EPA 823-R-07-006

# REPORT OF THE EXPERTS SCIENTIFIC WORKSHOP ON CRITICAL RESEARCH NEEDS FOR THE DEVELOPMENT OF NEW OR REVISED RECREATIONAL WATER QUALITY CRITERIA

**Airlie Center**
**Warrenton, Virginia**
**March 26-30, 2007**

**U.S. Environmental Protection Agency**
**Office of Water**
**Office of Research and Development**

**June 15, 2007**

# APPENDIX D: SUMMARY OF THE EUROPEAN COMMISSION DIRECTIVE

***Revised Bathing Water Directive (EP/CEU, 2006)***

The Directive sets out requirements for the following:

(a) the monitoring and classification of bathing water quality;
(b) the management of bathing water quality; and
(c) the provision of information to the public on bathing water quality.

It is meant to apply to identified European Union (EU) bathing waters used by "large numbers" of bathers which must be assessed against the criteria in Table 2 in Chapter 1 of these proceedings (using the previous 3 or 4 years of sampling data) though establishment of a sampling program to acquire data from each bathing water at locations where a bathing water "profile" suggests the greatest risk of pollution and/or the greatest numbers of bathers might be expected (Article 3.3b). Member States must monitor each bathing water in accordance with a monitoring calendar established at the start of the bathing season (Article 3.4). The monitoring calendar can be suspended during "abnormal" conditions and samples taken during "short term pollution" may be disregarded (Article 3.6) provided that Member States comply with the additional provisions outlined below.

Bathing waters are legally required to achieve "sufficient" microbiological status by 2015 (Article 5.3), although the numerical values will be reviewed in 2008 (Article 14).

However, bathing waters classified as "poor" in Table 2 may still remain in compliance with this Directive provided that Member States shall ensure that the following conditions are satisfied (Article 5.4a (i-iv)):

> adequate management measures, including a bathing prohibition or advice against bathing, with a view to preventing bathers' exposure to pollution and identification of the causes and reasons for the failure to achieve "sufficient" quality status is undertaken by Member States; and adequate measures to prevent, reduce or eliminate the causes of pollution; and in accordance with Article 12, alerting the public by a clear and simple warning sign and informing them of the causes of the pollution and measures taken, on the basis of the bathing water profile.

Member States must establish their bathing water profiles by March 24, 2011, which will be reviewed as specified in Annex III of the Revised Bathing Water Directive.

Article 12 further describes information which must be made available to the public at the bathing water and communicated promptly by means of a sign, which includes:

- the current bathing water classification and any bathing prohibition or advice against bathing;

- a general description of the bathing water, in non-technical language, based on the bathing water profile established in accordance with Annex III;
- in the case of bathing waters subject to short-term pollution: notification that the bathing water is subject to short-term pollution;
- an indication of the number of days on which bathing was prohibited or advised against during the preceding bathing season because of such pollution, and a warning whenever such pollution is predicted or present;
- information on the nature and expected duration of abnormal situations during such events;
- whenever bathing is prohibited or advised against, a notice advising the public and giving reasons;
- whenever a permanent bathing prohibition or permanent advice against bathing is introduced, the fact that the area concerned is no longer a bathing water and the reasons for its declassification; and
- an indication of sources of more complete information in accordance with paragraph 2.

In addition, "Member States shall use appropriate media and technologies, including the Internet, to disseminate actively and promptly the information concerning bathing waters referred to in paragraph 1 and also the following information in several languages, when appropriate" (Article 12.1 and 12.2).

Where a bathing water is subject to short-term pollution the public should also be informed on the following (Article 12.4d):

- conditions likely to lead to short-term pollution;
- the likelihood of such pollution and its likely duration; and
- the causes of the pollution and measures taken with a view to preventing bathers' exposure to pollution and to tackle its causes.

Member States are required to disseminate this knowledge using geo-referenced information and signage at bathing waters beginning March 24, 2008.

