

Appendix G. Bacteria Modeling for the Upper Sandusky Watershed

Fecal coliform bacteria were found likely to exceed the primary contact recreational use designation in twelve tributaries (spread over 6 assessment units) within the Upper Sandusky River watershed. A bacteria sampling run throughout the basin done in the summer of 2001, an assessment of the data from Ohio EPA's staff, and discussion with district personnel familiar with the area helped to pinpoint a number of areas that could potentially exceed the bacteria primary contact public recreation water quality standard (WQS).

Ohio's statewide criteria for the primary contact recreational use designation requires that at least five samples be collected within a thirty day period. Two samples were taken in a 30 day period at all but one of the sites of concern, therefore results could not be determined to meet or not meet the water quality standard (WQS) for bacteria. Instead, sample results were scrutinized and individual sites were picked as likely to exceed WQS. For these sites the geometric mean of the fecal coliform sample results were compared to the WQS of 1000 counts/100 mls.

This appendix describes the fecal coliform spreadsheet model and inputs used to determine loading sources and type of implementation needed to reduce the fecal coliform loading to below target levels.

1.0 Target Development

Bacteria samples were collected at 117 sites on 37 streams during the summer of 2001. The statewide numerical and narrative criteria for primary contact recreational use designation requires that for each designation at least one of the two bacteriological standards (fecal coliform or e. coli) must be met. These criteria apply outside the mixing zone and for fecal coliform state; the geometric mean content (either MPN or MF), based on not less than five samples within a thirty-day period, shall not exceed 1,000 per 100 ml and shall not exceed 2,000 per 100 ml in more than 10 percent of the samples taken during any thirty-day period. Since fewer than 5 samples were taken at each site the WQS could not be used as the sole determinate of the site meeting WQS. Instead sample results were scrutinized based on the geometric mean values, and proximity to potential sources of bacteria. From that, individual sites were picked as likely to exceed WQS.

The target selected for use in the modeling is the WQS used to compare to the geometric mean of the sample values, 1000 counts (or MPN)/100 ml. The geometric mean from samples were then compared to the WQS as described above. From the 117 sites sampled, 13 sites were selected as likely to exceed WQS and thus were modeled. Refer to table 1 for a list of the selected sites and their sampling results.

Table 1. Upper Sandusky River Bacteria Sampling Results

stream	RM at site	Field-measured bacteria for preliminary screening			geometric mean (> 1000 is an exceedance) (cnts/100 ml)
		sample 1	sample 2	sample 3	
		(cnts/100 ml)	(cnts/100 ml)	(cnts/100 ml)	
Paramour Creek	6.31	1800	320	10000L	1793
Unnamed trib. to Paramour Creek @ Hook Rd.	0.18	870	7900	na	2622
Westerly Creek	2.41	140	10000L	na	1183
Westerly Creek	0.13	1800	1200	na	1470
Indian Run	0.94	1200	1500	na	1342
Little Sandusky River	6.52	2800	10000L	na	5292
Honey Run	0.52	10000L	na	na	10000L
Negro Run	0.52	1300	10000L	na	3606
Prairie Run (2001data only)	1.02	2000	2500	na	2236
Warpole Creek	2.53	1300	1200	na	1249
"Lower" Little Tymochtee Creek	0.9	10000L	10000L	na	10000L
Unnamed tributary to Sycamore Creek	0.36	1200	1200	na	1200
Morrison Creek	2.36	1400	6000	na	2898

L = Means "greater than" the number in the value column, and is usually only used with bacteria, such as when they're too numerous to count or when they grow in colonies on top of each other that can't accurately be counted.

1.1 Current Deviation from Target

To determine the deviation from target, the target load was subtracted from the geometric mean load of the site samples, as seen in table 2. Load was calculated by multiplying the geometric mean site concentration by the average of the site flows taken on the sample dates. The target was calculated by multiplying the WQS, (1000 cnts/100 ml) by the site flow.

