Appendix 4, it is noted that, "BST does not tell you how much each source contributes to bacterial contamination, only the different kinds of sources." This suggests that BST is useful as a qualitative, rather than a quantitative tool. Based on our limited experience with BST, the cited rates of correct classification, and the identified research needs, this viewpoint seems supportable. It is difficult to endorse quantitative use of BST given the unresolved questions with the technique. We then wonder how reliable BST data will be as input to the various modeling tools.

Pages 32-33 - The recommended decision-making process outlines a procedure that might take several years. How quickly do bacterial strains mutate? It seems that there may be concerns about temporal variability of *E. coli* strains on relatively short time frames. Do we know if it is possible to use BST in a regulatory process that may span 5-10 years?

Recommended Decision-Making Process

Page 32 - The document has a section on the decision-making process for TMDL and implementation plan development, which identifies potential members for stakeholder work groups. As commentors have noted elsewhere in the document, stakeholder buy-in is critical to the success of the TMDL and implementation plan process. In order to facilitate understanding, communication and participation, we suggest that TCEQ and TSSWCB form a separate small work group in addition to the Task Force whose focus would be to create a blueprint for a successful stakeholder process. Such a blueprint could be used by staff of both agencies statewide in TMDL, implementation plan and watershed protection plan processes. We envision that it would address stakeholder group membership, attendance at meetings, and communication to stakeholders.

(TPWD comments continued)

It is critical that the state and local agencies be specifically included in the stakeholder group to ensure TMDL and other regulatory issues, are addressed in a manner appropriate to the relevant authority. Failure to do so could unwarranted expense or controversy.

Research and Development Needs

We do not disagree with any of the research needs that have been identified. That being said, in order to best serve the state, we believe that the list must be prioritized to address regulatory needs and to generate data that is defensible and that will stand up to the legal process. As it is now, the list seems to be ambitious for a 3-5 year horizon, even as a research "wish list."

Pages 41 and 42: We recommend adding bullets for BST research and development needs to develop standard methods to be used in library development and sampling for BST studies. Noting the issues listed under BST research and development needs along with the comments provided above suggests that BST is not presently at a point to be a critical component in a regulatory, legally defensible process. The use of BST should be at most as additional information in a weight-of-evidence approach to help in decisions using a three-way split (human, livestock, non-domestic animals).

Appendix 1

Please add Pat Radloff and David Sager to the list of experts.

Appendix 4

Have the authors found any example of any state which has successfully improved water quality by implementing a bacterial TMDL?

Appendix 5

In response to comment aw79: The commenter is correct. This should read: "Overall, the library needs to be extended to include more taxa with rigorously collected samples with adequate replication for each species."

Respectfully submitted on behalf of Texas Parks and Wildlife Department,

Dr. Patricia Radloff, Coastal Fisheries Division
Dr. David Sager, Inland Fisheries Division
Dr. Duane Schlitter, Wildlife Division

TEXAS DEPARTMENT OF TRANSPORTATION – HOUSTON DISTRICT
Comments on the Bacterial Total Maximum Daily Load Task Force Report Second Draft, December 4, 2006

Comments Submitted December 18, 2006

Introduction

As a stakeholder in many Texas bacteria TMDLs, the Houston District of the Texas Department of Transportation (the District) is very interested in the deliberations and findings of the Bacterial TMDL Task Force (Task Force). We appreciate the opportunity to provide comments on the Bacterial Total Maximum Daily Load Task Force Report Second Draft and to assist the Task Force in its work.

Task Force Charge

We believe that the charge to the Task Force should be placed in the introductory statements of the report, but we believe that it should be stated verbatim from the charge issued as posted on the TWRI Bacteria TMDL website[8].

Bacteria Fate and Transport Models

1. **Table 1 Bacteria Modeling Matrix:** The revisions to this section of the document have strengthened it with a higher level of detail. We feel that Table 1 should be moved to the end of the section to allow the reader to digest the different models, acronyms, and TMDL information presented within the section and the table should be introduced with a short paragraph that presents the matrix and explains how to use the matrix in detail. Other comments directed to Table 1 include:
    - The watercourse type breakdown is slightly confusing. We propose to rename Fresh/Saltwater Estuarine to simply Estuarine.
    - Several tools are described throughout the section such as SELECT and SPARROW, yet are not included in Table 1.
    - All of the mass balance (MB) watercourse boxes should be checked.
    - The MB, BLEST, BSLC, and BIT boxes for TMDL Implementation should be checked. Also, these methods account for some spatial variations, so perhaps the 1-D box should be checked.
    - The HSPF, SWAT, and SWMM boxes for 1-D should be checked.
    - The SWMM boxes for river/stream and TMDL development and implementation should be checked.
    - The HSPF and SWMM boxes for steady state time scale should be checked. A constant-value time series can be used to create a steady-state simulation.
    - The SWAT box for time varying should be checked. The model allows for a daily, monthly or yearly time step. The SWAT box for single storm event should be unchecked because of the large time steps.
    - Additional estuarine models should be included in the mechanistic/hydrologic/WQ section of the matrix that are capable of simulating coastal hydrodynamics and water quality.

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[8] See http://twri.tamu.edu/bacteriatmdl/

2. **Load Duration Curve:** The LDC section has been strengthened significantly, but the following sentence should be added: *Among the disadvantages of the LDC method is that TMDL duration and frequency targets cannot be directly compared to the LDC.* Also, we suggest adding the following short discussion: *There is a potential for linkage between models and bacteria source tracking (BST). These methods can be used to complement each other. For example, several bacteria TMDL studies have been utilized the LDC model combined with BST to determine bacteria loads and allocations.*

Bacteria Source Tracking

1. **Entry Pathways Not Identified:** Many of the comments that were expressed in Drafts 1 and 1.5 have been addressed by the revisions to this section. It should be noted in the Regulatory Expectations section that no BST method will identify the entry pathway to the water body and that the methods only identify the sources. This means that bacteria from a particular animal may be deposited in the watershed and then be conveyed to the water body by various transport mechanisms and conveyances, each owned and operated by different watershed stakeholders. This is critical to developing implementation actions. The report should acknowledge this missing information in this section.
2. **Identification of only Some Sources:** Another limitation that should be recognized is that the sources identified to date in BST work are not a complete inventory. In discussions following the last draft, it was noted that no unique signature had been identified for soil or stream sediment bacteria. The same is probably true for bacteria that grow in streams following wastewater disinfection. BST studies that focus on only selected intestinal sources are thus limited in their ability to characterize the full range of sources of indicator bacteria. The report should acknowledge this limitation.

Recommended Decision-Making Process for Texas TMDL and Implementation Plan Development

4. **Process Steps:** We support the inclusion of a road map for TMDL development and implementation. The steps outlined appear to be a good start in documenting the approach. We urge the Task Force to reconfigure the material into a flow diagram, with actions and decision points. This will allow the process to incorporate adaptive management, phased TMDL's and Phased Implementation.
5. **Margin of Safety:** A discussion of the determination of where the margin of safety will be incorporated into the TMDL should be included in Steps 4, 5, and 6. Step 5 of the decision-making process refers to a BST decision matrix. We recommend including this matrix in the BST section or if it is referring to the EPA decision matrix, the appropriate Appendix should be referenced.
6. **Steps 6 and 7 Should Incorporate Discussion of Adaptive Management, Phased TMDLs, and Phased Implementation:** We believe that the Task Force should include an up-to-date discussion and consideration of the most recent guidance from EPA regarding options for developing phased TMDL's , the use of adaptive management, and phased implementation. We urge the Task Force to consider and incorporate elements from the August 2, 2006 EPA memorandum from Benita Best-Wong to all EPA regions[9] so that these concepts can be

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[9] See http://www.epa.gov/owow/tmdl/tmdl_clarification_letter.html

7. included. Specifically, we suggest the following language be inserted into the Task Force Report:

   The TCEQ should adhere to the policy provisions of the EPA memorandum regarding TMDL implementation as follows:

   Phased TMDLs: *The use of the term "phased TMDLs" should be limited to TMDLs that for scheduling reasons need to be established despite significant data uncertainty and where the state expects that the loading capacity and allocation scheme will be revised in the near future as additional information is collected.*

