

Performance of human fecal anaerobe-associated PCR-based assays in a multi-laboratory method evaluation study

Blythe A. Layton¹, Yiping Cao¹, Darcy L. Ebentier², Kaitlyn Hanley², Elisenda Ballesté³, João Brandão⁴, Muruleedhara Byappanahalli⁵, Reagan Converse^{6,7}, Andreas Farnleitner⁸, Jennifer Gentry-Shields⁹, Maribeth L. Gidley¹⁰, Michèle Gourmelon¹¹, Chang Soo Lee⁹, Jiyoung Lee⁹, Solen Lozach¹¹, Tania Madi¹³, Wim G. Meijer³, Rachel Noble⁶, Lindsay Peed¹⁴, Georg H. Reischer⁸, Raquel Rodrigues⁴, Joan B. Rose¹⁵, Alexander Schriewer¹⁶, Chris Sinigalliano¹⁷, Sangeetha Srinivasan¹⁵, Jill Stewart⁹, Laurie C. Van De Werfhorst¹⁸, Dan Wang, Richard Whitman⁵, Stefan Wuertz^{16,20}, Jenny Jay², Patricia A. Holden¹⁸, Alexandria B. Boehm¹⁹, Orin Shanks¹⁴ and John F. Griffith¹

¹*Southern California Coastal Water Research Project, Costa Mesa, CA*

²*UCLA Civil and Environmental Engineering, Los Angeles, CA*

³*UCD School of Biomolecular and Biomedical Science, University College Dublin, Ireland*

⁴*Instituto Nacional de Saude, Dr. Ricardo Jorge, Avenida Padre Cruz, Portugal*

⁵*U.S. Geological Survey, Great Lakes Science Center, Lake Michigan Ecological Research Station, Porter, IN*

⁶*UNC Chapel Hill Institute of Marine Sciences, Morehead City, NC*

⁷*Oak Ridge Institute for Science and Education, Oak Ridge, TN*

⁸*Environmental Microbiology and Molecular Ecology Group, Vienna University of Technology, Vienna, Austria*

⁹*Department of Environmental Sciences and Engineering, University of North Carolina, Chapel Hill, NC*

¹⁰*The Cooperative Institute for Marine and Atmospheric Studies, University of Miami, Miami, FL*

¹¹*Laboratoire de Microbiologie, Unite Environnement, Microbiologie et Phycotoxines, Ifremer, Plouzane, France*

¹²*College of Public Health, Division of Environmental Health Science, The Ohio State University, Columbus, OH*

¹³*Source Molecular Corporation, Miami, FL*

¹⁴*U.S. Environmental Protection Agency, National Risk Management Research Laboratory, Cincinnati, OH*

¹⁵*Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI*

¹⁶*Department of Civil & Environmental Engineering, University of California, Davis, Davis, CA*

¹⁷*National Oceanic and Atmospheric Administration, Miami, FL*

¹⁸*University of California, Santa Barbara, CA*

¹⁹*Stanford University, Dept. of Civil & Environmental Engineering, Stanford, CA*

²⁰*Nanyang Technological University, Singapore*

ABSTRACT

A number of PCR-based methods for detecting human fecal material in environmental waters have been developed over the past decade, but these methods have rarely received independent comparative testing in large multi-laboratory studies. Here, we evaluated ten of these methods (BacH, BacHum-UCD, Bacteroides thetaiotaomicron (BtH), BsteriF1, gyrB, HF183 endpoint, HF183 SYBR, HF183 Taqman₊, HumM2, and Methanobrevibacter smithii nifH (Mnif)) using 64 blind samples prepared in one laboratory. The blind samples contained either one or two fecal sources from human, wastewater or non-human sources. The assay results were assessed for presence/absence of the human markers and also quantitatively while varying the following: 1) classification of samples that were detected but not quantifiable (DNQ) as positive or negative; 2) reference fecal sample concentration unit of measure (such as culturable indicator bacteria, wet mass, total DNA, etc); and 3) human fecal source type (stool, sewage or septage). Assay performance using presence/absence metrics was found to depend on the classification of DNQ samples. The assays that performed best quantitatively varied based on the fecal concentration unit of measure and laboratory protocol. All methods were consistently more sensitive to human stools compared to sewage or septage in both the presence/absence and quantitative analysis. Overall, HF183 Taqman₊ was found to be the most effective marker of human fecal contamination in this California-based study.

Due to distribution restrictions, the full-text version of this article is available by request only.