

SUBJECT: Microbial Risk Screening Tool

TASK: SC20-02: Microbial Indicators and Effects on Beneficial Uses

DATE: August 30, 2000

Abstract

The primary objective of this project was to create a computer-based program that can be used to assess the relative microbial risks to public health from recreational exposure to urban creek waters. Key components of this project included: summarizing the issues associated with estimating the acute risk recreational waters pose to an exposed population; conducting a literature review to determine the most appropriate relationships between bacterial indicator organisms and human illness that would be appropriate for creeks in urban areas; adapting a computer model of microbial risk to estimate the expected range of the number of infections or resulting illnesses from exposure to urban creek waters; and, developing a practical computer-based program which can be used on a screening level to estimate the relative level of risk posed to recreators from creek waters, given a set of monitoring data from that creek.

This investigation was motivated by the fact that sampling and analysis of some Bay Area creeks have shown sporadic exceedances of Basin Plan criteria for bacterial densities. Although no link has been established demonstrating a clear connection between the sampling results and human health risks, it has been suggested that the water contact recreation beneficial use may be impaired by these exceedances. A literature review on the subject indicates that the relationship between bacterial densities and human illness is not well agreed upon. Given the complexities associated with interpreting bacterial indicator data, a practical tool was proposed to streamline the process of evaluating the relative microbial risks to public health from exposure to urban creek waters.

Introduction

Use of Bacterial Indicator Organisms

The basic reason for carrying out microbiological water analysis is to safeguard the health of a community by testing for possible fecal pollution, the source of microorganisms causing waterborne disease. Pathogenic microorganisms usually appear in recreational waters intermittently and in low concentrations (Borrego et al., 1987). Indicator organisms are organisms that coexist with pathogens in the fecal environment and are easier and less expensive to test for than pathogens. For these reasons indicator organisms are often the focus of water analyses rather than pathogens. Ideally, an indicator organism would always be present when the pathogen is present, be present in equal or higher numbers than the pathogen of interest, be easy and inexpensive to assay, and would serve as an indicator of human fecal contamination (as opposed to animal contributions). The most commonly employed indicator organisms are total coliform, fecal coliform, enterococcus, and *E. coli*. Fecal streptococcus is also commonly employed in Europe and coliphages are quickly gaining increased acceptability as a viable alternative as an indicator for viral contamination. Some pathogens, particularly giardia and cryptosporidium are also

monitored. All of these organisms are included in the microbial risk screening tool described herein.

Sampling and analysis of some creeks throughout California and the United States have shown sporadic exceedances of Basin Plan criteria and EPA water quality objectives for bacterial indicator densities. Although no link has been established demonstrating a clear quantitative connection between the bacterial indicator densities and human health risks, it has been suggested that the water contact recreation beneficial use may be impaired by those exceedances and may be grounds for listing the corresponding creeks under the Clean Water Act Section 303(d).

A review of the available literature on the subject of bacterial indicator – human health illness relationships indicates that those relationships are not well agreed upon (Cabelli, 1983; Dufour, 1984; Fleisher, 1991; Kay et al., 1994, Gerba, et al., 1978; and Sobsey et al. 1995). In fact, it would be very difficult to generalize whether sporadic exceedances of the water quality objectives represent an increased risk to public health or not.

Role of Risk Assessment

Risk assessment involves the use of factual data to define the potential health effects of exposure to hazardous materials and situations for individuals or populations. Quantitative assessments of human health risks associated with the ingestion of waterborne pathogens have historically been conducted within the framework originally developed for chemical risk assessments (NRC 1983). Until recently, for the most part these assessments have focused on the probability of infection or disease to an individual as a result of a single exposure event (Dudley et al., 1976; Haas 1983; Rose et al., 1999).

When applied to infectious disease transmission, the chemical risk assessment framework has several methodological limitations. The chemical risk framework was never intended to address aspects unique to the transmission of infectious diseases such as person-to-person spread of infection or immunity. The limitations of treating infectious disease transmission as a static disease process, with no interaction between those infected or diseased and those at risk, has been illustrated in studies of giardia (Eisenberg et al., 1996), dengue (Koopman et al., 1994), and sexually transmitted diseases (Koopman et al., 1991). These limitations were formally recognized by US EPA in 1996 (ILSI, 1996).

Another critique of some of the chemical-style microbial risk assessments is that point estimates have commonly been used to characterize the probability that a particular exposure leads to infection or disease in a single individual. This type of estimate carries no significant information about the associated uncertainty or variability. From a public health perspective, the probable number of people infected in an exposed population is more meaningful than the probability of individual infection. To address this point, the probability of individual infection has sometimes been multiplied by the population number in an attempt to predict the disease incidence in the population. This strategy, however, may or may not be accurate depending on the appropriateness of the underlying assumptions.

A population-based microbial risk assessment approach for waterborne disease transmission was originally developed as part of a study for the U.S. Army (Cooper et al., 1986; Olivieri et al., 1986; Olivieri et al., 1989). In this work, a population perspective was taken by estimating the probability distribution of the number of infected/diseased people in the exposed population. Another unique feature of this model was its probabilistic treatment of dose-response data. Each

member of the population received a different dose and had a different probability of responding to this dose. The combination of these two factors resulted in each member of the population carrying a different probability of becoming infected or diseased.

This population-based approach has recently been extended by taking advantage of the available infectious disease and dose-response literature in the development of a mathematical model that characterizes the risk of human disease from waterborne pathogen exposure on a population level (EOA 1995a; EOA 1995b; EOA 1996; Eisenberg et al., 1996; Eisenberg et al., 1998). Based on the host/microbe interaction, this approach makes explicit the mechanistic aspects of the infectious disease process and provides a structure from which data are gathered. An existing dose-response model (Haas 1983; Regli et al., 1991) is embedded into an epidemiological framework, relying on a large base of literature describing the use of dynamic population models in the study of epidemics (Anderson and May, 1991). The dynamic nature of these epidemiological models emphasizes the importance of how the susceptible, infected, diseased, or immune status of individuals within a defined population group varies over time.

One important aspect of modeling the disease process is that, under a given set of assumptions, the population based modeling approach may converge with the individual based approach (Soller, et al., 1999). For example, this may be true if one were to assume that person to person transmission of disease within a population is unimportant and the whole population under study is susceptible to infection. Further, it should be noted that for each investigation, the risk assessor must evaluate the needs of the investigation and the data available for study, and then determine if the additional complexity of the population based approach is warranted. Both the individual and population based approaches have been shown to produce valuable results.