   The phased TMDL approach would be used in situations where limited existing data are used to develop a TMDL and the state believes that the use of additional data or data based on better analytical techniques would likely increase the accuracy of the TMDL load calculation and merit development of a second phase TMDL. Such significant uncertainty may arise, for example, because the State is using a surrogate to interpret a narrative standard, or because there is little information regarding the loading capacity of a complex system such as an estuary and it is difficult to predict how the a water body will react to the planned load reductions. An example of a phased TMDL could be a TMDL for phosphorus in a lake watershed where there are uncertain loadings from the major land uses and/or limited knowledge of in-lake processes. In such a case, the loading capacity of the water body may be difficult to establish and the State may decide to include a schedule for establishing a revised TMDL based on follow-up monitoring. ***Phased TMDLs may also occur when a revision of the applicable standard is underway and will necessitate development of a second phase, revised TMDL to comply with the new standard [emphasis added].***

   All phased TMDLs must include all elements of a regular TMDL, including load allocations, wasteload allocations and a margin of safety. As with any TMDL, each phase must be established to attain and maintain the applicable water quality standard. In addition, EPA recommends that a phased TMDL document or its implementation plan include a monitoring plan and a scheduled timeframe for revision of the TMDL. (These elements would not be an intrinsic part of the TMDL and would not be approved by EPA, but may support a rationale for approving the TMDL.)

   Since phased TMDLs will in all likelihood need to be revised and therefore require more overall effort, States should carefully consider the necessity of such TMDLs, for example to meet consent decree deadlines or other mandatory schedules Upon revision of the loading capacity, wasteload, or load allocations, the TMDL would require re-approval by EPA.

   TMDLs with Adaptive Implementation Provisions: *Adaptive implementation is an iterative implementation process that makes progress toward achieving water quality goals while using any new data and information to reduce uncertainty and adjust implementation activities. The National Research Council report suggests that adaptive implementation include "immediate actions, an array of possible long-term actions, success monitoring, and experimentation for model refinement." By using the adaptive implementation approach, one can utilize the new information available from monitoring following initial TMDL implementation efforts to appropriately target the next suite of implementation activities.*

   Phased TMDLs are an example of the adaptive implementation approach because each new phase utilizes new information to reevaluate the original TMDL. However, even for TMDLs where there is little uncertainty regarding the loading capacity of the water body and the *necessary load reductions, an adaptive implementation approach can be a useful tool. Implementation of TMDLs can take many years and when uncertainty about the effectiveness of implementation activities exists, TMDLs would benefit from containing elements that would facilitate adaptive implementation such as, for example, provisions for a flexible load allocation/waste load allocation scheme. EPA is currently working to clarify how TMDLs can be written to provide for adjustments in the load and wasteload allocations in approved TMDLs.*

EPA understands that not all TMDLs can be implemented using adaptive implementation methods due to the more intensive monitoring and added administrative steps associated with this iterative approach. Nonetheless, EPA believes that in appropriate cases it should be feasible for States to develop TMDLs that facilitate implementation of practicable controls while additional data collection and analysis are conducted to guide implementation actions. Follow-up monitoring is integral to the adaptive implementation approach. Monitoring addresses uncertainty in the efficacy of implementation actions and can provide assurance that implementation measures are succeeding in attaining water quality standards, as well as inform the ongoing TMDL implementation strategy. If adaptive implementation activities reveal that a TMDL loading capacity needs to be changed, the revision would require EPA approval. In most cases adaptive implementation is not anticipated to lead to the re-opening of a TMDL. Instead, it is a tool used to improve implementation strategies.

***TMDLs with Staged Implementation:** The third type of TMDL, described in the Great Lakes Initiative, is different from the two preceding types. While not a "phased TMDL," it is a TMDL that anticipates implementation in several distinct stages. It is also different from the adaptive implementation scenario because it is anticipated that the load and wasteload allocations will not require any significant adjustments. Instead, implementation actions will be staged over a period of time. For example, EPA has approved mercury TMDLs where the wasteload allocation to point sources (which would be implemented within five years through the NPDES process) was predicated on long-term reductions in atmospheric mercury deposition. We believe that the appropriate terminology for such a TMDL, if a label needs to be applied, would be "staged implementation."*

8. **Step 6 Should Incorporate Discussion of Wet Weather Concentrations and Loads:** Urban stormwater frequently can contain elevated bacteria concentrations and loads, however, the impact of these episodic events on attainment of contact recreational uses is not clear and certainly, no consensus on how to deal with wet weather has emerged. Approaches to consider stormwater loads during TMDL development are similarly not straightforward. We urge the Task Force to consider the November 22, 2002 EPA memorandum from Robert Wayland to all EPA regions[10] so that wet weather issues can be addressed when developing TMDL's with stormwater loads. Specifically, we suggest the following language be inserted into the Task Force Report:

   TMDL's with NPDES-regulated storm water discharges should be developed using the following approaches:

   a) NPDES-regulated storm water discharges must be addressed by the wasteload allocation (WLA) component of a TMDL.

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[10] See http://www.epa.gov/npdes/pubs/final-wwtmdl.pdf

(TxDOT—Houston District comments continued)

- b) *NPDES-regulated storm water discharges may not be addressed by the load allocation (LA) component of a TMDL.*
- c) *Storm water discharges from sources that are not currently subject to NPDES regulation may be addressed by the load allocation component of a TMDL.*
- d) *It may be reasonable to express allocations for NPDES-regulated storm water discharges from multiple point sources as a single categorical wasteload allocation when data and information are insufficient to assign each source or outfall individual WLAs.*
- e) *In cases where wasteload allocations are developed for categories of discharges, these categories should be defined as narrowly as available information allows.*
- f) *The WLAs and LAs are to be expressed in numeric form in the TMDL.*
- g) *EPA expects TMDL authorities to make separate allocations to NPDES- regulated storm water discharges (in the form of WLAs) and unregulated storm water (in the form of LAs). EPA recognizes that these allocations might be fairly rudimentary because of data limitations and variability in the system.*

9. **Step 7 Should Incorporate Discussion of Wet Weather Concentrations and Loads:** Urban stormwater frequently can contain elevated bacteria concentrations and loads, however, the impact of these episodic events on attainment of contact recreational uses is not clear and certainly, no consensus on how to deal with wet weather has emerged. Approaches to consider stormwater loads during TMDL implementation planning are similarly not straightforward. We urge the Task Force to consider the November 22, 2002 EPA memorandum from Robert Wayland to all EPA regions[11] so that wet weather issues can be addressed when developing TMDL implementation plans with stormwater loads. Specifically, we suggest the following language be inserted into the Task Force Report:

   TMDL implementation plans with NPDES-regulated storm water discharges should be developed using the following approaches:

   - a) *WQBELs for NPDES-regulated storm water discharges that implement WLAs in TMDLs may be expressed in the form of best management practices (BMPs) under specified circumstances. If BMPs alone adequately implement the WLAs, then additional controls are not necessary.*
   - b) *EPA expects that most water quality based effluent limits (WQBELs) for NPDES-regulated municipal and small construction storm water discharges will be in the form of BMPs, and that numeric limits will be used only in rare instances.*
   - c) *When a non-numeric water quality-based effluent limit is imposed, the permit's administrative record, including the fact sheet when one is required, needs to support that the BMPs are expected to be sufficient to implement the WLA in the TMDL.*
   - d) *The NPDES permit must also specify the monitoring necessary to determine compliance with effluent limitations. Where effluent limits are specified as BMPs, the permit should also specify the monitoring necessary to assess if the expected load reductions attributed to BMP implementation are achieved (e.g., BMP performance data).*
   - e) *NPDES permit conditions must be consistent with the assumptions and requirements of available WLAs.*

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[11] See http://www.epa.gov/npdes/pubs/final-wwtmdl.pdf

(TxDOT—Houston District comments continued)

f) *The storm water permit should also provide a mechanism to make adjustments to the required BMPs as necessary to ensure their adequate performance.*

Research and Development Needs

1. **Previous Comments:** Some of our comments concerning research and development needs were submitted in a separate document on December 13, 2006. These comments are repeated here:

   - **Research Indicator Bacteria Sources in Runoff:** There is a need to understand why indicator bacteria concentrations in rainfall runoff tend to be very high—frequently two orders of magnitude greater than the concentration deemed suitable for swimming. Such high runoff concentrations can be understood in watersheds where there is a high density of intestinal waste sources (e.g. a cow pasture), but it is more difficult to understand in watersheds that have minimal wildlife uses such as parking lots, streets, or large roofs. Monitoring for many years by the City of Austin has demonstrated that runoff from all types of watersheds, from those with no impervious cover to 100% impervious cover, have Event Mean Concentrations of both Fecal Coliform and Fecal Streptococcus that are high. The geometric mean of FC observations was 42,625 cfu/dL and the Fecal Strep geomean was 69,004 cfu/dL (COA-ERM/WQM 2006-1). Research to better quantify the sources of bacteria from a range of watershed types would be essential to understanding how we might expect to achieve the existing criteria for swimming in streams that have a significant runoff component.
   - **Research Pathogen Sources in Stormwater:** A related research need is to address other bacteria forms such as *Shigella, Campylobacter,* and *Staphylococcus* in runoff from these watersheds. The historical focus on indicator bacteria to identify a human sewage source has been useful, but has been complicated by the knowledge that the same indicator bacteria are common in runoff from all types of watersheds, as well as being common in stream sediments and soils. While it may be tempting to dismiss the risk of disease from swimming in waters with high concentrations of indicator organisms that are not from human waste, it is not so easy to dismiss the risk from other potential pathogens such as those listed above. Research on the sources and the human health significance of these bacterial forms is needed.
   - **Conduct Studies to Better Define Indicators and Disease Risk for Freshwater Streams and Bayous:** Original EPA studies to identify indicator bacteria criteria to protect contact recreational uses were conducted in lakes with designated swimming areas and nearby wastewater discharge points (EPA, 1986). Studies need to be performed to develop a scientific basis for appropriate freshwater contact recreation criteria for streams, bayous, and rivers, particularly in tropical climates. Criteria should address incidental contact with riparian waters during boating and wading activities.

2. **Consider National Guidance and Recommendations First:** The EPA and the National Academy of Sciences have both produced significant publications identifying research needs. The District urges the Task Force to consider these publications when identifying research needs for Texas. These publications include Reckhow, Donigian, et. al., 2001;[12] Shoemaker, Dai, and Koenig, 2006;[13] and EPA, July 2002.[14] While these references don't explicitly and

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[12] See http://www.nap.edu/catalog/10146.html#orgs

[13] See http://www.epa.gov/ORD/NRMRL/pubs/600r05149/600r05149.pdf

3. directly address bacteria TMDL issues, they do include important findings regarding the process, policy issues, scientific rigor, and equity issues that impact bacteria TMDL development and implementation. Specifically, we suggest the following language be inserted into the Task Force Report:

   From Reckhow, Donigian, et. al., 2001:

   - ***Suggested TMDL Program Changes:*** *Develop appropriate use designations before water body assessment and refine them before TMDL development and employ use of adaptive implementation.*
   - ***Water Quality:*** *Assigning tiered designated uses is an essential step in setting water quality standards. Once designated uses are defined, criterion chosen to measure use attainment should be logically linked to the designated use.*
   - ***TMDL Development:*** *Uncertainty must be explicitly acknowledged. End the practice of arbitrary selection of the margin of safety (MOS) and require uncertainty analysis to determine the MOS. Assessment and monitoring programs need to be coordinated so that TMDL development and modeling data needs are more closely met.*
   - ***TMDL Implementation:*** *A Use Attainability Analysis (UAA) should be considered for all water bodies before a TMDL plan is developed.*

   From Shoemaker, Dai, and Koenig, 2006:

   - ***Statistical Modeling of Pathogens.*** *Guidance and additional techniques for modeling pathogens using statistical techniques are needed. Building statistical models that associate sources or localized loading potentials could help support evaluation of management alternatives. Simple spreadsheet tools could be developed to facilitate analysis.*
   - ***Guidance.*** *Examples, guidance and applications of modeling E. coli and enterococci should be developed. An expanded dataset and compilation of available source loading and die-off characteristics would assist in parameterizing models. Increased data collection will assist in developing calibrated applications.*
   - ***Genetic Tracer Analysis.*** *Genetic source typing can provide a discrete representation of the sources present at a particular location. Guidance and examples are needed on how to link genetic source typing information with dynamic modeling applications.*
   - ***Growth and Die-off Rates.*** *Models typically represent bacteria behavior by using a first-order decay term. However, in many systems, bacteria appear to die-off or regrow depending on environmental conditions. Development of second-order equations or functional relationships that more accurately represent bacteria growth and die-off rates would significantly improve modeling accuracy. The regrowth potential is of particular concern in coastal areas with shellfish beds and beaches.*
   - ***Shellfish Areas.*** *In tidally influenced areas, often located in the vicinity of shellfish beds and beaches, specialized modeling techniques are needed to evaluate loading and associated pathogen counts. The ability to comply with water quality standards for pathogens in tidal areas strongly correlate to the tidal circulation and configuration of*

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[14] See http://www.epa.gov/owow/tmdl/20needsreport_8-02.pdf

the shoreline. Areas with poor flushing potential are particularly prone to high pathogen counts, in some cases due to highly localized sources. Some options proposed for simulation of these tidal areas include linkage of watershed models such as HSPF and LSPC to the Tidal Prism Model. Other techniques have included simplified loading estimates using monitoring data or genetic tracer information in combination with receiving water models such as the Tidal Prism Model. Additional research is needed to better characterize sources and develop protocols for linking monitoring with models.

From EPA, 2002:

- ***Improve guidance for allocation development and methods to translate allocations into implementable control actions.*** *Once the linkage is made between pollutant sources and instream water quality, the available assimilative capacity is allocated among the watershed's point and nonpoint sources. Allocation is a critical juncture in the steps of TMDL development from modeling through implementation of point and nonpoint control actions. Social and economic considerations also complicate allocation decision-making. Office of Research and Development activities such as alternative futures assessment, watershed risk assessment, modeling, sustainable ecosystems, socioeconomic and pollutant trading research are all potentially relevant.*

- ***Improve information on BMP, restoration or other management practice effectiveness, and the related processes of system recovery.*** *As management practices are typically implemented under limited budgets, post-evaluation is often dropped despite the fact that this is among the most widely cited needs. Practically every type of Best Management Practice (BMP) or restoration technique needs effectiveness research. Researchers must also consider that recovery of impaired systems is intimately linked to effectiveness, and recovery is not just the inverse of degradation. EPA's investment in effectiveness research is substantial, and Office of Research and Development should continue to closely track the programs and practitioners who are their clients.*

- ***Develop adaptive implementation approaches for doing TMDLs.*** *The National Research Council recommended that "TMDL plans should employ adaptive implementation.... foster the use of strategies that combine monitoring and modeling and expedite TMDL development." There is widespread agreement that adaptive management on a watershed basis is a sound and practical approach for TMDLs, but the need for more specific research remains. EPA researchers might develop or evaluate adaptive management strategies, or focus on related tools such as recovery forecasting models, post-implementation monitoring methods, and alternative futures analysis.*

- ***Revisit the scientific basis for use designations.*** *The National Research Council panel called "tiered designated uses" an essential step, claiming that there should be substantial stratification and refinement of uses with scientific, social and economic input about the desired state for each water body. EPA researchers might study the few states that have begun to use tiered uses; Office of Research and Development might also use their skills in endpoint development to facilitate states' refinement of designated uses. Research in watershed classification and reference condition of different water body types may prove important.*

- ***Assist states in translating narrative standards into numeric criteria.*** *The uncertainties inherent in evaluating impairment qualitatively rather than quantitatively even affect the top three listed impairments (sediment, nutrients, and pathogens), which in many states*

(TxDOT—Houston District comments continued)

have qualitative or weak quantitative criteria. But among TMDL developers, numeric criteria are sometimes but not always preferred. Office of Research and Development's narrative/numeric translation support could work with states on translators, develop the basis for new numeric criteria (e.g., for effluent dominated streams, odor, aesthetics, fish advisories), further incorporate flow considerations, and support Office of Water in triennial reviews of state water quality standards.