Member States are free to simply use the numerical standards in Table 2. However, they may take advantage of the opportunity to discount samples collected during short-term pollution events provided they have produced a bathing water profile and have complied with the requirement to provide public information specified in Article 12, which requires real time water quality prediction. No more than 15% of planned samples that are predicted to be of poor quality (i.e., resulting in public advisories) can be discounted in this manner prior to the calculation of the compliance statistics.

**References**

EP/CEU (European Parliament/Council of the European Union). 2006. Directive 2006/7/EC of the European Parliament and of the Council of 15 February 2006 Concerning the Management of

Bathing Water Quality and Repealing Directive 76/160/EEC. *Official Journal of the European Union* L64: 31-51. Available at: http://europa.eu.int/eur-lex/lex/LexUriServ/site/en/oj/2006/l_064/l_06420060304en00370051.pdf.

# APPENDIX E: INDICATOR TERMINOLOGY

**Table E-1. Definitions for Indicator and Index Microorganisms of Public Health Concern.***

| Group | Definition |
|---|---|
| Indicator | A group of organisms that demonstrates the efficacy of a process, such as total heterotrophic bacteria or total coliforms for chlorine disinfection |
| Fecal indicator | A group of organisms that indicates the presence of fecal contamination, such as the bacterial groups fecal coliforms or *E. coli*; thus, they only infer that pathogens may be present |
| Index and model organisms | A group/or species indicative of pathogen presence and behavior respectively, such as *E. coli* as an index for *Salmonella* and F-RNA coliphages as models of human enteric virus behavior in the environment |
| Pathogen indicator | A specific pathogen belonging to a broader group of pathogens which would serve as a surrogate for the presence and/or health risks for that group (e.g., *Cryptosporidium* serving as a surrogate for all parasitic protozoa), or an indicator microorganisms whose presence is correlated to the presence of a broad group of pathogens (e.g., spores of *Clostridium perfringens* serving as a surrogate for human or dog parasitic protozoa) |

*See Text Box E-1 for definitions of microbial groups (adapted from Ashbolt et al., 2001).

**Text Box E-1. Definitions of Key Fecal Indicator Microorganisms**

**Coliforms**: Gram-negative, non spore-forming, oxidase-negative, rod-shaped facultative anaerobic bacteria that ferment lactose (with β-galactosidase) to acid and gas within 24 to 48 hours at 36±2°C. *Not* specific indicators of fecal pollution.

**Fecal coliforms**: coliforms that produce acid and gas from lactose at 44.5± 0.2°C within 24±2 hours, also known as thermotolerant coliforms due to their role as fecal indicators.

***Escherichia coli (E. coli)***: thermotolerant coliforms that produce indole from tryptophan, but also defined now as coliforms able to produce β-glucuronidase (although taxonomically up to 10% of environmental *E. coli* may not). Most appropriate group of coliforms to indicate faecal pollution from warm-blooded animals.

**Fecal streptococci (FS)**: Gram-positive, catalase-negative cocci from selective media (e.g., azide dextrose broth or m Enterococcus agar) that grow on bile aesculin agar and at 45°C, belonging to the genera *Enterococcus* and *Streptococcus* possessing the Lancefield group D antigen.

**Enterococci**: all fecal streptococci that grow at pH 9.6, between 10° and 45°C, and in 6.5% NaCl. Nearly all are members of the genus *Enterococcus*, and also fulfil the following criteria: resistance to 60°C for 30 minutes and ability to reduce 0.1% methylene blue. The enterococci are a subset of fecal streptococci that grow under the conditions outlined above. Alternatively, enterococci can be directly identified as micro-organisms capable of aerobic growth at 44±0.5°C and of hydrolysing 4-methlumbelliferyl-β-D-glucoside (MUD, detecting β-glucosidase activity by blue florescence at 366nm), in the presence of thallium acetate, nalidixic acid, and 2,3,5-triphenyltetrazolium chloride (TTC, which is reduced to the red formazan) in the specified medium (ISO/FDIS 7899-1 1998).

