MICROBIOME CHANGES IN CLEAR LAKE WATERSHED AFTER HURRICANE HARVEY-INDUCED FLOODING

Theodore Richardson¹, Yan Zhang², Michael LaMontagne³, and Michael S. Allen²

¹Department of Biology, Texas A&M University, College Station, TX 77843
²Department of Microbiology, Immunology, and Genetics, University of North Texas Health Science Center, 3500 Camp Bowie Blvd, Fort Worth, TX 76107
³Department of Biological and Environmental Sciences, University of Houston-Clear Lake, 2700 Bay Area Blvd, Houston, TX 77058

Abstract

Hurricanes can have large-scale effects on ecosystems. These effects include the readily apparent macro-scale changes, as well as less obvious changes to micro-ecosystems. This research sought to identify changes in bacterial populations in the waters the received floodwater from the Clear Lake watershed in the aftermath of Hurricane Harvey. Six water samples were collected from around Houston on August 25 (pre-storm) and again on August 30 (post-storm). DNA was extracted from the samples and the microbial communities were profiled by 16S rRNA gene sequencing using Illumina MiSeq. The pre- and post-storm sequences showed dramatic differences in bacterial community composition. Post-storm showed a higher relative abundance of Comamonadaceae and Cytophagaceae than the pre-storm samples (Comamonadaceae was significant at p<1x10⁻⁵; Cytophagaceae was significant at p<2.2x10⁻⁵). Post-storm samples taken on August 30 also showed distinct similarities to sewer water samples, indicating the presence of wastewater contamination. This suggests floodwaters generated by Harvey posed a health risk and suggests particular bacteria that could be used to quantify and track fecal contamination of waterways during extreme weather events.

Key Words: Betaproteobacteria, Comamonadaceae, Cytophagaceae, Flood Water, Harvey, Hurricanes, Microbiome, Proteobacteria

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