- ***Clarify and quantify selected parameters used in criteria definitions.*** *On this issue the National Research Council panel stated, "All chemical criteria and some biological criteria should be defined in terms of magnitude, frequency, and duration." Even beyond clarifying these three key parameters, criteria can and should go farther (in definition and in application) when necessary to establish a more reliable relationship between the designated use and the criterion meant to protect it. Temporal considerations are particularly in need of improvement, and regionalized syntheses of episodic stressor behavior would be useful. Researchers might also address flows at which standards must be met, wet weather conditions, and sediment lethality.*
- ***Evaluate defensible scientific standards for listing and de-listing.*** *Specifically, the National Research Council panel's recommendation of a two-part impaired waters list (preliminary and final lists) has implications for monitoring research, sampling methods development and statistical analysis, usually occurring in a data-limited environment. Strengthening the scientific basis might include statistical guidance for listing decisions, methods for combining multiple lines of evidence (e.g. biomonitoring and chemical monitoring), improving the analysis of the role of flow as ultimately affecting the designated uses, and methods for uncertainty analysis.*

HARRIS COUNTY
PUBLIC INFRASTRUCTURE DEPARTMENT

1001 Preston, 5th Floor
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(713) 755-4400

December 15, 2006

C. Allan Jones, Ph.D., Director
Texas Water Resources Institute
1500 Research Parkway, Ste. 240
College Station, TX 77843-2118

SUBJECT: BTMDL Task Force Report – Second Draft, December 4, 2006

Dear Dr. Jones:

Harris County appreciates the opportunity to comment on the referenced report. We are deeply appreciative of the time and effort taken by you and the other members of the Task Force in guiding future work in the field of water quality. Transmitted herewith for consideration by the Task Force please find attached Harris County's comments on the Second Draft of the Report.

If you have any questions regarding these comments or need further information, please call me at (713) 316-4877 or Alisa Max at (713) 290-3089.

Sincerely,

John Blount, P.E.
Deputy Director
Planning & Operations

Attachments: Comments on BTMDL Task Force Report

cc: Kevin Wagner – TWRI
Alisa S. Max, P.E. – Harris County
Trent Martin – Harris County
Joe Myers, P.E. – Harris County Flood Control District
Catherine Elliot – Harris County Flood Control District

Comments on Bacteria Total Maximum Daily Load Task Force Report
Second Draft – dated December 4, 2006

John Blount, P.E. – Harris County

1. The Bacteria Source Tracking section describes several commonly-used BST tools. However, a TCEQ study for Buffalo and White Oak Bayous and another for Orange County was recently initiated to examine enteric viruses. These studies have a source tracking component. Since enteric viruses appears to be a currently-used tracking methodology, Harris County recommends changing the name of this section from "Bacteria Source Tracking" to "Microbial Source Tracking" and include a discussion and analysis on enteric viruses.

2. Recommended Decision-Making Process for Texas TMDL and I-Plan Development – Page 32. "Step 2" describes "Sanitary Surveys". The connotation of this phrase denotes sanitary sewerages. However, surveys in this context involve efforts far beyond the scope of WWTPs and collection systems. Therefore, Harris County recommends changing the name from "Sanitary Survey" to "Source Survey".

   Also, please change the phrase, "cities and municipalities" to "local governments". This broader concept includes special districts and counties, in addition to cities and municipalities.

3. Recommended Decision-Making Process for Texas TMDL and I-Plan Development – Page 33. "Step 3" states that monitoring should not begin until input from the stakeholders is received. Harris County is in full agreement with this statement and appreciates its inclusion.

   Also, we request that a statement be added that water quality in one waterway should not be extrapolated and applied for another waterway.

   Lastly, in "Step 5", it is our understanding that BST does not distinguish the means in which the bacteria arrived in a stream (ie- did the human bacteria come out of a pipe or did it regrow from other human bacteria already in the stream). These means are different inputs into most models and could also influence greatly the implementation approaches proposed. Understanding how the bacteria arrived in the stream is also vital in determining what the ratio of human: non-human truly means with respect to reducing point loads into the stream.

4. Recommended Decision-Making Process for Texas TMDL and I-Plan Development – Page 34, "Step 7". Harris County requests that a discussion of adaptive management occur here, including mention of the potential for adverse economic impact in implementing BMPs that are not shown to be effective. Harris County is adamant, as an entity that will be responsible for implementation, that due science prove the effectiveness of a BMP before its use is required. We do not believe that wasting taxpayers' money on ineffective "solutions" is palatable.

(Harris County comments continued)

5. "Bacteria Source Tracking", Page 20. Please include a discussion on the limitations of BST regarding regrowth of bacteria. If regrowth of bacteria occurs, such as is seen in urban streams, then researchers must address if bacteria from different sources re-grow at the same rates; otherwise, differential regrowth rates would badly skew any conclusions.

   Also, fecal indicator bacteria has been found in high numbers from a number of non-animal sources, from rooftops and gardens to mulch stockpiles and forests. Some study designs, such as the BST Study completed for Buffalo and White Oak Bayous in Harris County, assign all bacteria isolates to an animal group. This approach ignores contributions of bacteria from non-animal sources. We recommend including in this discussion an examination and recommendation to address subject bacteria from non-animal sources.

6. Research and Development Needs – Page 35. This section addresses tools and methods for TMDL and I-Plan development. Although important, an equally-important - if not more important - need is the research required for development of tools and methods for *implementation*. That is, once a TMDL and I-Plan is in place, how can local governments and stakeholders feasibly and effectively achieve desired results?

7. Characterization of Sources – Page 36. Please add among the studies needed, studies to quantify bacteria production/shedding from non-animal sources, such as mulch, gardens, or other organic-rich environments.

8. Characterization of Sources – Page 37. The description of studies to improve characterization of loadings from WWTPs states that "(r)e-growth of bacteria after incomplete disinfection can be another concern worthy of more study." Please remove the word "incomplete" from this sentence. Harris County has found that even fully-disinfected WWTP effluent provides a superb growth media for indicator bacteria.

9. Characterization of Kinetic Rates and Transport Mechanisms – Page 40 The last paragraph describes studies to quantify suspended bacteria in stream water column and sediments. Included for consideration is a "…need to consider die-off and regrowth of bacteria under various…"conditions. Harris County requests that bacteria die-off and regrowth be studies of their own; *i.e.*; have its own bullet point. In addition to the conditions listed (sediment, nutrient, water temperature) please include "occurrence of WWTP effluent".

10. In general, this report does not delve into implementation, which was a stated objective for the Task Force. If the Task Force agrees that an assessment of implantation needs and strategies is beyond its scope, then Harris County requests

(Harris County comments continued)

11. that the Task Force recommend that an independent group, comprised of practitioners as well as academia and under the auspices of TSSWCB and TCEQ, be developed to form a white paper on this subject.

12. Table 1 – please add a row to address complexity and/or cost. Also, please note that no model is believed to adequately model bacteria regrowth. This could be a particular hindrance for effluent dominated streams.

13. The concept in the Load Reduction Curve of "Exceeds Feasible Management" is a great concept that should be added to other models.

14. Determination of Effectiveness of Control Measures, Page 42. Harris County disagrees with the statement that determination of effectiveness of various controls is beyond the scope of TMDL and I-Plan development. It is critical to recognize where to draw the line for "exceeds reasonable management". The only true way to know this is to understand how effective treatment controls are. Rather than considering effectiveness of controls as a separate issue from TMDL and I-Plan development, Harris County would like to see a fuller treatment of this subject incorporated into these discussions.

    Also, please change the word "could" to "should" in the second sentence of each bullet point.

15. Harris County's comments from the First Draft are referenced by hyperlink. Please include these and future comments from Harris County in full text. The County can provide comments in electronic format if it would facilitate this request.

16. Several comments from our previous review have not been addressed in this draft. They include Comments # 1, 2, 3, 4, 8, 9, 10, 11, 12, 13, 14, and 15. Please address those comments as well.