**Sulphite-reducing clostridia (SRC)**: Gram-positive, spore-forming, non-motile, strictly anaerobic rods that reduce sulphite to $H_2S$.

***Clostridium perfringens***: as for SRC, but also ferment lactose, sucrose and inositol with the production of gas; produce a stormy clot fermentation with milk; reduce nitrate, hydrolyse gelatine, and produce lecithinase and acid phosphatase. Bonde (1963) suggested that all SRC in receiving waters are not indicators of fecal pollution; thus, *C. perfringens* is the appropriate indicator.

**Bacteroidales:** a family of strictly anaerobic bacteria present in the guts of warm-blooded animals. The family to which *Bacteroides* belongs.

***Bacteriodes***: Gram-negative, mainly straight *Bacteroides* species that are: (a) obligately anaerobic, chain saturated, anteiso-methyl, and iso-methyl branched acids, (b) saccharolytic, producing acetate and succinate as the major metabolic end products; (c) contain enzymes of the hexose monophosphate shunt-pentose phosphate pathway; (d) have a DNA-base composition in the range 40-48 mol% GC; (e) membranes contain sphingolipids, and contain a mixture of long-chain fatty acids; (f) possess menaquiones with MK-10 and MK-11 as the major components; and (g) contain *meso*-diaminopimelic acid in their peptidoglycan. This definition restricts the *Bacteroides* to the following ten species: *B. fragilis*, *B. thetaiotaomicron*, *B. vulgatus*, *B. ovatus*, *B. distasonis*, *B. uniformis*, *B. stercoris*, *B. eggerthii*, *B. merdae*, and *B. caccae*, with *B. fragilis* as the type strain. The *Bacteroides*, along with *Prevotella* and *Porphyromonas*, form one major subgroup in the bacterial phylum Cytophaga-Flavobacter-Bacteroides. This phylum diverged quite early in the evolutionary lineage of bacteria, and thus the *Bacteroides*, although Gram-negative organisms, are not closely related to the enteric Gram-negatives such as *Escherichia coli*.

***Bacteriodes*** phages: Those viruses (bacteriophages) that use *Bacteroides* as a host for replication.

## References

Ashbolt, NJ; Grabow, WOK; Snozzi, M. 2001. Indicators of Microbial Water Quality. Pp: 289-316 in: *Water Quality: Guidelines, Standards and Health* Fewtrell, L; Bartram, J. (eds.). London: IWA Publishing.

# APPENDIX F: SUMMARY OF MEASUREMENTS CURRENTLY PLANNED FOR THE DOHENY AND MALIBU BEACH (CALIFORNIA) EPIDEMIOLOGY STUDY

**Table F-1. Summary of Measurements Currently Planned for the Doheny and Malibu Beach (California) Epidemiology Study.**

| Indicator | Method | Investigator |
|---|---|---|
| **Traditional** | | |
| Enterococci | IDEXX | South Orange County Wastewater Authority (SOCWA) |
| Enterococci | Membrane-filtration (MF) | SOCWA |
| Fecal coliforms | MF | SOCWA |
| *E. coli* | MF or IDEXX | Southern California Coastal Water Research Project (SCCWRP) |
| Total coliforms | MF | SOCWA |
| **Rapid Traditional** | | |
| Enterococci | Quantitative polymerase chain reaction (qPCR) | Noble |
| Enterococci | qPCR | Stewart |
| Enterococci | PCR-Luminex | Stewart |
| Enterococci | Transcription-mediated amplification/nucleic acid sequence-based amplification (TMA/NASBA) | Moore |
| Enterococci | Immunomagnetic separation (IMS) | Bushon |
| *E. coli* | qPCR | Noble |
| *E. coli* | IMS | Bushon |
| *E. coli* | IMS | Jay |
| **Marker Genes** | | |
| Entero-Raptor, *Esp* gene | qPCR-Raptor | Harwood/Lim |
| Enterococci *Esp* gene | qPCR | Scott |
| *E. coli* virulence genes | qPCR | Sadowsky |
| *Bacteroides* human marker | qPCR | Field |
| *Bacteroides* human marker | qPCR | Wuertz |
| **Phage** | | |
| Phage | Culture | Stewart |
| Phage | Culture | Sobsey |
| Rapid phage | Antibody | Sobsey |
| **Human Virus** | | |
| Adenovirus | qPCR | Sobsey |