Genesis of the Microbial Risk Screening Tool

The variability and uncertainty associated with environmental data are significant. With respect to bacterial indicator and pathogen data, variability and uncertainty stem from 1) uncertainty in the analytical results (i.e. confidence range for the reported results may span an order of magnitude) 2) the highly variable bacterial densities at any given location, and, for indicator data, 3) the uncertainty in the relation between the indicator and human infection.

A modeling tool must account for these uncertainties when providing risk estimates. Due to these uncertainties, it is very difficult to accurately characterize the absolute risk associated with a given situation, and many models focus on the relative risks between different scenarios. For example, one possible result may be that the risk associated with scenario A, in which humans are exposed to a pathogen, is in all cases higher than for scenario B. An alternative result may be that the risk from scenarios A and B are indistinguishable.

A practical tool based on the chemical risk framework has been developed to streamline the process of evaluating the relative microbial risks to public health from exposure to urban creek waters. The purpose of the computer-based screening tool described herein is to help determine whether or not a thorough risk assessment is required. Given monitoring data from an urban creek, the tool will estimate the relative magnitude of the potential public health impact.

If used properly, the microbial risk screening tool may provide valuable information for decision making. However, because of the complexities involved in microbial risk assessment, this tool is not intended to serve as a rigorous quantitative estimate of risk to the exposed population. The tool may be used to determine when or if a rigorous risk assessment may be warranted in comparison to

situations in which the relative risk is clearly lower than a given standard. Given that the intent of this investigation is to develop a tool that can be used to estimate the relative risk to public health from exposure to urban creek waters, the most applicable relations between indicator or pathogen densities and public health effects for urban creek waters were identified via literature review.

The user of the screening tool inputs microbiological data (indicator or pathogen) into the program. The tool uses the previously discussed relations between indicator or pathogen densities and public health, along with an estimated ingested rate, to characterize the relative risk to public health. This estimated risk may then be compared to an “accepted” level of risk for freshwater¹, if desired. In this manner, the tool may be used to facilitate the interpretation of the available microbiological data.

This memorandum explains the function and utilization of the microbial risk screening tool that has been developed. A case study has been performed with the microbial risk screening tool and is explained in detail under separate cover (EOA, 2000). That case study uses bacterial indicator data from an urban creek in the San Francisco Bay area, California.

Scope

One central issue in biological risk assessment is how to extract information from biological data, which tend to be highly uncertain and variable. In particular, the uncertainty and variability of factors affecting infectious disease transmission limit the usefulness of traditional curve-fitting techniques. In this application, an alternative approach is used. The approach consists of assigning probability distributions to the parameters, and sampling these distributions via Monte Carlo simulations. By repeating this process many times, a relative risk associated with a given set of input parameters is obtained. The screening tool is implemented as an add-in to Microsoft Excel.

It is important to realize that the biological significance of a model’s output is dependent on the appropriateness and accuracy of the assumptions used to build the model. Assumptions employed in the construction of the screening tool are documented below.

- Bacterial indicator or pathogen data are obtained from an urban creek environment;
- The data input are representative of the water body under study, and any preliminary data screening has been carried out prior to inputting the data into the screening tool. The existence of outliers may impact the results of the computations carried out in the screening tool, and data not considered representative must be removed prior to running the program;
- Exposure to pathogens occurs through recreational contact (i.e. swimming). If other routes of exposure are significant, the screening tool may not be suitable;
- Exposure events are independent;
- The output from the program is the estimated distribution of risk to infection per person per exposure event. Factors not accounted for in this estimate include person to person transmission of disease, immunity (protection from infection due to prior exposure), and differential susceptibility within the population;
- The primary risk from recreational exposure is to enteric viruses;

¹ According to the U.S. EPA’s ambient water quality criteria for bacteria, 8 illnesses/1000 swimmers is considered to be an acceptable level of risk (US EPA, 1986)

- This program is intended only as a screening tool to determine if further investigations of health risk are appropriate.

Data Input

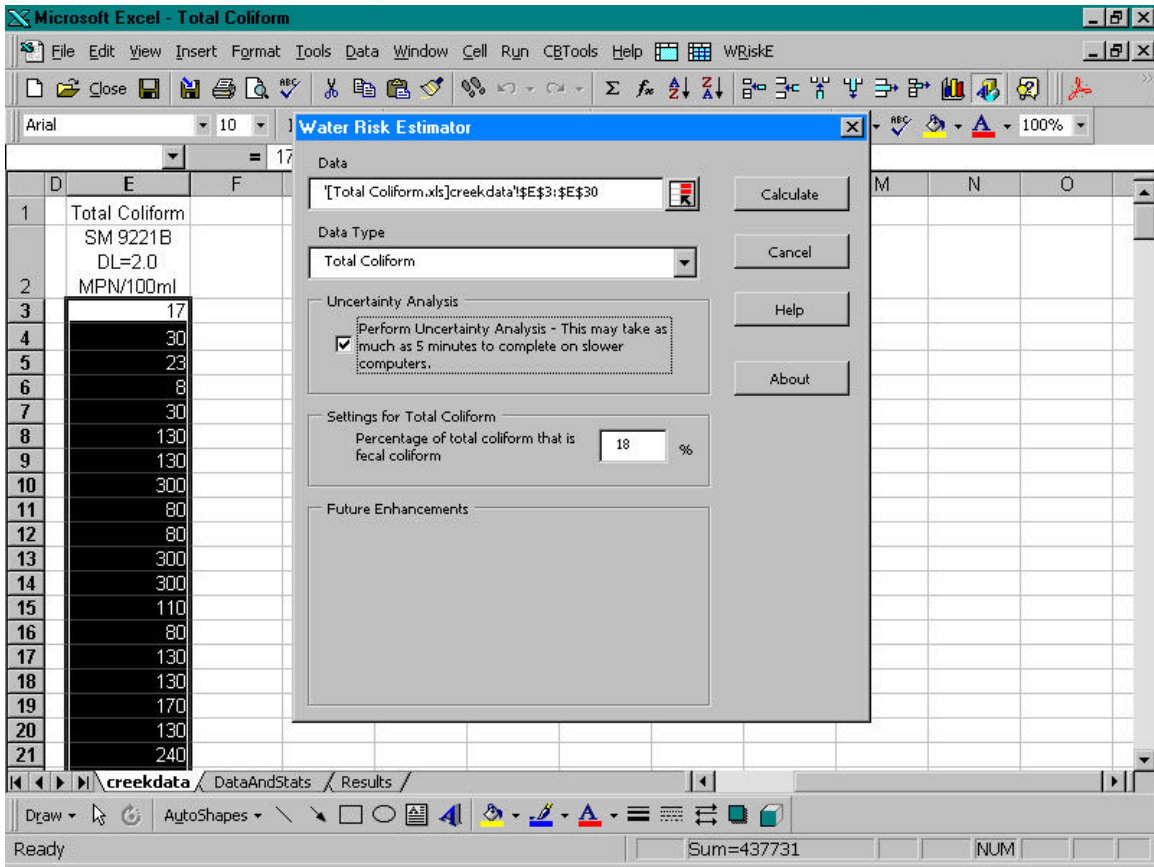
The screening tool takes as input fecal indicator and pathogen data. Indicators included in the tool are total coliform, fecal coliform, fecal streptococcus, E. coli, enterococcus, and F+RNA coliphage; pathogens included are giardia and cryptosporidium. The screening tool is implemented as an add-in to Microsoft Excel. The add-in was developed using Excel 2000. Input data should therefore be stored as or converted to an Excel Worksheet. It should be clear that the results from the screening tool are limited by the quality of the data input to the program. If the input data do not adequately characterize the water quality of the stream of interest, the results output by the screening tool will be of little value. It cannot be over-emphasized that methodical sampling and quality assurance programs are critical components to accurately characterizing the risk associated with recreational exposure to pathogens.