UNITED STATES ENVIRONMENTAL PROTECTION AGENCY
REGION 6
1445 ROSS AVENUE, SUITE 1200
DALLAS, TX 75202-2733

DEC 20 2006

Dr. Allan Jones
Director, Texas Water Resources Institute
1500 Research Parkway, Suite 240
2118 TAMU
College Station, TX 77843

Dear Dr. Jones,

Thanks for your leadership and active involvement with the Texas Bacteria Task Force (TBTF) which was formed on September 27, 2006. Since the TBTF was formed, we have had several discussions within EPA on the technical and scientific issues inherent with the establishment of bacteria criteria and the development of Total Maximum Daily Loads (TMDLs) nationwide and particularly in Texas. At the same time, several members of my staff have participated in the TBTF teleconferences held on October 24, 2006, and November 27, 2006, respectively.

Enclosed with this letter, you will find a table summarizing various approaches used by other states to develop bacteria TMDLs, a document with a list of options related to bacteria modeling, and a document with possible options for establishing bacteria criteria. Electronic copies of the TMDLs will be sent via e-mail directly to you. Please note that this information does not include all available TMDLs and options used by other states nationwide.

EPA looks forward to seeing recommendations from the TBTF for expedited development of bacteria TMDLs using more practical methods such as mass balance or load duration curve. As we have stated previously, requiring bacteria source tracking (BST) data as part of the TMDL development will significantly delay timely development and approval of TMDLs. EPA supports the use of BST, as needed, in the implementation phase of TMDLs.

I look forward to receiving a copy of the final recommendations developed by the Texas Bacteria Task Force by the end of January 2007. If you would like to discuss the enclosed information or need additional information, please contact me at (214) 665-7101.

Sincerely,

Miguel I. Flores
Director
Water Quality Protection Division

Enclosures
Attachment 1 – Examples of Bacteria TMDLs
Attachment 2 – Options for Bacteria TMDL Modeling
Attachment 3 – Options for Establishing Bacteria Criteria

Attachment 1: Examples of Bacteria TMDLs

	State/ Region	TMDL Project	EPA Approval Date	Modeling Approach	Water Quality Standard	BST Study Completed	Wildlife	Stakeholder Group
1	SC/4	Hanging Rock and Lick Creek Fecal Coliform TMDLs	Aug-03	Watershed Characterization System (WCS) and the Non-Point Source Model (NPSM).	200/100mL (geometric mean); No more than 10% of the samples collected during any 30 day period shall exceed 400/100mL.	No	Deer used as surrogate for all wildlife.	No
2	SC/4	Thompson Creek Fecal TMDL	Jan-04	Bacterial Indicator Tool (BIT) and Hydrolocial Simulation Program Fortran (HSPF) at one station; Load Duration Curve (LDC) at the second station.	200/100mL (geometric mean); No more than 10% of the samples collected during any 30 day period shall exceed 400/100mL.	No	Deer and raccoon population density used to estimate in-stream contributions from the wildlife sources. Assumed 30 ct/100 mL background concentration under base flow conditions.	No
3	GA/4	Ogeechee River Basin Fecal Coliform TMDLs	Mar-05	Load Duration Curve (LDC)	200/100mL (geometric mean) May-Oct; 1000/100mL (geometric mean) Nov-Apr; 4000/100mL (single sample maximum) Nov-Apr; 300/100mL lakes, reserviors; 500/100mL freshwater streams.	No	White-tailed Deer have a significant presence in the basin, but no individual loading is calculated.	Involved in implementation phase.
4	IN/5	Plummer Creek E. Coli TMDLs	Jun-06	Load Duration Curve (LDC)	126/100mL (geometric mean); 235/100mL (single sample maximum)	No	Wildlife contribution acknowledged, but not quantified.	No
5	MO/7	Shoal Creek Fecal Coliform TMDL	Nov-03	Soil and Water Assessment Tool (SWAT)	200/100mL shall not be exceeded during the recreational season in waters designated for whole-body-contact recreation or at any time in losing streams. The recreational season is from April 1 to October 31.	DNA Source Tracking	Turkey, Deer, Geese and Raccoons.	Involved in assessment and TMDL development.
6	MO/7	Little Sac Fecal Coliform TMDL	Aug-06	Soil and Water Assessment Tool (SWAT)	200/100mL shall not be exceeded during the recreational season in waters designated for whole-body-contact recreation or at any time in losing streams. The recreational season is from April 1 to October 31.	DNA Source Tracking	Wild Geese have a significant presence in the watershed.	Involved in assessment and TMDL development.
7	KS/7	Chetopa Creek Fecal Bacteria TMDL	Oct-02	Load Duration Curve (LDC)	2000/100mL (single sample maximum)	No	No	No
8	NE/7	Loup River Basin E. Coli TMDLs	Jan-06	Load Duration Curve (LDC)	126/100mL (geometric mean) May- Sept.	No	Big game, upland game, furbearers, waterfowl and other non-game species. Considered part of background, but not quantified.	No
9	NM/6	Middle Rio Grande Fecal Coliform TMDL	May-02	No	Segment-specific standards apply. 1000/100mL (geometric mean); 2000/100mL (single sample maximum).	No	Wildlife contribution acknowledged, but not quantified.	No
10	LA/6	Sabine River Fecal Coliform TMDL	Oct-06	Load Duration Curve (LDC)	400/100mL (Primary) May-Oct; 2000/100mL (Secondary) and Nov-Apr.	No	Wildlife contribution acknowledged, but not quantified.	No
11	LA/6	Bayou Segnette	Jul-04	Bacterial Indicator Tool (BIT)	400/100mL (Primary) May-Oct; 2000/100mL (Secondary) and Nov-Apr.	No	Wildlife and Waterfowl considered part of background. Quantified based on population density estimates.	No
12	LA/6	Bayou Lafourche	Jul-04	Bacterial Indicator Tool (BIT)	400/100mL (Primary) May-Oct; 2000/100mL (Secondary) and Nov-Apr.	No	Wildlife and Waterfowl considered part of background. Quantified based on population density estimates.	No

(EPA comments continued)

Attachment 2: Options for Bacteria TMDL Modeling

1. Include Level of Stakeholder Concern in Decision Matrix for Model Selection

An action item that resulted from the most recent conference call held by the task force on November 27, 2006, is to develop a decision matrix to assist with model selection. Since the TMDL development process in Texas includes significant stakeholder involvement, it may be helpful to include an assessment of the level of stakeholder concern or involvement as a criterion in model selection. Based on the draft report distributed by the task force on November 21, 2006, several modeling approaches (simple to complex) are being evaluated. It has been suggested that stakeholders tend to prefer complex models such as the Soil and Water Assessment Tool (SWAT). In light of this, it may be feasible to use simple modeling approaches such as mass balance or Load Duration Curve (LDC) in cases where stakeholder concern is minimal.

2. Comparison of Modeling Results obtained from a Simple Modeling Approach with those from a Complex Model

TCEQ has already drafted a number of bacteria TMDLs using complex models such as the Hydrological Simulation Program Fortran (HSPF). It may be helpful to recalculate the reductions for one of the draft bacteria TMDLs using a simple approach such as the Load Duration Curve (LDC). If both methods yield similar reduction requirements, it will help demonstrate the usefulness of the LDC method and help address stakeholder concerns.

Attachment 3: Options for Establishing Bacteria Criteria

1. Revise the Single Sample Maximum Criteria for Enterococci in Saltwater

The enterococci criterion of 89 colonies per 100 ml in the 2000 *Texas Surface Water Quality Standards* is based on EPA's *Quality Criteria for Water - 1986*, EPA 440/5-86-001 (the "Gold Book"). However, the recommended value for freshwater was inadvertently adopted in the TX WQS as the single sample maximum for saltwater. Additionally, EPA's Gold Book contains errors on several single sample maximum values for both freshwater and saltwater criteria. The correct value for an enterococci criterion in saltwater (moderate use level) is 158 colonies per 100 ml. EPA recommends that the state update the single sample maximum enterococci criterion for saltwater in the next revision. EPA's 1986 criteria document for bacteria is found at the following website: http://www.epa.gov/waterscience/beaches/files/1986crit.pdf.

2. Update the Standard Deviation in the Calculation of the Single Sample Maximum Criteria

EPA's 1986 criteria document recommends the use of state data to calculate a standard deviation, rather than the default values. In the 2000 Texas standards, the single sample maximum criteria for *E. coli* in freshwater is calculated with a state-specific standard deviation. Since most states, including Texas, focused on fecal coliform bacteria for assessing contact recreation uses, data for *E. coli* was limited to 126 stations in seven river basins. The Texas Surface Water Monitoring Program has collected extensive data for both *E. coli* and enterococci in recent years. This information may be used to recalculate the standard deviation used in the *E. coli* criterion and to develop a state-specific standard deviation for the enterococci criteria.