| Indicator | Method | Investigator |
|---|---|---|
| Enterovirus | qPCR | Stewart |
| Hepatitis A virus | qPCR | Fuhrman |
| Norovirus | qPCR | Stewart |
| Norovirus | qPCR | Sobsey |
| Polyomavirus | qPCR | Harwood |
| **Community Profiling** | | |
| *Bacteroides thetaiotamicron* | Sequencing | Moorthy |
| *Heliobacter pylori* | Sequencing | Moorthy |
| *Campylobacter jejuni* | Sequencing | Moorthy |
| *Clostridium perfringens* | Sequencing | Moorthy |
| *Salmonella enteritica* serovar Typhimurium | Sequencing | Moorthy |
| *Shigella dysenteriae* | Sequencing | Moorthy |
| *Shigella flexneri* | Sequencing | Moorthy |
| *Shigella boydii* | Sequencing | Moorthy |
| **Bacterial Markers** | | |
| *Bacteroides thetaiotamicron* | qPCR | Noble |
| *Bacteroides thetaiotamicron* | PCR | Leddy |
| Multiple methanogens | PCR | Ufnar |
| *Methanobrevibacter smithii* | PCR-Luminex | Stewart |
| *Methanobrevibacter smithii* | qPCR | Stewart |
| *Legionella* spp. | qPCR | Gast |

# APPENDIX G: DEVELOPMENT OF DETERMINISTIC MODELS

The discussion of the modeling workgroup members included the present and future use of statistically-based models. This relates to the fact that they are currently being used to supplement monitoring information and can be implemented in a resource-effective manner in existing beach advisory programs. In general, deterministic models have not been included in the main part of this discussion (see Chapter 6) because it was the common opinion of the workgroup members of the modeling workgroup that their application represents a longer-range measure that might be considered in the context of research and development beyond the 2 to 3 year (near-term) window envisioned by the current criteria development effort; however, there were differences of opinion on the importance of this relative to development of new or revised recreational water quality criteria.

Although not discussed in detail at this workshop, deterministic process-based models represent an entire range of additional modeling tools that could be used to inform water quality criteria development and implementation over the range of criteria framework options that have been discussed during the course of this conference. Applications of such models to beach environments are discussed in the EPA report *Review of Potential Modeling Tools and Approaches to Support the BEACH Program*, (US EPA, 1999). They range from those that are simply based on precipitation to newer models that consider other factors such as sediment resuspension, hydrodynamics, microbial growth and decay, and non-point source basin scale inputs. For example, a process-based deterministic model has been recently used to predict fecal indicator concentrations in coastal reaches of southern Lake Michigan (Liu et al., 2006) and Huntington Beach, California (Boehm et al., 2005; Grant et al., 2005). Deterministic models also are being used in the development of total maximum daily loads (TMDLs) for pathogens and in evaluations of non-point and sources of biological contaminants in watersheds.

In this appendix, deterministic models for evaluating pathogens in watersheds are briefly discussed. TMDLs often have to consider non-point sources from watersheds. This discussion is not intended to be comprehensive; rather, it is designed to illustrate the range of tools available to this area of consideration.