After loading the tool into Excel addins², the user clicks on the “Run Water Risk Estimator” option on the “WriskE” drop down menu. This will start the screening tool. The user then inputs the location of the concentration data for one of the appropriate indicators or pathogens. Input data must consist of numeric concentration values (no non-numeric entries or missing values!) with units of “per 100mL” (MPN\100mL, oocysts\100mL, etc.).

To run the uncertainty analysis, the user simply checks the button. For the total coliform indicator, the user may change the percentage of total coliform that is fecal, provided it is known, or simply use the default of 18% as discussed below. Pressing the “calculate” button on the initial screen will prompt the microbial risk screening tool to begin calculations to estimate the distribution of risk of infection. Figure 1 shows the input screen with the options described above.

² Solver (a Microsoft add-in) must be loaded prior to loading the microbial risk screening tool.

Figure 1: Input Screen for Microbial Risk Screening Tool



Generating a “Dose” from the Input Data

Using skewness as the significant criteria to identify an appropriate family of distributions, the input data are fit to a distribution using the method of maximum likelihood. If the data are positively skewed, a lognormal distribution is selected; whereas, if the raw data are negatively skewed, a weibull distribution is employed (Ott, 1995).

For the following indicators, the data are converted from indicator concentration to enteric virus concentration using the relations reported by Havelaar and co-workers (1993):

$$\text{Log (y)} = 0.17 + 0.98 * \text{Log (x)} \text{ for F + RNA coliphage}$$

$$\text{Log (y)} = -1.16 + 1.56 * \text{Log (x)} \text{ for fecal coliform}$$

$$\text{Log (y)} = -0.2 + 1.81 * \text{Log (x)} \text{ for fecal streptococcus}$$

where y is the concentration of enteric virus (per L) and x is the concentration of indicator (per mL).

Total Coliform is calculated in a similar way; however, it must first be converted to an “equivalent” fecal coliform concentration. The U.S. EPA (1986) water quality criteria are based on a relationship in which fecal coliform concentration is 18% of total coliform concentration. This is the default in the microbial risk screening tool. The user may either use this relationship

between total and fecal coliform or input a different site-specific percentage, provided it is known. After total coliform data have been converted to a fecal coliform “equivalent”, the relationship for fecal coliform is used as discussed above.

For E. coli and enterococcus, no conversion to enteric viruses is necessary because the illness rates are based on epidemiologic data that relate densities of these organisms directly to illness (Cabelli, 1983; Dufour, 1984). For the pathogens, giardia and cryptosporidium, no concentration conversion is necessary.

The next step in the microbial risk screening tool is to calculate an ingestion rate distribution. The screening tool applies results reported by Roseberry and Burmaster (1992) to the generally accepted rate of water ingestion during recreational activities (50mL). The result is a lognormal distribution with a mean value of 50 mL per exposure event, with 90% of ingestion events between 25 and 75 mL.

Enteric virus concentrations (for total coliform, fecal coliform, fecal streptococcus, and F+RNA coliphage), indicator concentrations (for E. coli and enterococcus), or pathogen concentrations (giardia and cryptosporidium), and the ingestion rate distribution are used to calculate the dose ingested. For F+RNA coliphage, fecal coliform, total coliform, and fecal streptococcus, a dose is calculated by sampling once from the pathogen concentration distribution (converted from indicator concentrations) and once from the ingestion rate distribution. Those values are multiplied to obtain an expected dose of pathogen ingested. For E. coli, enterococcus, giardia and cryptosporidium, a dose is calculated by sampling once from the indicator or pathogen concentration distribution and once from the ingestion rate distribution, and then multiplying these two resulting values. This process is repeated 500 times, yielding a dose (number organisms/event) distribution. For E coli and enterococcus, this distribution is indicator dose; whereas, for all of the other organisms, the calculated distribution is pathogen dose.

Dose-Response

For F+RNA coliphage, fecal coliform, total coliform, and fecal streptococcus, the relationship between enteric virus and risk of infection is based on a maximum likelihood fit of data obtained from a rotavirus dosing trial (Ward, et al., 1986) using a beta Poisson function (Haas, 1983). The following dose-response function describes the relationship:

$$r = 1 - (1 + y/b)^{-a}$$

where r is the risk of infection per person per exposure event, y is the dose of enteric viruses, and a and b are 0.26 and 0.42, the parameters of the dose-response function.

For E. coli and enterococcus, the US EPA (1986) developed the following equations based on epidemiological studies at freshwater recreation areas:

$$Y = -11.74 + 9.397 \log (x)$$

where Y is the illness rate per 1000 swimmers and x is the E. coli density per 100 mL, and

$$Y = -6.278 + 9.40 \log (x)$$

where Y is the illness rate per 1000 swimmers and x is the enterococcus density per 100 mL.