Upper Sandusky River Watershed TMDLs

Table 2. Bacteria Target Deviation (* based on 1000 cnts/100 ml WQS)

Stream	HUC number 04100011-	RM at site	site flow (ml/hr)	geometric mean load from field samples (cnts/hr)	target fecal coliform load * (cnts/hr)	deviation from geometric mean target (cnts/hr)	% reduction needed
Paramour Creek	020	6.31	2.34E+07	4.20E+08	2.34E+08	1.86E+08	56
Unnamed trib. to Paramour Creek @ Hook Rd.	020	0.18	2.40E+07	6.29E+08	2.40E+08	3.89E+08	38
Westerly Creek	202	2.41	3.98E+07	4.71E+08	3.98E+08	7.28E+07	85
Westerly Creek	020	0.13	5.30E+07	7.79E+08	5.30E+08	2.49E+08	68
Indian Run	030	0.94	5.30E+07	7.11E+08	5.30E+08	1.81E+08	75
Little Sandusky River	040	6.52	1.16E+08	6.14E+09	1.16E+09	4.98E+09	19
Honey Run	040	0.52	6.73E+07	6.73E+09	6.73E+08	6.06E+09	10
Negro Run	040	0.52	1.02E+08	3.68E+09	1.02E+09	2.66E+09	28
Prairie Run (2001data only)	050	1.02	2.24E+07	5.01E+08	2.24E+08	2.77E+08	45
Warpole Creek	050	2.53	2.14E+07	2.67E+08	2.14E+08	5.33E+07	80
"Lower" Little Tymochtee Creek	060	0.9	8.97E+07	8.97E+09	8.97E+08	8.07E+09	10
Unnamed tributary to Sycamore Creek	060	0.36	1.12E+07	1.34E+08	1.12E+08	2.24E+07	83
Morrison Creek	090	2.36	8.05E+07	2.33E+09	8.05E+08	1.53E+09	35

1.3 Method of Calculation

The model used is the United States Environmental Protection Agency's (USEPA's) Bacterial Indicator Tool. It is a spreadsheet that estimates the bacteria contribution from multiple sources. It is setup currently for fecal coliform, the modeled parameter in this study. The tool was designed to use the output as input to WinHSPF and the Hydrological Simulation Program Fortran (HSPF) water quality model in BASINS. However, for the purposes of this report due to the small areas in the problem subbasins it was used as a stand alone model. The tool estimates the monthly accumulation rate of fecal coliform bacteria on four land uses (cropland, forested, built-up, and pastureland), as well as the asymptotic limit for the accumulation should no washoff occur. The tool also estimates the direct input of fecal coliform bacteria to streams from grazing agricultural animals and failing septic systems (USEPA, 2000).

The Bacteria Indicator Tool requires three types of values: user-defined, default, and literature. User-defined values must be inputted into worksheets by the user, and are to be specific to the study area. User-defined values required by the tool are land use distribution, numbers of agricultural animals, wildlife densities, number of septic systems, and the failure rate of septic systems. Default values are supplied by the tool, but it is suggested that they are modified to reflect patterns in the study area. Default values include fraction of each manure type applied each month; fraction of manure type that is incorporated into the soil; and time spent grazing and confined by agricultural animals. Like default values, literature values are supplied by the tool, but they may be replaced with user values if better information is available for the study area. Literature values required by the tool are animal waste production rates and fecal coliform bacteria content; fecal coliform bacteria accumulation rates for built-up land uses; and raw sewage fecal coliform bacteria content and waste production.

To see the Bacteria Indicator Tool User's Guide or download the software refer to <http://www.epa.gov/waterscience/ftp/basins/system/BASINS3/bit.htm>.

4.2 Critical Conditions and Seasonality

The critical stream condition for bacteria concentration depends on the location and source of the bacteria. The first inch of rainfall typically removes most of the bacteria available for entrainment in runoff, (Moore, et al., 1982). If the source is pastured livestock, cropland applied manure or wildlife, rains will wash manure off fields and elevate bacteria counts in the vicinity of the source shortly after the water begins to runoff. If the source is far upstream of the sampling site, due to the time of travel the bacteria counts may not elevate until after the first flush. If the source is failing aeration systems which are actively flowing to the stream or homes which have no treatment and are straight piped to the stream the critical condition occurs during low stream flows. If the source is failing leach bed systems the bacteria may not reach the stream until it is

flushed out during a rain event.