3. Consider the Adoption of Single Sample Maximum Criteria based on the level of use

EPA's 1986 criteria document provides geometric mean densities as well as four different single sample values (75th percentile, 82nd percentile, 90th percentile, and 95th percentile) that are appropriate for different levels of recreational usage. The moderate use level (82nd percentile) is used for the single sample maximum criteria in the 2000 Texas standards. Criteria based on a higher level of use (75th percentile) could be adopted for waters frequently used for swimming (e.g., Barton Springs, Padre Island beaches). Criteria based on a lower level of use (90th or 95th percentile) may be appropriate for other water bodies.

4. Consider Other Risk Levels for the Criteria to Protect Recreation Uses

The 2000 Texas standards include a risk level of 0.8% (i.e., 8 illnesses per 1000 swimmers). For freshwater, EPA recommends that states adopt criteria reflective of risk levels up to and including 1.0% (i.e., 10 illnesses per 1000 swimmers). For marine waters, EPA recommends that states adopt criteria reflective of risk levels up to and including 1.9% (or 19 illnesses per 1000 swimmers). Please table below for comparison of geometric mean and single sample maximum values at different risk levels for freshwater *E. coli* criteria.

EPA could consider approving criteria for the protection of primary contact recreation in inland freshwaters, at risk levels above 1% (up to a maximum of 1.9%) provided that states submit scientifically defensible information to show that the relationship between illness and indicator concentrations holds beyond 1.0% in freshwater. However, without this additional information, EPA expects criteria with a risk level above 1.0% would not be protective of the primary contact recreation use. This is because EPA's existing epidemiological data for freshwater are not adequate to establish a relationship between illness rates higher than 1.0% and the corresponding bacteria concentrations.

(EPA comments continued)

E. coli criteria for freshwater (bold font indicates current criteria in §307.7(b)(1)(A)(i) of 2000 Texas *Surface Water Quality Standards*).

Risk Level (% of swimmers)	Geometric Mean Density	Single Sample Maximum Allowable Density (colonies per 100 ml)			
		75th percentile	82nd percentile	90th percentile	95th percentile
0.8	**126**	235	298 *	409	575
0.9	161	301	382	523	736
1.0	206	385	489	668	940

* The single sample maximum in the 2000 Texas standards is 394 colonies per 100 ml. This value was calculated with a standard deviation based on water quality data from the state's monitoring programs (see additional information in option 2).

5. Conduct Use Attainability Analyses

For water bodies where there is reason to believe that recreational activities do not occur, even on a limited basis, a use attainability analysis could be conducted to determine if the recreation use is attainable. Use attainability analyses are required to demonstrate that a Clean Water Act §101(a)(2) goal use (e.g., contact recreation) is not attainable. If the use attainability analysis successfully makes this demonstration, a standards revision is required to change the designated or presumed use.

6. Use the Single Sample Maximum Criteria for Specific Purposes rather than Use Attainment Decisions

EPA notes that the term "maximum" in single sample *maximum* has led to some confusion as a plain reading would lead one to infer that a single sample maximum is a value not to be exceeded. The single sample maximum values in the 1986 bacteria criteria were not established as "never-to-be exceeded" or "maximum" values. States have the discretion to determine whether to include a single sample maximum in their water quality standards for inland waters. For example, states could establish water quality standards that include single sample maximum criteria for inland waters, but only for use in beach monitoring and notification programs. Likewise, while a single sample maximum criterion for coastal waters must be included in water quality standards, the state may decide not to use this value for determining attainment of standards under the Clean Water Act as long as this is clearly specified in the state's standards.

Single sample maximum criteria are useful in several Clean Water Act applications. Single sample maximums provide a valuable tool against which to measure individual grab samples as part of a monitoring and notification program to protect public health. Single sample maximums can also be helpful in water body assessments, particularly when states collect insufficient data to reliably average and compare to the geometric mean component of the criteria. Lastly, single sample maximums can serve as daily limits in certain NPDES permits.

7. Limit Application of Bacteriological Criteria in Waters Affected Solely by Non-human Sources

The following paragraph is found in the final rule promulgating EPA's recommended indicators and criteria for use in coastal recreation waters. (Rule and other information at: http://www.epa.gov/waterscience/beaches/bacteria-rule.htm). While this rule is specific to coastal waters, the policy regarding the application of bacteriological criteria in waters impacted by non-human sources applies to inland freshwaters as well:

"States and Territories must apply the *E. coli* and enterococci criteria to all coastal recreation waters. If, however, sanitary surveys and epidemiological studies show the sources of the indicator bacteria to be non-human and the indicator densities do not indicate a human health risk, then it is reasonable for the State or Territory to not consider those sources of fecal contamination in determining whether the standard is being attained. This is the approach taken in the 1986 bacteria criteria document. It would be reasonable for a State or Territory to use existing epidemiological studies rather than conduct new or independent epidemiological studies for every water body if it is scientifically appropriate to do so."

TAMU’s Biological and Agricultural Engineering Comments

January 9, 2007

Pathogen Transport in Surface and Subsurface Systems at Different Space and Time Scales - A Roadmap: Fundamental Understanding to Advanced Modeling

The task force has produced a very comprehensive report on the need and possible approaches to be undertaken to address the daunting task of bacteria TMDL for sustaining and improving the quality of water resources in the state of Texas in the coming years and decades. While we agree with most of the issues and approaches proposed, we tried to summarize the vision of the Biological and Agricultural Engineering faculty emphasizing a focused need of basic science and engineering questions relating bacteria TMDL below:

Faculty Expertise:
Binayak Mohanty – Flow and Transport Physics and Conceptual Modeling, Biogeochemistry in un/saturated medium, Spatial Variability, Scaling Techniques, Forward/Inverse Numerical Modeling, Air/Space-Based Remote Sensing, and
4-Dimensional Data Assimilation

Vijay Singh – Watershed Hydrology, Surface Hydrologic Modeling, Entropy Theory / Monitoring Design, and Data Analyses

Patti Smith – Surface Hydrologic Modeling, Land Cover Land Use Change Effects on Hydrology, Stochastic Modeling and Uncertainty Analyses

Raghupathy Karthikeyan – Contaminant Fate and Transport and Applications of GIS

Clyde Munster – Watershed Hydrology, Best Management Practices, Field Experiments, GIS, and Applied Modeling

Yong Huang – Physicochemical Processes in Water Engineering, Dynamics of Colloidal Processes in Aquatic Systems, Geochemistry, Contaminant Transport, and Field Studies

Saqib Mukhtar – Animal Waste Management, Water Quality, Education and Outreach

Bruce Lesikar – Waste Water Treatment, Education and Outreach

&
Others

Biological and Agricultural Engineering
Texas A&M University

January 9, 2007

(TAMU BAEN comments continued)

Statement of need/Description: This program will address the critical issue facing the State of Texas regarding the presence of pathogens in our water resources. The Total Maximum Daily Load (TMDL) process has identified pathogens as a major contributor to the degradation of the State's water resources. While we agree that there does need to be a methodology in place that maximizes benefit while reducing time of implementation and cost as described in "Recommended Decision-Making Process for Texas TMDL and I-Plan Development", we also believe that fundamental research remains to be done in all areas concerning the fate and transport of bacteria in Texas waterways. Effective methods are needed to remove, track, describe and model pathogens.

Relevance/Background: Bacterial TMDLs are being developed for the Leon River, White Oak Bayou and Buffalo Bayou. These TMDLs are attempting to allocate the pathogen load in the water resources to the sources in the watershed. The end goal is to improve the quality of the water resource by reducing the concentration of pathogens to a level below acceptable water quality standards. Effective implementation of this program will require a thorough understanding of where the pathogens are originating, how effective are the best management practices at preventing pathogens from reaching the streams, what processes are occurring during transport to the water resource, what happens to the pathogens while in the water resource and how can this process be modeled. In addition, we need to quantify the limitations of current technologies and models used to measure, monitor and predict indicator bacteria species, in the form of uncertainty estimates on measured and predicted values. All of these questions will need to be answered through a comprehensive approach to evaluating pathogen cycling in the environment.