Eisenberg, et al. (1996) applied the following equation for giardia:

$$Y = 1 - \exp(-ay)$$

where Y is the illness rate per swimmer, y is the dose of giardia and a is the parameter of the dose-response function, corresponding to 0.024 with 95% confidence between 0.008 and 0.04.

Eisenberg, et al. (1998) applied the following equation for cryptosporidium based on the largest known waterborne outbreak of disease in Milwaukee, Wisconsin in 1993:

$$Y = 1 - \exp(-ay)$$

where Y is the illness rate per swimmer, y is the dose of cryptosporidium, and a is the parameter of the dose-response function, corresponding to 0.0055 with 95% confidence between 0.001 and 0.01.

For F+RNA coliphage, fecal coliform, total coliform, and fecal streptococcus, risk is calculated by randomly sampling the dose distribution and plugging the result into the dose-response functions described above. For E. coli and enterococcus, risk is calculated by randomly sampling the indicator concentration distribution and plugging the result into the function described above. For giardia and cryptosporidium, risk is calculated by randomly sampling the pathogen dose distribution and plugging the result into the dose-response functions described above.

The random sampling calculations are performed 500 times yielding a distribution of risk of infection per person per exposure event. The maximum likelihood distribution of indicator organism or pathogen concentration, the ingestion rate distribution, the dose histogram, the dose-response function, and the resultant and cumulative distributions of risk are shown in the output of the program.

Uncertainty Analysis

It should be understood that each risk assessment has some degree of uncertainty embedded in it. To make explicit the known variability and uncertainty in the computations carried out for the microbial risk screening tool, functionality characterizing uncertainty has also been built into the screening tool.

For F+RNA coliphage, fecal coliform, total coliform, and fecal streptococcus, uncertainty bounds for the risk estimate are calculated by varying six parameters and finding the 5th and 95th percentiles about the resultant risk distribution. For these indicators, the parameters varied are the two parameters describing the maximum likelihood fit of the raw concentration data, the two parameters describing the shape of the dose-response function, and the two parameters describing the relationship between indicator and enteric virus concentration.

For E. coli and enterococcus, four parameters are varied: the two parameters describing the maximum likelihood fit of the raw data and the two parameters describing the shape of the “dose-response” function.

For giardia and cryptosporidium, three parameters are varied: the two parameters describing the maximum likelihood fit of the raw data and the one parameter describing the shape of the dose-

response function. For all indicators, the 5th and 95th percentile probabilities are plotted with the maximum likelihood risk distribution in the program output.

Conclusions

A microbial risk screening tool has been developed to estimate the relative level of risk associated with exposure to pathogens via recreational contact (i.e. swimming) in an urban creek or stream environment. The screening tool takes as input microbial indicator or pathogen data and generates, through a series of Monte Carlo simulations and maximum likelihood distribution fits, a distributional estimate of relative risk of infection to pathogenic microorganisms.

The microbial risk screening tool does not generate quantitative risk estimates in the strictest sense, but is rather a tool that may be used to determine if more detailed investigations are appropriate or needed. It is assumed that the data input to the program is representative of the water quality to which the population is exposed, and that the data have been subject to appropriate quality control and filtering prior to running the screening tool.

It is anticipated that the microbial risk screening tool will be used by public agencies to interpret microbial indicator or pathogen data with respect to impairment of beneficial uses. In that respect, it should be understood, that the rigor of a population-based assessment of microbial risk has been sacrificed for the practicality of a tool that may be used on a screening level to interpret microbial data. The intention of the tool is to facilitate in sufficient detail that interpretation, without requiring the assistance of a specialized risk analyst.

References

- Borrego, et al., 1987. Coliphages as an indicator of fecal pollution in water, its relationship with indicator and pathogenic microorganisms. *Wat. Res.* V.21(12), 1473-80.
- Anderson, R.M. and R. May, "Infectious Diseases of Humans: Dynamics and Control", New York: Oxford University Press, 1991.
- Cabelli, V.J., 1983. Public health and water quality significance of viral disease transmitted by drinking water and recreational water. *Wat. Sci. Tech.* Vol. 15, pp1-15.
- Cooper, R.C., A.W. Olivieri, R.E. Danielson, P.G. Badger, R.C. Spear, and S. Selvin, "Evaluation of Military Field-Water Quality, Volume 5: Infectious Organisms of Military Concern Associated With Consumption: Assessment of Health Risks and Recommendations for Establishing Related Standards", Lawrence Livermore National Laboratory, 1986.
- Dudley, R.H., K.K. Hekimain, and B.J. Mechalas, "A Scientific Basis for Determining Recreational Water Quality Criteria," *Journal of the Water Pollution Control Federation*, 48, 2761-2777, 1976.
- Dufour, A.P. 1984. Health Effects Criteria for Fresh Recreational Waters. US EPA EPA-600/1-84-004.
- Eisenberg, J.N., E.Y. Seto, A.W. Olivieri, R.C. Spear, "Quantifying Water Pathogen Risk in an Epidemiological Framework", *Society for Risk Analysis*, pp.549-563, 1996.