Horsley & Whitten found that the first flush from areas adjacent to a stream will enter the stream more quickly than the first flush from areas higher in the watershed. The net result is the water quality trend exhibited in the stream data (bacteria concentrations increasing with increasing flow). As more bacteria reach the stream from higher in the watershed the stream bacteria concentration increases (Horsley & Whitten, 1996).

The data for this study occurred in July and August of 2001. Older data from the mid 1990s was available for the Prairie Run site, however it was deemed too old since the values collected then were significantly less than the samples from 2001, and so was not used. The differences could be due to a combination of different weather, soil conditions, or a new source.

Since precipitation is required for runoff to occur, precipitation data was examined during and up to four days prior to each sampling date to see if it had an effect on Fecal coliform concentrations. The data shows that little significant rain occurred during or just prior to the sampling dates. On 7/26/2001 a 1.15 inch rain occurred in the Morrison Creek basin which seems to have raised the concentrations from samples taken with no rain, see Table 3.

Table 3. Comparison of Fecal Coliform Concentration to Precipitation

Stream	River Mile	Date of Sample & Precipitation	Measured site FC count (cnts/100 ml)	Precipitation (inches)
MORRISON CK	2.36	7/26/2001	6000	1.15
MORRISON CK	2.36	8/9/2001	1400	0
MORRISON CK	9.34	7/26/2001	1100	1.15
MORRISON CK	9.34	8/9/2001	470	0

In order to see the relevance of precipitation graphically, sample dates were compared to sample values, see figure 1. Figure 1 seeks to find date based trends, for instance if on one of the sample days all values tended high or low one may surmise that something on or near that date like precipitation, the lack of precipitation, agricultural activities or some other date related response may have played a role in the trend. No trend was noted.