Commonly used TMDL models allow users to discretize the watershed spatially and bacteria loads spatially and temporally, although this capacity is limited. As discussed in ASABE (2006),

> the models are also limited in their ability to simulate bacterial life cycles and bacteria concentrations. Even with their limitations, these models are useful when developing TMDLs if for no other reason than their use provides educational opportunities for both stakeholders and modelers throughout the TMDL process. The load duration method of developing TMDLs provides a good representation of overall water quality and needed water quality improvement, but intra-watershed bacteria contributions must be determined through supplemental sampling or through subsequent hydrologic and water quality modeling. Identified research needs include improved bacteria source characterization procedures and supporting data, and specific modeling advances.

New models are now becoming available for evaluating non-point sources of pathogens derived from watersheds and catchments.

- The L-THIA model (http://www.ecn.purdue.edu/run-off/lthianew/) combined with GIS-referenced inputs from Digital Watershed are being used as tools to evaluate runoff of fecal coliform and fecal streptococcus (enterococci) in watersheds. Digital Watershed (http://www.iwr.msu.edu/dw/) allows the user to view the watershed tributary to any given point in the continental United States, on an 8-digit or (in parts of the Midwest) a 12-digit HUC code level of detail. L-THIA calculates the surface and groundwater impacts of current land use, land use changes and potential best management practices (BMPs) for quality and quantity for the bacteria. L-THIA will be directly linked to STORET water quality and SSURGO soils databases within a year. In the Midwest it is also available as a web-based GIS tool at the 12-digit HUC code level through the watershed delineation tool at http://pasture.ecn.purdue.edu/~watergen/.
- The SPARROW model (SPAtially Referenced Regression on Watershed attributes) (http://water.usgs.gov/nawqa/sparrow/index.html) is being used to investigate the sources and fate of fecal contamination in streams and to assess the effects of the spatial resolution of the stream network and landscape data on model parameters and predictions. SPARROW has been used to evaluate the following indicators: fecal coliforms, *E. coli*, *C. perfringens*, somatic coliphage, F+ RNA phage, and the bacterial pathogen *Campylobacter*. The explanatory data for the SPARROW models include land use and other data that describe the climatic, hydrologic, and physical conditions of the catchments. The models also reveal the effects of climate, soils, and instream processes on the transport of fecal contaminants.
- LSPC is the Loading Simulation Program in C++, a watershed modeling system that includes streamlined Hydrologic Simulation Program Fortran (HSPF) algorithms for simulating hydrology, sediment, and general water quality on land as well as a simplified stream transport model. LSPC has been used in Alabama for developing pathogen TMDLs (see http://www.epa.gov/athens/wwqtsc/Toolbox-overview.pdf and http://www.epa.gov/ATHENS/wwqtsc/html/lspc.html).

In addition to these models, a 1999 EPA report describes other potential models that can be used for evaluating non-point sources of biological contaminants from catchments. These include, for example, HSPF. HSPF is one of the models that is included in the BASINS3 watershed model system that is maintained by EPA (http://www.epa.gov/waterscience/BASINS/).

## References

ASABE (American Society of Agricultural and Biological Engineers). 2006. Modeling bacteria fate and transport in watersheds to support TMDLs. Proceedings from the ASAE Annual Meeting. Paper 062295.

Boehm, AB; Keymer, DP; Shellenbarger, GG. 2005. An analytical model of enterococci inactivation, grazing, and transport in the surf zone of a marine beach. *Water Research* 39(15): 3565-3578.

Grant, SB; Kim, JH; Jones, BH; Jenkins, SA; Wasyl, J; Cudaback, C. 2005. Surf zone entrainment, along-shore transport, and human health implications of pollution from tidal outlets. *Journal of Geophysical Research* 110: C10025.

Liu, L; Phanikumar, M; Molloy, S; Whitman, RL; Shively, D; Nevers, D; Schwab, D; Rose, J. 2006. Modeling the transport and inactivation of *E. coli* and enterococci in the near-shore region of Lake Michigan. *Environmental Science and Technology* 40(16): 5022-5028.

US EPA (U.S. Environmental Protection Agency). 1999. *Review of Potential Modeling Tools and Approaches to Support the BEACH Program.* EPA-823-R-99-002. Washington, DC: US EPA.