- Eisenberg, J.N., E.Y. Seto, J.M. Colford, A.W. Olivieri, R.C. Spear, "An Analysis of the Milwaukee Cryptosporidiosis Outbreak Based on a Dynamic Model of the Infection Process", *Epidemiology*, 9: #3, May, 1998.
- EOA, Inc. and U. C. Berkeley, "Microbial Risk Assessment for Reclaimed Water", Prepared for Irvine Ranch Water District and the National Water Resource Association, May 1995a.
- EOA, Inc., "Mamala Bay study Infectious Disease Public Health Risk Assessment", 1995b.
- EOA, Inc., "City of Stockton NPDES Studies Health Risk Assessment", 1996.
- EOA, Inc., Santa Clara County Microbial Risk Case Study, 2000.
- Fleisher, J.M., 1991. A reanalysis of data supporting U.S. federal bacteriological water quality criteria governing marine recreational waters. *WPCF Research Journal*, V.63 (3).
- Gerba, C.P., S.M. Goyal, R.L. LaBelle, I.Cech, and G.F Bodgan, 1978. Failure of indicator bacteria to reflect the occurrence of enteroviruses in marine waters, *Am. J. Public Health*, 69(11): 1116-9.
- Haas, C.N., "Estimation of Risk Due to Low Doses of Microorganisms: A Comparison of Alternative Methodologies", *Am. J. Epidemiol*, 55:573-582, 1983.
- Havelaar, A.H., M. Van Olphen, and Y.C. Drost, 1993. F-specific bacteriophages are adequate model organisms for enteric viruses in fresh water. *Applied & Environmental Microbiology*, pp.2956-62.
- International Life Sciences Institute, Risk Science Institute Pathogen Risk Assessment Working Group, "A Conceptual Framework to Assess the risks of Human Disease Following Exposure to Pathogens", *Risk Analysis*, 16:841-848, 1996.
- Kay, et al., 1994. Predicting likelihood of gastroenteritis from sea bathing: results from randomized exposure. *Lancet*, Vol. 344, pp905-909.
- Koopman JS, Longini IM, Jacquez JA, 1991. Assessing Risk Factors for Transmission of Infection. *American Journal of Epidemiology*, 133:1199-1209.
- Koopman JS, Longini IM. 1994. The Ecological Effects of Individual Exposures and Nonlinear Disease Dynamics in Populations. *American Journal of Public Health*, 84:836-842.
- National Research Council, "Risk Assessment in the Federal Government, Managing the Process", National Academy Press, Washington, D.C., 1983.
- Olivieri, A.W. et al., "Risk Assessment of Waterborne Infectious Agents," Proceedings of the International Conference on Development and Application of Computer Techniques to Environmental Studies, Los Angeles, 1986.

- Olivieri, A.W. et al., "Risk of Waterborne Infectious Illness Associated with Diving in the Point Loma Kelp Beds, San Diego, CA," Proceedings of the ASCE 1989 Specialty Conference on Environmental Engineering, Austin, Texas, 1989.
- Ott W.R., "Environmental Statistics and Data Analysis", Lewis Publishers, Boca Raton, FL, 1995.
- Regli, S., J.B. Rose, C.N. Haas, and C.P. Gerba, "Modeling the Risk from Giardia and Viruses in Water", Journal Am. Water Works Association, pp.76-84, 1991.
- Rose J.B., et al., "King County Combined Sewer Overflow Water Quality Assessment for the Dumanish River and Elliott Bay, Appendix B-2: Risks to People", Prepared for the Duwamish River and Elliott Bay Water Quality Assessment Team Working Draft, 1999.
- Roseberry, A. M. and D. E. Burmaster, 1992. "Log-normal Distributions for Water Intake by Children and Adults". Risk Analysis, 12 (1): 99-104.
- Sobsey, M.D., D.A. Battigelli, T.R. Handzel, and K.J. Schwab, 1995. Male specific coliphages as indicators of viral contamination of drinking water, AWWARF and AWWA.
- Soller, J.A., J.N. Eisenberg, and A.W. Olivieri, "Evaluation of Pathogen Risk Assessment Framework", Prepared by EOA, Inc. for ILSI Risk Science Institute, January 1999.
- US EPA, 1986. Ambient Water Quality for Bacteria, EPA440/5-84-002, 1986.
- Ward, R. L., D. I. Bernstein, E. C. Young, J. R. Sherwood, D. R. Knowlton and G. M. Schiff, "Human Rotavirus Studies in Volunteers: Determination of Infectious Dose and Serological Response to Infection," Journal of Infectious Disease, 154, 871-880, 1986.

Appendix A

Microbial Indicators and Effects on Beneficial Uses Work Plan

Microbial Indicators and Effects on Beneficial Uses

Work Plan

1.0 Purpose and Motivation

The primary objective of this project is to create a computer-based program (tool) that can be used to assess the relative microbial risks to public health from recreational exposure to urban creek waters. Key components of this project are to:

- Summarize the issues associated with estimating the acute risk recreational waters pose to an exposed population;
- Conduct a literature review to determine the most appropriate relationships between bacterial indicator organisms and human illness that would be appropriate for creeks in Santa Clara Valley;
- Adapt a computer model of microbial risk to estimate the expected range of the number of infections or resulting illnesses from exposure to urban creek waters; and
- Develop a practical computer-based program which can be used on a screening level to estimate the relative level of risk posed to recreators from creek waters, given a set of monitoring data from that creek.

The primary motivation for this investigation is that sampling and analysis of some Bay Area creeks has shown sporadic exceedances of Basin Plan criteria for bacterial densities (fecal coliform in particular). Although no link has been established demonstrating a clear connection between the sampling results and human health risks, it has been suggested that the water contact recreation beneficial use may be impacted by these exceedances. A review of the available literature on the subject indicates that the relationship between bacterial densities and human illness is not well agreed upon. In fact, it would be very difficult to generalize whether sporadic exceedances of the fecal coliform objectives represent an increased risk to public health or not.

Given the complexities noted above, a practical tool was proposed to streamline the process of evaluating the relative microbial risks to public health from exposure to urban creek waters. Given monitoring data from an urban creek, related information about the potential sources of fecal contamination in that creek, and exposure information, the tool will estimate the relative scale of the potential public health impact. The Work Plan to carry out the development of that tool and associated documentation is described herein.

The relative health risk will be based on the estimated occurrence of selected pathogens in the creek under study (based on bacterial indicator densities), pathogen characteristics, number of persons exposed, mode of exposure, population immune status, and other factors. The utility and application of the tool will be demonstrated for a selected creek reach and interpreted to assess the significance of bacterial indicator densities with respect to relative risk to public health. Documentation will be provided to facilitate the input and analysis of data for other creek reaches and to interpret the relative microbial risks to public health from exposure to pathogens via recreational contact in an urban creek environment.

2.0 Introduction

2.1 History of Bacterial Water Quality Objectives

Water quality criteria objectives are specified in the Basin Plan (RWQCB, 1995) for total and fecal coliform bacteria for water contact recreation, shellfish harvesting, non-contact water recreation, and municipal supply beneficial uses. Additionally, EPA bacteriological criteria for freshwater water contact recreation are specified for enterococci and E. coli. For water contact recreation the Basin Plan objectives and fresh water criteria may be summarized as follows:

Organism	Criteria	Value	Units
Fecal Coliform	log mean	<200	MPN/100 ml
	90th %ile	<400	
Total Coliform	median	<240	MPN/100 ml
	maximum	<10,000	
Enterococci	steady state	33	colonies/100ml
	max at beach	61	
	max at lightly used area	108	
E Coli	steady state	126	colonies/100ml
	max at beach	235	
	max at lightly used area	406	

The following is a summary of information originally prepared by the US EPA (1986). Federal water quality criteria recommendations were first proposed in 1968 by the National Technical Advisory Committee (NTAC) of the Department of the Interior. The microbiological criterion suggested by the NTAC for bathing waters was based on a series of studies conducted in the 1940s and 1950s by the United States Public Health Service. The studies were conducted at bathing beaches located on Lake Michigan in Chicago, IL, on the Ohio River in Dayton, KY, and on Long Island Sound, NY. In each case two beaches with different water quality were selected, cooperating families recorded their swimming activity and illnesses on a daily basis for the entire summer.