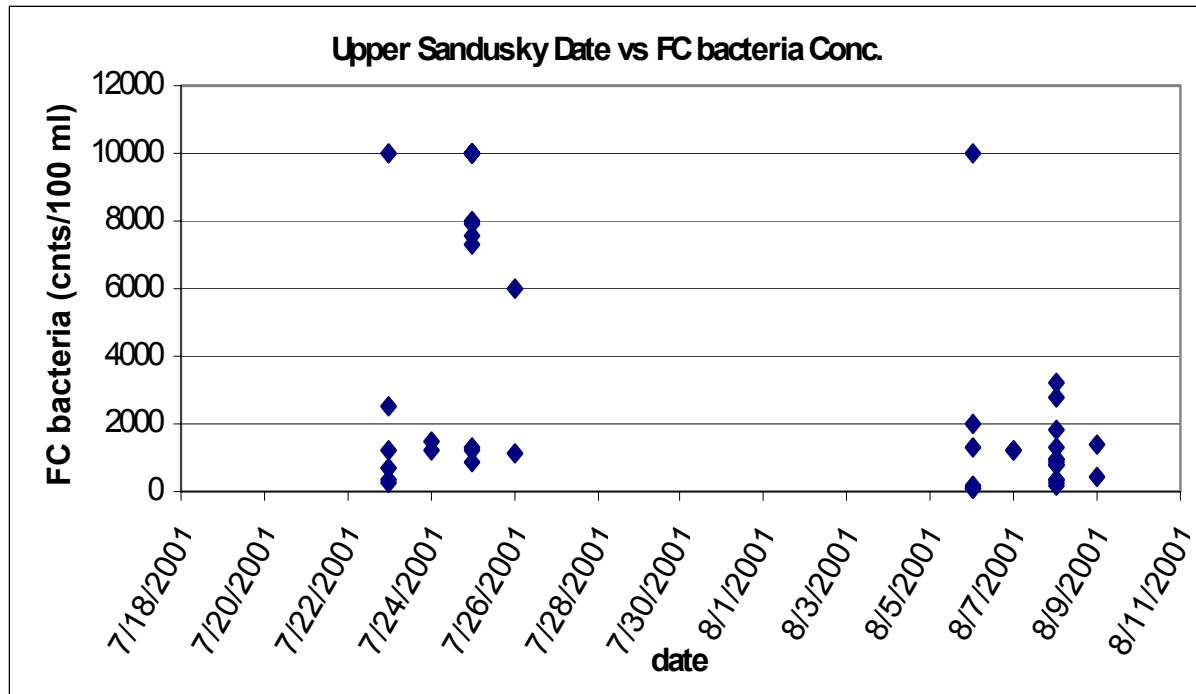


Figure 1. Comparison of Fecal Coliform Concentration to Date

In order to see if flow played a role in Fecal coliform concentration the various samples and their corresponding site flows from one site were compared. Figure 2 looks at 9 samples ranging from years 2001 to 1995 for the Prairie Run RM 1.02 site. If flow plays a role in concentration then a pattern should emerge. At lower flows concentrations are both high and low, at higher flows there are only two samples to compare but concentrations are on the lower end of the scale. There is no distinct pattern but it does support the information from district personnel familiar with the area which blames failing septic systems for high Fecal coliform concentrations. As one would expect with failing septic systems lower stream flows yield higher concentrations and higher flows yield lower concentrations.

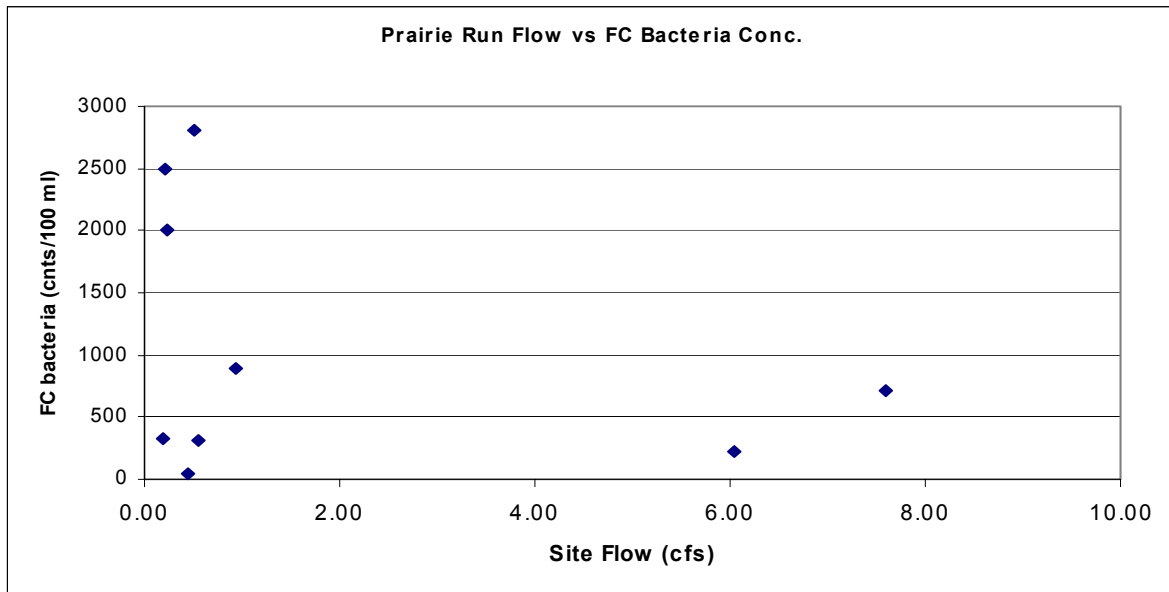


Figure 2. Comparison of Prairie Run Fecal Coliform Concentrations to Flows

4.3 Margin of Safety

The (MOS) for the Upper Sandusky River bacteria modeling is implicit as it was not purposefully built into the model. The premise of the models for this report is to quantify the problem of failing home septic treatment systems and/or runoff problems in and around the Upper Sandusky River study area. This bacteria TMDL serves to; demonstrate that the HSTS problem, cattle in streams and/or runoff problems are real, show that correcting the problems will result in decreased in stream bacteria and improved water quality for recreation use, and show how much improvement will occur with implementation. The MOS was calculated by dividing the post model result by the target and converting to a percentage, see Table 8. Note: This table shows the effect that reducing the HSTS failures, cattle in streams and/or runoff problems has on the model result and compares the reduction of fecal coliform load to each site's target value, this comparison is expressed in percent margin of safety.

