

The Extreme Microbiome Project (XMP) and Development of New Standards for Metagenomics and Microbiome Applications. S. Green¹, S. Tighe², D. Baldwin³, E. Afshinnekoo⁴, N. Ajami⁵, N. Bivens⁶, R. Carmical⁷, T. Hunter⁸, S. Joye⁹, J. Lee¹⁰, S. Levy¹¹, C. Mason¹², K. McGrath¹³, D. Reeves¹⁴, M. Settles¹⁵, N.G.R. Vinas¹⁶ and K. Thomas¹⁷, ¹University of Illinois at Chicago, 835 S. Wolcott, Chicago, IL, 60612, GreenDNA@uic.edu, ²University of Vermont, scott.tighe@uvm.edu, ³Pathonomics, Inc, donabaldwin65@yahoo.com, ⁴Weill Cornell Medical College, ebbyafshinnekoo@gmail.com, ⁵Baylor College of Medicine, Nadim.ajami@bcm.edu, ⁶University of Missouri, bivensn@missouri.edu, ⁷Baylor College of Medicine, Carmical@bcm.edu, ⁸University of Vermont, timothy.hunter@uvm.edu, ⁹University of Georgia, mandyjoye@gmail.com, ¹⁰American Type Culture Collections, jolee@atcc.org, ¹¹Hudson Alpha Laboratories, slevy@hudsonalpha.org, ¹²Weill Cornell Medical College, chm2042@med.cornell.edu, ¹³Australian Genome Research Facility, Ken.McGrath@agrif.org.au, ¹⁴Weill Cornell Medical College, dar326@cornell.edu, ¹⁵University of Idaho, msettles@uidaho.edu, ¹⁶Mississippi State University, nvinas@igbb.msstate.edu, ¹⁷University of New Hampshire, kelly.thomas@unh.edu.

The Extreme Microbiome Project (XMP) is a research endeavor within the Association of Biomolecular Research Facilities Metagenomic Research Group (ABRF MGRG) that focuses on the characterization of extremophilic and unique environments through metagenomic analyses. Whole genome shotgun sequencing of samples from several sites has been conducted, including from Lake Hillier in Western Australia, the “Door to Hell” crater in Turkmenistan, deep ocean brine lakes, and deep ocean sediments from Greenland, permafrost tunnels in Alaska, and the International Space Station, among others. The goals of the XMP are multifaceted: i) to refine techniques for the detection and characterization of novel microbes, ii) evaluate nucleic acid extraction techniques for extremophilic samples, iii) and to improve or develop bioinformatic pipelines for the compositional analysis of microbial communities. The MGRG is also involved in developing new reference standards, reagents, and workflows needed for standardizing methods. This includes, development of microbial controls and DNA, advancement of poly-lytic enzyme mixes, and refined bioinformatics pipelines. The present reference standard under development includes six biosafety level I bacteria comprised of Class I genomes at varying GC content with the goal of releasing it as a publically available resource. Future reference standards with Class II and Class III microbial genomes, and representatives from other kingdoms, will be subsequently developed.