Data from the Ohio River study indicated that swimmers who swam in water with a median coliform density of 2300 total coliform/100ml had an excess of gastrointestinal illness when compared to an expected rate calculated from the total study population. An analysis of the Lake Michigan study comparing a one week time period following three days of high coliform density, with a corresponding time period following three days of low coliform density corroborated the Ohio River study results. The results of the two marine bathing beach studies showed no association between illness and swimming in water containing approximately 400 and 800 coliforms/100ml.

The coliform water quality index used during the studies noted above was translated into a fecal coliform index in the mid-1960s by using a ratio of fecal coliform to total coliform at the location on the Ohio River where the original study had been conducted in 1949. About 18% of the coliforms were found to be fecal coliforms and this proportion was used to transform the density at which a statistically significant swimming-associated gastrointestinal illness was observed to a fecal coliform standard (400/100ml). The NTAC suggested that a detectable risk was undesirable, and therefore one half of the density at which a health risk occurred, 200/100ml was proposed.

The recommended criterion for fecal coliform was thus generated. Although this criterion was criticized on a number of technical issues, it was again recommended by the US EPA in 1976.

The US EPA, in 1972 initiated a series of studies at marine and fresh water bathing beaches which were designed to correct the perceived deficiencies of the PHS studies. One goal of these EPA studies was to determine if swimming in sewage-contaminated water carries a health risk for bathers, and if so, to what type of illness. If a quantitative relationship between water quality and health risk was obtained, two additional goals were to determine which bacterial indicator is best correlated to swimming associated health effects and if the relationship is strong enough, to provide a criterion.

The results of the EPA bathing beach studies are described by Cabelli (1983) and Dufour (1984). In these studies, quantitative relationships between the rates of swimming-associated health effects and bacterial indicator densities were determined using regression analysis. The studies included an examination of a number of potential indicators including total and fecal coliform, enterococci, *E. coli*, *klebsiella sp.*, *Enterobacter sp.*, *citrobacter sp.*, *Clostridium perfringens*, *Pseudomonas aeruginosa*, *Aeromonas hydrophilia*, and *Vibrio parahemolyticus*. The selection of the best indicator was based on the strength of the relationship between the rate of gastroenteritis and the indicator density. The marine studies concluded that enterococci showed the strongest relationship, *E. coli* was a poor second, and all others showed very weak association to the observed gastroenteritis. In the fresh water studies *E. coli* and enterococci had similar regression coefficients, and fecal coliform showed a weaker relation to gastroenteritis.

Based on the results of these studies, EPA did not change the stringency of its bacterial criteria for recreational waters. EPA's evaluation of the bacteriological data indicated that using the fecal coliform indicator group at the maximum geometric mean of 200/100ml would cause an estimated 8 illness per 1000 swimmers at fresh water beaches and 19 illnesses per swimmers at marine beaches. *E. coli* and enterococcus criteria were developed using those accepted illness rates. The equations developed by Cabelli (1983) and Dufour (1984) were used to calculate the geometric mean indicator densities corresponding to the accepted gastrointestinal illness rates. Those densities are the ones shown in the table presented previously. EPA recommends the application of these criteria unless sanitary and epidemiological studies show the sources of the indicator bacteria to be non-human suggesting that the indicator densities are not indicative of a health risk to those swimming in such waters.

2.2 Modeling of Waterborne Infectious Disease Transmission

2.2.1 Individual-Based Microbial Risk Assessment

Risk assessment involves the use of factual data to define the potential health effects of exposure for individuals or populations to hazardous materials and situations. Quantitative assessments of human health risks associated with the ingestion of waterborne pathogens have historically been conducted within the framework developed for chemical risk assessments (NRC 1983). Until recently these assessments have, for the most part focused on the probability of infection or disease to an individual as a result of a single exposure event (Dudley et al., 1976; Haas 1983; Rose et al., 1999).

When applied to infectious disease transmission, the chemical risk assessment framework has several methodological limitations. The chemical risk framework was never intended to address

aspects unique to the transmission of infectious diseases such as: 1) person-to-person spread of infection; 2) immunity; and 3) the environmental population dynamics of pathogens (regrowth or dieoff). The limitations of treating infectious disease transmission as a static disease process, with no interaction between those infected or diseased and those at risk, has been illustrated in studies of *Giardia* (Eisenberg et al., 1996), dengue (Koopman et al., 1994), and sexually transmitted diseases (Koopman et al., 1991).

Another critique of some of the previously cited microbial risk assessments is that point estimates have commonly been used to characterize the probability that a particular exposure leads to infection or disease in a single individual. This type of estimate carries no significant information about the associated uncertainty or variability. From a public health perspective, the probable number of people infected in an exposed population is more meaningful than the probability of individual infection. To address this point, the probability of individual infection has sometimes been multiplied by the population number in an attempt to predict the disease incidence in the population. This strategy, however, may or may not be accurate depending on the appropriateness of the underlying assumptions.

2.2.2 Population-Based Microbial Risk Assessment

A population-based risk assessment approach for waterborne disease transmission was originally developed by members of this project team as part of a study for the U.S. Army (Cooper et al., 1986; Olivieri et al., 1986; Olivieri et al., 1989). In this work, a population perspective was taken by estimating the probability distribution of the number of infected/diseased people in the exposed population. One unique feature of this model was its probabilistic treatment of dose-response data (i.e., data which provide a quantitative linkage between the number of organisms ingested and the probability of infection or overt disease). From this model's population perspective, each member of the population received a different dose and also had a different probability of responding to this dose. The combination of these two factors resulted in each member of the population carrying a different probability of becoming infected or diseased.