4.4 TMDL Calculations

The units for fecal coliform concentration as determined by Ohio Environmental Protection Agency's lab is # (or MPN) / 100 ml. The concentration used for comparison to the WQS for each site was the geometric mean of the 2 samples collected at each site. The load, in counts (or #) / hour, for each study area was determined by multiplying the concentration in counts/100 ml by the flow for the site in ml/hr, i.e. ((2309

counts/100 ml) * 6.70E+08 ml/hr)/100 = 1.55E+10 counts/hr. For each site the model flow was calculated by multiplying the sites drainage area by the flow yield from various nearby or appropriate USGS gages.

The Bacteria Indicator tool model is sensitive to a number of inputs, some of which are text book or assumed values. Some of these values, since they are assumed and may need adjusted to local conditions, could be used to adjust the model outcome to a desired point, in other words could be used to calibrate the model. For the model's runoff sheets these inputs include number of animals from the animal sheet (wildlife only for these sites), a user assumed "die off" rate for wildlife related fecal coliform and the percentage of each type of urban land in the basin from the built up sheet. From the septic sheet the two important inputs are the failure rate of home sewage treatment systems and the assumed fecal coliform concentration reaching the stream.

An attempt was made to find a justifiable value for each of these inputs and use them consistently for each of the models. Particular attention was paid to the model's septic sheet value for fecal coliform concentration reaching the stream. This value is very important to the outcome of the model yet is a difficult one to measure. In order to know the actual concentration one would have to measure at the stream the seepage from failing home sewage treatment systems throughout each study area. This would be a huge under taking and was not in the scope of this study. Text book values were used, however the literature warns that this is a very difficult value to obtain as fecal coliform concentrations reaching the stream change with temperature, soil radiation, soil moisture, residence time, filtration adsorption and degree of treatment system failure. The study *An Analysis of the Potential Impacts on Groundwater Quality of On-Site Wastewater Management Using Alternate Management Practices* cites three references with values for fecal coliform septic tank effluent concentrations ranging from 10E+6 to 10E+8 Most Probable Number (MPN), (Venhuizen, 1995). In *Identification and Evaluation of Nutrient and Bacterial Loading to Maquoit Bay Brunswick* the range of literature values found were from 10E+4 to 10E+7 fecal count (FC)/100 ml and selected for use in their model was 10E+6 FC/100ml (Horsley and Whitten, 1996). The cited range of values is for septic concentration which may differ from the fecal concentration that leaks, seeps or drains to the stream.

An effort was made to be consistent with text book values. The lower end of the text book range was used to calibrate the subbasin models. The value used for assumed fecal coliform concentration that reaches the stream is 1.50E+05. Using values consistently in the subbasins and staying within an order magnitude range of the measured fecal concentration helped to place more emphasis on the other more measurable variables such as number of homes and land use makeup.

Table 5 lists the model inputs and attempts to weight the importance of each input to the model (model sensitivity) and to qualify the degree of accuracy of each input.