Goals: These recommendations will develop methods to describe and predict the processes associated with pathogen load, transport, die-off, and regrowth in our water resources.

1. Source, Fate and Transport – Data Collection, Process Understanding, and Modeling

    a. Determine background levels of bacteria in representative watersheds in the various regions throughout the State of Texas. Samples would be collected at the source, catchment, stream, and lakes/reservoirs. Study catchments will include both rural and urban settings. This would permit an assessment of existing bacteria levels as a function of climate, land use, topography, soil type, wildlife population, etc. Bacteria growth/die-off/regrowth patterns will be very different in the humid gulf coast region to the more arid regions of west and north Texas.

b. Determine the effect of sediment resuspension on the rate of bacteria growth/die-off/regrowth patterns.
c. Develop multi-scale data collection protocols in the surface and subsurface systems. In the surface system samples will be collected at the source, catchment, stream, and lakes/reservoirs. Study catchments will include both rural and urban settings. In the subsurface system data will be collected for a better understanding of spatio-temporal evolution of bacteria at the pore, core, pedon and plume scales. Relative significance of surface versus subsurface transport processes will be evaluated. In addition, most important surface and subsurface environmental factors controlling bacteria fate and transport will be determined.
d. Determine the true bacterial loads from “permitted” WWTP.
e. Establish protocols and QC plans for the collection of water samples for evaluation of bacteria concentrations including quantifying the uncertainty in these measured data.
f. Develop biogeochemistry-based fate and transport modeling and scaling rules for pathogen loads in surface and subsurface systems across space-time scales.

2. <u>Develop tools and models for tracking pathogen</u>
    a. Utilize advanced genetic / molecular biology (including nano- and atomic scale) techniques to monitor/characterize the pathogen characteristics which tie pathogens in our surface and subsurface water resources to their source.
    b. Develop streamline based history matching techniques and other inverse modeling tools to model bacterial fate and transport in surface and subsurface systems.

3. <u>Describe the processes associated with pathogen transport during the use of various best management practices (BMPs) utilized to manage waste</u>.
    a. Evaluate the effectiveness of current BMPs used for sediment/nutrient control to reduce bacterial loads. It seems that some of the current BMPs used for stormwater control won’t be effective for retaining bacteria.
    b. Develop new BMPs that address all constituents of concern in stormwater runoff.

4.

5. Evaluate methods to improve the current models used to predict pathogen transport from the various sources to our water resources.
    a. Evaluate the parameter uncertainty in models to use as a guide for pinpointing where time and effort is best spent to improve predictions of water quality. A recent uncertainty analysis of HSPF showed that peak in-stream fecal coliform concentrations are most sensitive to the parameter used to represent the maximum storage of fecal coliform bacteria on pervious land segments and to the amount of surface runoff needed to remove 90% of the water quality constituent from a pervious land segment. A subsequent First Order Analysis showed that 99.86% of the variance in simulated peak in-stream fecal coliform concentration was contributed by the maximum storage parameter. These results were directly related to the difficulty in finding reliable values for these types of parameters given the current state of research. This leads to the question, can the model as it is be improved or would it be better to develop a new bacteria subroutine that relies less on assumption and more on the basic transport and dynamic nature of bacteria in water and on the land surface? The other question that needs to be asked is if we do develop more physically based models that include an even wider range of parameters does this decrease or increase the uncertainty in the model results. Certainly a more physically based, process model may reduce model uncertainty, but may increase parameter uncertainty as more and more parameters are added to the mix.
    b. Establish modeling protocols for urban vs. rural watersheds. The approach to modeling these is likely to be very different.

6. Develop basic approaches to modeling pathogen transport from the source to State water resources.
    a. Perform experiments from lab to field scale to understand how bacteria move both across the surface and through the soil profile.

7. Develop the informational resources to convey this knowledge to the engineering consultants, decision makers and general public.
    a. Key to this process is risk assessment and communication. What are the risks associated with the various pathways of human contamination by fecal coliform? How do you communicate the science to stakeholders? The perception today is that we are just guessing (what we like to call estimating). How do we change that perception?

(TAMU BAEN comments continued)

Capitalizing on the expertise of BAEN water faculty, the following six overarching research objectives are proposed to accomplish a comprehensive understanding of bacteria/pathogens fate and transport and to develop predictive models.

Broad Research Objectives

1. *To identify, characterize, and quantify pathogen sources.*

Key Sources:

- Livestock
- Wildlife
- Pets
- Human

2. *To study key governing processes of fate and transport of microbial pathogens in terrestrial water and soil (porous media).*

Key Processes:

- Advection and Dispersion
- Deposition/Adsorption and Release
- Inactivation and Die-off
- Coupled Bio-Geo-Chemical processes
- Dominant Transport Mechanism under Laminar and Turbulent Flow Conditions
- Preferential Transport over Land and in Subsurface
- Other (Space and Time) Scale-Appropriate Transport Processes!

3. *To investigate key anthropogenic and environmental factors and their characteristic properties (and inter-relationships) controlling the fate and transport processes of microbial pathogens in surface water and porous media for rural/urban catchments/watersheds.*

Key Factors:

- 3-D Hydrologic Setup, Initial/Boundary Conditions, and Forcings
- Precipitation
- Temperature
- Stream flow
- Runoff
- Infiltration
- Irrigation and Drainage
- Pathogen Type

(TAMU BAEN comments continued)

- Soil and Mineralogy
- Topography
- Vegetation
- Animal Populations
- Sediment
- Nutrients
- Agricultural/Cropping Practice
- Waste water treatment facilities
- Soil and Water Management Practice
- Surface/Ground Water Interface and Interaction

4. *To develop (deterministic/stochastic) conceptual and numerical models to describe the transient pathogen transport in runoff, stream, and unsaturated/saturated porous media with embedded hydrological, and biogeochemical heterogeneity at multiple spatial scales.*

Spatial Scales:

- Molecular/Process scale
- Pore Scale
- Continuum/Column Scale
- Representative Elementary Area/Volume Scale
- Plot/Pedon Scale
- Field/BMP Scale
- Catchment Scale
- Watershed/Aquifer Scale

5. *To test the conceptual and computer model with controlled experiments at lab and field scales and develop inverse modeling algorithms for model parameter(s) estimation and study the process/parameter uncertainty*

- Micromodel Experiments
- Controlled Lab Column/Lysimeter Experiments
- Field/Catchment-Scale Experiments
- In-Stream Pathogen-Sediment-Nutrient Interaction Experiments
- Novel BMP/Pathogen Experiments
- Watershed Monitoring and Data Analyses
- Inverse Modeling and Data Assimilation
- Parameter Uncertainty Analyses

(TAMU BAEN comments continued)

6. *To identify and quantify scaling features (spacing, extent, support) for developing long-term monitoring protocol for pathogens across space and time in terrestrial environment*

- Time Series Analyses
- Entropy Analyses
- Geostatistical Analyses
- GIS Tools
- Insitu vs. Possible Remote Sensing Techniques
- Discrete vs. Lumped Measurement Techniques

United States Department of the Interior

U. S. GEOLOGICAL SURVEY

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January 25, 2007

MEMORANDUM

To: Robert L. Joseph
Director, USGS Texas Water Science Center

From: Donald M. Stoeckel
Hydrologist, USGS Ohio Water Science Center

Subject: Texas Bacteria TMDL Task Force -- Report draft 12/4/2006 and meeting 12/18/2006

At your request, I've been a participant in the Texas Bacteria TMDL Task Force meetings that began in October 2006. The task force is closing in on a final product. I would like to offer the following comments related to the most recent report draft and the discussions at the meeting on 12/18/2006. As requested by the Task Force leaders, my comments are formulated as recommended text for the final report (plain text) with explanations (italics).

deleted USGS internal comments—DMS

Thank you for inviting me to participate in this process. The experience has been an education for me and I hope I've been able to provide useful information to the Task Force.

The statement made during the meeting of 12/18 that library-dependent MST is capable of providing quantitative allocation of fecal contamination to sources is debatable. My perspective is that quantitation by library-dependent MST is so uncertain as to be suitable for simple presence and absence categorization (or possibly major, minor, or absent categorization). The following hypothetical data set illustrates this point.