We have recently extended this population-based approach by taking advantage of the available infectious disease and dose-response literature in the development of a mathematical model that characterizes the human disease risk of waterborne pathogen exposure (EOA 1995a; EOA 1995b; EOA 1996; Eisenberg et al., 1996; Eisenberg et al., 1998). Based on the host/microbe interaction, this approach makes explicit the mechanistic aspects of the infectious disease process and provides a structure from which data are gathered. An existing dose-response model (Haas 1983; Regli et al., 1991) is embedded into an epidemiological framework, relying on a large base of literature describing the use of dynamic population models in the study of epidemics (Anderson and May, 1991).

The dynamic nature of these epidemiologic models emphasize the importance of how the susceptible, infected, diseased, or immune status of individuals within a defined population group vary over time. In addition to these epidemiologically-based variables, this model incorporates the environmental dynamics of the pathogen.

2.2.3 Recent Developments

In 1996, the US EPA Office of Water and the American Water Works Association Research Foundation contracted the International Life Sciences Institute to convene a panel of experts to develop a conceptual framework to assess the risks of human disease associated with exposure to waterborne pathogenic microorganisms. The panel acknowledged the limitations of the chemical risk assessment framework when applied to microorganisms, and developed a generalized framework applicable for microbial risk assessment (ILSI 1996).

Recently, members of this research team were asked to critique the microbial risk assessment framework by conducting a quantitative risk assessment case study (Soller et al., 1999). In general, it was found that the ILSI framework provides an efficient process which may be used to develop the conceptual structure of the risk assessment, and to identify important components to be included in the risk characterization. Our critique of the Framework recommended several modifications to more directly address aspects of the infectious disease process. The methodology described in this Work Plan is consistent with the ILSI framework and the recommended modifications.

One important aspect of modeling the disease process is that, under a given set of assumptions, the population based modeling approach may converge with the individual based approach. For example this may be true if one were to assume that secondary infection within a population is unimportant and the whole population under study is susceptible to infection. Further, it should be noted that for each investigation, the risk assessor must evaluate the needs of the investigation and the data available for study, and then determine if the additional complexity of the population based approach is warranted. Both the individual and population based approaches have been shown to produce valuable results. Based on the scope of this project, the incorporation of a full-blown population model will not be necessary. The proposed use of this computer-based screening tool is to help decide whether or not a thorough risk assessment is required.

2.3 Identifying Appropriate Relationships Between Bacterial Indicator Organisms and Human Illness

The basic reason for carrying out microbiological water analysis is to safeguard the health of a community by testing for possible fecal pollution, the source of microorganisms causing waterborne disease. Pathogenic microorganisms usually appear in recreational waters intermittently and in low concentrations (Borrego et al., 1987). Indicator organisms, organisms which coexist with pathogens in the fecal environment and are easier and less expensive to test for than pathogens, are often the focus of water analyses rather than pathogens. Ideally, an indicator organism would be present in higher numbers than the pathogen of interest, always be present when the pathogen is present, be easy and inexpensive to assay, and would serve as an indicator of (preferably human) fecal contamination.

Over the years, coliforms, enterococci, *E. coli*, fecal streptococci, coliphages, and others have been proposed as indicator systems of risk to public health. In all of these studies the limited applicability of these indicators were outlined. As suggested in Kay et al. (1994), after examining the data from each of these studies, no universal relation between any single microbiological indicator of water quality and disease has emerged. However, relations have been developed between a number of indicators and risk to human health under specific conditions. Given the

nature of the specificity of these relations, it should be clear that some of those relations may be more applicable to creek waters in Santa Clara County than others.

Given that the intent of this investigation is to develop a tool which can be used to estimate the relative risk to public health from exposure to urban creek waters, we propose to determine the most applicable relations between indicator densities and public health effects for creek waters in Santa Clara County. This will be carried out through a review of the available literature. During the literature search, we will attempt to find relations for total coliform, fecal coliform, enterococci, E. coli, fecal streptococci, and F+RNA coliphage. Documentation will be provided describing the relation between indicator densities and human health effects for each organism where an applicable relation was found. Assumptions associated with each of the relations will also be documented.

2.4 Rationale for a computer-based tool for assessing microbial risks

A computer-based tool provides a systematic way of integrating and summarizing data. If used properly the tool described herein may provide valuable information for decision making. However, it must be understood that this tool provides screening level estimates of relative risk and not a rigorous assessment of risk. One valuable aspect of this tool is that it may be used to determine when or if a rigorous risk assessment may be warranted in comparison to situations in which the relative risk is clearly lower than a given standard.

The uncertainties in the available data and the underlying processes, as well as the variability inherent in environmental systems are significant. A modeling tool must account for these uncertainties when providing estimates. Due to these uncertainties, the utility of these models is in their abilities to compare the effects of different scenarios. For example, one possible result may be that the distribution of risk associated with scenario A, in which humans are exposed to a pathogen, is in all cases higher than for scenario B. An alternative result may be that scenario A and B are indistinguishable when comparing their output distributions of risk. In all cases the result from this tool will be a broad assessment of relative risk rather than an absolute risk estimate.

For this project, applicable relations between indicator organism densities and health effects will be incorporated into the tool. The user of the tool will input whatever indicator organism data are available into the program (provided that a relation was determined for that organism). The tool will use the previously discussed relations between indicator densities and public health to estimate the relative risk to public health by comparing the distribution of risk to the “accepted” level of risk for freshwater. In this manner, the tool will be used to facilitate the interpretation of the available indicator organism data.

3.0 Tasks

3.1 Problem formulation and analysis

This task will include the development of a conceptual model for exposure and the relevant population level epidemiology. A literature review will be conducted based on the conceptual

model. Consistent with the microbial risk assessment framework (ILSI, 1996), the refinement of these components will be an iterative process.

The following components need to be addressed and defined in this phase of the project.

Route of exposure;

Pathogen of interest (Preliminary indications are that human enteric viruses are most relevant for this project, and that rotavirus is the primary etiological agent);

Population exposed;

Dose of the pathogen to which the population is exposed; and

Relative benefit of including population level effects;

Based on the problem definition, the conceptual model, and manuscripts obtained during the literature search, data and requisite assumptions will be organized into exposure and health effects “profiles”. Following is a generic description of the information typically contained in each of the profiles.