Table 5. Important Model Sensitive Inputs

model inputs	model sensitivity rank				
	<-----most sensitive least sensitive----->				
	1	2	3	4	5
site FC geomean	B				
drainage area of basin			A		
site flow					A
landuse breakdown			A		
builtup percentages					B
No. of wildlife		B			
No. of livestock	B				
no. of septic		B			
no. of people/septic system			A		
failure rate for septic systems	B				
FC conc. That reaches stream	C				
manure incorporation into soil rate	nu				
cattle in streams	C				

A = Based on solid evidence
 B = Estimate based on evidence
 C = Est. based on literat. values, BPJ or model calibra.
 nu = not used for any of these basin models

The models for each of the basins were calibrated by first inputting the known and assumed values into a model for each subbasin (13 models) then comparing the model output to the geometric mean of the measured values at the study area. At first the same assumed values were used for each subbasin. Once the inputs for all the models were in, the outputs were compared to the measured values of bacteria for each subbasin. Surprisingly the initial results were within the one order magnitude range limit for most of the models. For the subbasins where the limit was exceeded the wildlife population (deer), percentage of built up and percentage of failing septic system inputs were adjusted until the model output reasonably reflected the geometric mean of the field samples, see Table 6.

Table 6. Comparison of Target to Field Values and Calibration Model Results

stream	RM at site	target fecal coliform load based on 1000 cnts/100 ml WQS (cnts/hr)	geometric mean load from field samples (cnts/hr)	calibration model results of fecal coliform load (cnts/hr)
Paramour Creek	6.31	2.34E+08	4.20E+08	4.36E+08
Unnamed trib. to Paramour Creek @ Hook Rd.	0.18	2.40E+08	6.29E+08	6.48E+08
Westerly Creek	2.41	3.98E+08	4.71E+08	4.79E+08
Westerly Creek	0.13	5.30E+08	7.79E+08	7.40E+08
Indian Run	0.94	5.30E+08	7.11E+08	6.85E+08
Little Sandusky River	6.52	1.16E+09	6.14E+09	6.14E+09
Honey Run	0.52	6.73E+08	6.73E+09	5.91E+09
Negro Run	0.52	1.02E+09	3.68E+09	3.60E+09
Prairie Run (2001data only)	1.02	2.24E+08	5.01E+08	5.37E+08
Warpole Creek	2.53	2.14E+08	2.67E+08	2.59E+08
"Lower" Little Tymochtee Creek	0.9	8.97E+08	8.97E+09	2.30E+11
Unnamed tributary to Sycamore Creek	0.36	1.12E+08	1.34E+08	1.51E+08
Morrison Creek	2.36	8.05E+08	2.33E+09	2.67E+09

Based on biological sampling and observation agricultural influences are believed to impact Paramour Creek, Indian Run, Honey Run, Lower Little Tymochtee Creek and perhaps others. An analysis of rain data from nearby precipitation gages reveals that conditions were unaffected by precipitation during the sample runs at all these sites. Therefore runoff would not be a source of bacteria in any of the samples. For this reason the models were set to add up fecal loads from wildlife, cattle in streams (where appropriate) and septic systems only. The assumed percent available runoff of wildlife manure fecal coliform based on best professional judgement and model calibration was 40 percent, a 60% "die off" rate.

The modeled subbasins are situated in six counties; Sandusky, Crawford, Richland, Wyandot, Marion and Seneca. A document from Ohio EPA's North West District Office states there is a 10% - 20 % failure rate of home sewage treatment systems in Crawford County and 10% in Seneca County, (McKibben, 9/9/2003). It also mentions that the percentage could well be higher since it is difficult to account for the systems that discharge to field tiles prior to discharging to streams. Because this is the only available information on failure rates for HSTSs and because all the modeled subbasins are similar in topography and landuse that percentage failure rate range was used for all modeled subbasins. It makes sense that these assumed rates would not be high enough at least in some cases as these are average county wide failure rates. Because these study areas are selected because they have high bacteria it makes sense that the HSTS failure rate may be higher than average.

Deer and raccoons were the two species of wildlife considered in the models and the sources are Ohio Department of Natural Resources (ODNR) Waterloo Experimental Station (Mike Reynolds) and the Crane Wildlife Station, respectively. The estimate for deer density is 5 to 10 per square mile in Western Ohio. North Western Ohio has the sparsest habitat in the state, for that reason I used the low end of the deer density estimate for most of the subbasin models. In some basins where there was a significant portion taken up by an urban area, where row crop agricultural is intense or where appropriate for model calibration I used less than 5 deer per square mile.