Taken at face value, the results in the following example indicate that each source contributes to each sample except, probably, wildlife in sample 4. The ARCC of 62% would be taken by many

(USGS comments continued)

MST researchers as evidence that the library was capable of accurately classifying isolates. In the current state of the science, water-quality modelers would be tempted to take the data at face value and, for sample 1, allocate 10% of the fecal load to human sources, 52% to domestic animals, and 38% to wildlife.

Hypothetical sample data

# isolates	**Total**	**Human**	**Domestic**	**Wildlife**
Sample 1	100	10	52	38
Sample 2	100	35	46	19
Sample 3	100	15	72	13
Sample 4	100	42	56	2

Hypothetical quality-control data (compare to Wiggins et al., 2003, Stoeckel et al., 2004 and Moore et al., 2005)

# isolates	**Total**	**Human**	**Domestic**	**Wildlife**
Human (+)	100	**62**	12	26
Domestic (+)	100	23	**58**	19
Wildlife (+)	100	12	23	**65**

Rates of correct classification are **BOLD**
The average rate of correct classification is 62%
NOTE: higher accuracy than observed in studies cited

Minimum detectable percentage (MDP; calculated as in Whitlock et al., 2002 and Wiggins et al., 2003)

	Human	**Domestic**	**Wildlife**
Frequency of misclassification	18%	18%	23%
Average misclassification	19%		
Standard deviation:	3%		
MDP (Avg+4*SD):	**31%**		

Credible evidence of presence based on MDP

	Human	**Domestic**	**Wildlife**
Sample 1	No	Present	Present
Sample 2	Present	Present	No
Sample 3	No	Present	No
Sample 4	Present	Present	No

Proportion true identity in each class (P; bold is true positive)

# isolates	**Human**	**Domestic**	**Wildlife**
Human (test)	**0.64**	0.24	0.12
Domestic (test)	0.13	**0.62**	0.25
Wildlife (test)	0.24	0.17	**0.59**

Lower confidence limit per sample (True positive*test result)

	Human	**Domestic**	**Wildlife**
Sample 1	6	32	22
Sample 2	22	29	11
Sample 3	10	45	8
Sample 4	27	35	1

Upper confidence limit per sample (test + false negative)

	Human	**Domestic**	**Wildlife**
Sample 1	26	61	52
Sample 2	45	58	35
Sample 3	27	78	33
Sample 4	50	66	21

Credible evidence that one source contributes more than another

	Human	**Domestic**	**Wildlife**
Sample 1	<Domest	>Human	No
Sample 2	No	No	No
Sample 3	<Domest	>Others	<Domest
Sample 4	>Wildlife	>Wildlife	<Others

(USGS comments continued)

Refinement of interpretation to include a minimum detectable percentage (MDP) is recommended (USEPA MST guide document) to guard against false-positive results. In general, library-dependent methods have been shown to find all sources in all samples. (See the results of the Southern California Coastal Waters Research Program methods-comparison study, Journal of Water and Health, Harwood et al., Myoda et al., 2003.) The MDP calculated from the hypothetical quality-control data in this example is 31% -- in sample 1, there is not credible evidence that humans contribute at all. In fact, by this criterion, no more than two sources can be credibly depicted as "present" in any of the four hypothetical samples.

The process for bracketing percent classifications with confidence intervals has not yet been proposed in the literature. In the example, I calculated a conservative minimum confidence limit by reducing the observed values by the misclassification rate for positive-control isolates in the quality-control data. I calculated a conservative maximum limit by increasing the observed values by the number of isolates that might have been misclassified to another source. Credible evidence that one source contributes more than another was indicated if the upper and lower confidence limits for two categories did not overlap. Continuing with the example of sample 1, there was no credible difference between domestic and wildlife inputs (human was previously categorized as "no credible evidence of presence").

I hope this example is a convincing illustration of my perspective that, in most cases, library-dependent methods cannot provide quantitative allocation of fecal contamination loads to source with sufficient certainty to be incorporated into water-quality models.

This issue is raised, in part, in the summary passage for regulatory expectations on page 28 "Alternatively, a higher number of E. coli isolates (e.g. 50) can be analyzed from fewer water samples to identify statistically significant differences in pollution sources. However, this will only provide pollution source identification on very limited time scales, and not an overall assessment of the waterbody." *The implication is that statistically significant differences may be calculated by use of library-dependent methods. This implication was stated explicitly during the meeting of December 18th.*

Consider adding the following:

Although quantitative allocation of fecal contamination to source categories is a goal of most TMDL projects, uncertainty in classification limits our capacity for absolute quantitation. In some cases, library-dependent methods may enable identification of a source that contributes more fecal contamination than other sources, or identification of sources for which there is no credible evidence of substantial contamination. The results of library-dependent classification are conservatively seen as semiquantitative and suitable for sample-level classification of sources as "contribution not detected" or "contribution detected" with possible refinement to "contribution detected greater than (alternative source)." This information may not be suitable for incorporation into quantitative water-quality models.

ERIC-PCR

Consider adding two aspects to this section:

ERIC primers are used much less commonly than the BOX A1R primer in the literature; many of the early MST studies and related studies used REP primers.

(USGS comments continued)

Repetitive DNA elements include BOX, ERIC, and REP (reference Versolavic). Each has been used for rep-PCR in microbial source tracking studies (reference Carson, Dombek, Hassan , Stoeckel, and/or Myoda, in addition to the others).

In general, rep-PCR fingerprints are not reproducible from lab-to lab. Though the major bands in a fingerprint are generally present, the calculated similarities can be quite low. At this point, the only way to share rep-PCR fingerprints among laboratories is to use Sadowsky's HFERP or Diversilab's reagent packs and/or the Bioanalyzer. Consider the following sentence to complement the mention of the Ribotyper in the next section.

Though the rep-PCR banding patterns for a primer tend to be generally stable, minor differences between laboratories result in low between-laboratory similarity and currently limit the ability to generate a composite library in multiple laboratories. Two analytical strategies that enhance data similarity between laboratories are the use of horizontal fluorophore-enhanced rep-PCR (HFERP; Johnson et al., 2004) or a commercially packaged product such as the DiversiLab system (http://www.bacbarcodes.com/).

Future directions

I have comments on two passages in this section:

"More importantly, these library-independent methods can only detect a limited range of pollution sources. For example, the Bacteroidales PCR (Bernhard and Field 2000; Dick, Bernhard et al. 2005) can detect fecal pollution from ruminants, humans, horses and pigs; but no further discrimination is possible."

Further discrimination may be possible as the field progresses – the limitation is in the number of source-associated markers that have been developed and validated thus far.

"Identification libraries consisting of thousand of isolates from different geographical regions in Texas have already been established for ERIC-PCR, PFGE, RiboPrinting, CSU and KB-ARA patterns. In addition, several thousand more E. coli isolates from source samples have been archived and are available to researchers. Library development is one of the most costly components of BST studies. It would be most economical to build upon the libraries already established in Texas. It is recommended that agencies use contractors that use BST methods that will strengthen and expand the current Texas library."

Questions raised related to the geographical and temporal stability of library-independent markers are also relevant to libraries (as mentioned in the next paragraph of the document). The apparent advantage of having existing libraries may be not be useful in all areas of Texas, and the investment represented by existing libraries will almost certainly diminish in value over decades. Maintenance and updating the existing library with additional isolates to keep it relevant is a heavy liability.

I believe the economic tradeoff between developing and validating more source-associated markers and investing further in library development is not as clear as stated. The process of extracting the composite sample DNA and testing for markers is less costly than cultivating multiple fecal indicator isolates and typing them by molecular methods.

(USGS comments continued)

Also, the recommendation to use contractors and expand the current Texas library may be a reflection of opinion as much as it is a reflection of the state of the science. It will be very difficult to ensure comparability of data as multiple facilities add to the library database. Library expansion and application over larger areas and timeframes may not generate the anticipated high-quality data needed for application in TMDL efforts. Consider the following test for this paragraph:
If pursued, expansion of the current Texas library should incorporate accepted and consistent methods by experienced organizations, with substantial quality control, so data potentially can be combined into a statewide database.

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