3.1.1 Exposure profile:

The goal of the exposure profile is to consolidate and summarize all of the data relevant to exposure for the scenario under investigation. In this investigation, the information in the profile include: 1) the potential types of pathogen sources in the creek; 2) the applicability of the reported relations between indicator organism densities and health effects. Relations will be investigated for fecal coliform, total coliform, fecal streptococci, enterococci, E. coli, and F+RNA coliphage; 3) the uncertainty and/or variability associated with those relations; 4) the dose of pathogen to which the exposed population may encounter.

3.1.2 Health effects profile

The purpose of this component is to consolidate and summarize all of the data relevant to individual or population level health effects for the scenario under investigation. The exposure pathway model will serve as input into the health effects model. The information in this profile will be used to estimate the public health effects of the defined exposures and estimated in the exposure pathway model.

3.2 Risk characterization development

The risk characterization phase of a risk assessment provides an estimate of the likelihood and/or magnitude of effects to be observed in the exposed population under a specified exposure scenario, including all of the inherent assumptions and uncertainties. In this particular risk assessment, the risk characterization phase will include parameterization of a mathematical model(s), numerical simulation, and summarization of results.

The first step in this risk characterization phase will be to translate the model from conceptual models of exposure and health effects to computer code. Parameterization will be carried out by integrating the data obtained through literature review. All applicable relations between indicator organisms and health effects will be incorporated. Routines will then be added to read input files (indicator organism data) into the model. Data input to the model will be fit to a distribution which will be used to the characterize the input data from that point forward. Distributions will be fit

with a maximum likelihood routine using skewness as the significant criteria to establish the appropriate distribution family.

The input distribution will be mapped into a risk estimate using the appropriate relation via numerical simulation. Monte Carlo simulation techniques will be used to sample the input distributions and appropriate parameters in the model. Output from the model will be a comparison of risk between the modeled scenario and the level of acceptable risk for fresh water recreation.

3.3 Case study

In this task we will use the software developed and conduct a case study. The case study will use data collected on a specific creek reach in Santa Clara County. Data from this creek reach will be input to the program and an estimate of relative risk will be generated. The results of the case study, along with illustrative examples will be documented in detail in the final project report.

3.4 Documentation

Documentation will be provided in the form of a final project report and a memorandum describing the use of the final product, a tool which may be used to estimate the relative risk associated with recreational contact with creek waters in Santa Clara County.

4.0 References

- Anderson, R.M. and R. May, "Infectious Diseases of Humans: Dynamics and Control", New York: Oxford University Press, 1991.
- Cabelli, V.J. 1983. Health Effects Criteria for Marine Recreational Waters. US EPA, EPA-600/1-80-031.
- Cooper, R.C., A.W. Olivieri, R.E. Danielson, P.G. Badger, R.C. Spear, and S. Selvin, "Evaluation of Military Field-Water Quality, Volume 5: Infectious Organisms of Military Concern Associated With Consumption: Assessment of Health Risks and Recommendations for Establishing Related Standards", Lawrence Livermore National Laboratory, 1986.
- Dudely, R.H., K.K. Hekimain, and B.J. Mechalas, "A Scientific Basis for Determining Recreational Water Quality Criteria," Journal of the Water Pollution Control Federation, 48, 2761-2777, 1976.
- Dufour, A.P. 1984. Health Effects Criteria for Fresh Recreational Waters. US EPA EPA-600/1-84-004.
- Eisenberg, J.N., E.Y. Seto, A.W. Olivieri, R.C. Spear, "Quantifying Water Pathogen Risk in an Epidemiological Framework", Society for Risk Analysis, pp.549-563, 1996.
- Eisenberg, J.N., E.Y. Seto, J.M. Colford, A.W. Olivieri, R.C. Spear, "An Analysis of the Milwaukee Cryptosporidiosis Outbreak Based on a Dynamic Model of the Infection Process", Epidemiology, 9:#3, May, 1998.
- EOA, Inc. and U. C. Berkeley, "Microbial Risk Assessment for Reclaimed Water", Prepared for Irvine Ranch Water District and the National Water Resource Association, May 1995a.
- EOA, Inc., "Mamala Bay study Infectious Disease Public Health Risk Assessment", 1995b.
- EOA, Inc., "City of Stockton NPDES Studies Health Risk Assessment", 1996.

- Haas, C.N., "Estimation of Risk Due to Low Doses of Microorganisms: A Comparison of Alternative Methodologies", *Am.J. Epidemiol*, 55:573-582, 1983.
- International Life Sciences Institute, Risk Science Institute Pathogen Risk Assessment Working Group, "A Conceptual Framework to Assess the risks of Human Disease Following Exposure to Pathogens", *Risk Analysis*, 16:841-848, 1996.
- Koopman JS, Longini IM, Jacquez JA, 1991. Assessing Risk Factors For Transmission of Infection. *American Journal of Epidemiology*;133:1199-1209.
- Koopman JS, Longini IM. 1994. The Ecological Effects of Individual Exposures and Nonlinear Disease Dynamics in Populations. *American Journal of Public Health*;84:836-842.
- National Research Council, "Risk Assessment in the Federal Government, Managing the Process", National Academy Press, Washington, D.C., 1983.
- Olivieri, A.W. et al., "Risk Assessment of Waterborne Infectious Agents," Proceedings of the International Conference on Development and Application of Computer Techniques to Environmental Studies, Los Angeles, 1986.
- Olivieri, A.W. et al., "Risk of Waterborne Infectious Illness Associated with Diving in the Point Loma Kelp Beds, San Diego, CA," Proceedings of the ASCE 1989 Specialty Conference on Environmental Engineering, Austin, Texas, 1989.
- Regli, S., J.B. Rose, C.N. Haas, and C.P. Gerba, "Modeling the Risk from Giardia and Viruses in Water", *Journal Am. Water Works Association*, pp.76-84, 1991.
- Rose J.B., et al., "King County Combined Sewer Overflow Water Quality Assessment for the Dumanish River and Elliott Bay, Appendix B-2: Risks to People", Prepared for the Duwamish River and Elliott Bay Water Quality Assessment Team Working Draft, 1999.
- RWQCB San Francisco Bay Basin Region, Water Quality Control Plan, 1995.
- Soller, J.A., J.N. Eisenberg, and A.W. Olivieri, "Evaluation of Pathogen Risk Assessment Framework", Prepared by EOA, Inc. for ILSI Risk Science Institute, January 1999.
- US EPA, 1986. Ambient Water Quality for Bacteria, EPA440/5-84-002, 1986.