The only data for raccoons from the ODNR is a hunter observation survey the results of which are in number of raccoons observed per 1000 hunter hours. It is difficult to accurately convert this to a density. The way it was done for the purposes of this report was to divide the number of observed raccoons per 1000 hunter hours for a county and divide that by the square miles for the county then multiply by 25, see Table 7. The assumption based on BPJ is that only 1/25th of all existing raccoons in each county are observed. In other words, for each racoon a hunter observes there are 25 others. Raccoons are mostly nocturnal and are mostly not visible during daylight. This method is rough but it does produce believable results and is based on counts by county population trends, so the higher the observation rate the higher the number of raccoons per square mile are assumed.

Table 7. County Raccoon Population Calculations

County	# of raccoons observed by hunter per 1000 hrs.		county (sq mi)		multiplier		Raccoons per square mile
Crawford	41	/	403	*	25	=	2.5
Sandusky	42	/	421	*	25	=	2.5
Wyandot	41	/	407	*	25	=	2.5
Seneca	47	/	554	*	25	=	2.1
Richland	31	/	499	*	25	=	1.6
Marion	50	/	402	*	25	=	3.1
Formula = # raccoons obs. / county sq mi. * 25 = no. raccoons per sq mi							

The results of the modeling show that by reducing the failing HSTs, and removing cattle from streams for two of the basins, the bacteria load WQS based on a concentration of 1000 counts/100 ml can be met, see Table 8.

Table 8. Post Treatment Model Results

stream	RM at site	existing percentage of failing septic systems	calibration model results of fecal coliform load (cnts/hr)	% of failing HSTSs after improvements	post treatment model results of fecal coliform load (cnts/hr)	percent margin of safety (1-(post model result/target))*100
Paramour Creek	6.31	4	4.36E+08	0	1.70E+08	27
Unnamed trib. to Paramour Creek @ Hook Rd.	0.18	8	6.48E+08	1	2.30E+08	4
Westerly Creek	2.41	15	4.79E+08	5	3.60E+08	10
Westerly Creek	0.13	3	7.40E+08	1	3.98E+08	25
Indian Run	0.94	10	6.85E+08	3	4.76E+08	10
Little Sandusky River	6.52	48	6.14E+09	2	1.03E+09	11
Honey Run	0.52	10	5.91E+09	10 ^E	5.65E+08	16
Negro Run	0.52	55	3.60E+09	5	9.13E+08	10
Prairie Run (2001 data only)	1.02	10	5.37E+08	1	1.98E+08	12
Warpole Creek	2.53	5	2.59E+08	2	2.09E+08	2
"Lower" Little Tymochtee Creek	0.9	70	2.30E+11	1 ^E	8.48E+08	5
Unnamed tributary to Sycamore Creek	0.36	5	1.51E+08	0	1.11E+08	1
Morrison Creek	2.36	10	2.67E+09	1	6.61E+08	18

6.0 Implementation and Monitoring Recommendations

Restoration methods to bring an impaired water body into attainment with water quality standards generally involve an increase in the water body's capacity to assimilate pollutants, a reduction of pollutant loads to the water body, or some combination of both.

6.1 Implementation Strategies

To eliminate the bacteria impairments emphasis will need to be placed on education about HSTS maintenance and funding for HSTS improvements will need to be provided as an incentive to residents.

Failing home sewage treatment systems (HSTS) are the identified source of water quality impairments from various subbasins in the Upper Sandusky River study area. Solutions to HSTS problems have traditionally fallen into two general categories: individual HSTS repairs/upgrades or replacement of individual HSTS with a centralized collection and treatment system.

Individual HSTS repairs or upgrades are feasible where local soils, groundwater, and bedrock conditions are favorable and lot sizes are adequate for on-site treatment. Where the above-mentioned local conditions are not available, the only feasible long-term solution to pollution problems is centralized wastewater collection and treatment. However, the small number of homes among which the cost of such a project must be distributed often makes this option cost-prohibitive, unless there is already a local centralized system nearby that can serve the area.

Ohio EPA has two sources of funding available to address failing or poorly maintained HSTSs that result in water quality problems:

- Section 319 grant funds administered by the Division of Surface Water (DSW) Nonpoint Source Section available over a three year implementation period.
- Low interest loan funds from the Ohio Water Pollution Loan Fund (WPCLF) linked deposit loan program administered by the Division of Environmental and Financial Assistance (DEFA). Through the linked deposit system, local banks can offer interest rates that are generally 5% below market rates to credit-worthy homeowners for the upgrade or replacement of home sewage treatment systems, as approved by the County Health Department. Terms of the loan are typically three, five, or seven years.

There are differences in the way the two funding sources are administered, but the key to accessing these funds is the same for both programs. Funding is available only to counties that have produced an Ohio EPA approved county-wide or watershed-wide HSTS Plan. The approved contents of the plan will drive the activities which occur during the entire 319 grant/ WPCLF loan project and will be used to evaluate the county's progress during the funding period.

The purpose of this plan is to:

- a) outline a county-wide system for the identification, inventory, and correction of improperly located, badly maintained, malfunctioning, and/or failing home sewage treatment systems in a county, particularly where this is causing a water quality impact;
- b) outline a long-term plan for ongoing inspection, corrective action, tracking progress and success, and monitoring of the county-wide system both during and after the funding period ends.

The timing of HSTS Plan submission, in relation to funding availability, will vary depending on whether grant only, loan only, or a grant/loan combination will be used by the county to pay for HSTS improvements.

Ohio EPA does not provide funding for HSTS upgrades or repairs that result in a discharging system. Frequently home sewage treatment systems are discharging systems. Therefore in order for a homeowner to access sources of funding provided by Ohio EPA the correction to will need to result in a system that does not discharge.

Three of the six counties for which subbasins were modeled (Crawford, Wyandot and Seneca) have completed a HSTS study and have drawn conclusions about how and where to attack the problems. In each of the 3 county studies there is a section in the back titled Corrective action Plan which discusses implementation for failing HSTS problems, see Appendices B, C & D.

Livestock is a suspected source of bacteria in four of the basins. Due to a lack of precipitation during and prior to sampling in these basins runoff was not considered in the overall bacteria loading calculations. Based on field work observations two of the basin models, Honey Run and the Lower Little Tymochtee Creek, considered cattle in streams as a Fecal coliform loader. To determine post implementation bacteria loads in the model it was assumed all cattle would be excluded from streams. This will require landowner cooperation and assistance and funding from the local Soil and Water Conservation Offices.

6.3 Process for Monitoring and Revision

The adaptive management approach is recommended for the restoration of the Upper Sandusky River Study Area. Adaptive management suggests that a hypothetical restoration plan be developed and implemented, and then the stream reassessed. If at that time the stream is not meeting use designations another restoration plan will be developed incorporating most recent data.

REFERENCES

- Horsley & Whitten, Inc., Identification and Evaluation of Nutrient and Bacterial Loading to Maquoit Bay Brunswick, ME and Freeport, ME, 1996.
- Horsley & Whitten, Inc., Identification and Evaluation of Nutrient and Bacterial Loading to Maquoit Bay Brunswick, ME and Freeport, ME, Appendix A, The FecalLoad MODEL Users Guide, 1996.
- McKibben, 9/9/2003, Excerpts from Sandusky River Watershed Home Sewage Treatment System plans.
- Moore, et al, 1982, Evaluating Dairy Waste Management Systems' Influence on Fecal Coliform Concentration in Runoff, Department of Agricultural Engineering, Agricultural Experiment Station Bulletin 658, Oregon State University, Corvallis, (As referenced in Horsley & Whitten, Inc., Identification and Evaluation of Nutrient and Bacterial Loading to Maquoit Bay Brunswick, ME and Freeport, ME, 1996.
- United States Environmental Protection Agency, Bacterial Indicator Tool Users Guide, March 2000, Office of Water, EPA-823-B-01-003.
- Venhuizen, David, An Analysis of the Potential Impacts on Groundwater Quality of On-Site Wastewater Management Using Alternate Management Practices, 1995.