EVALUATING VULNERABLE LOCATIONS IN THE CITY OF ATLANTA, GA DRINKING WATER DISTRIBUTION SYSTEM FOR MICROBIAL INTRUSION AND REGROWTH USING AN AUTOMATED MONITORING AND SAMPLING DEVICE

Ethell Vereen, Karen Levy, Samina Panwhar, Amy Kirby, Ashleigh Streby, and Christine Moe

AUTHORS: Emory University - Environmental Health, 1518 Clifton Road NE, Atlanta, Georgia 30322 REFERENCE: *Proceedings of the 2013 Georgia Water Resources Conference*, held April 10–11, 2013, at the University of Georgia

Abstract. The integrity of the drinking water distribution system (DS) is considered the final, and one of the most important barriers for providing safe drinking water. The City of Atlanta (COA) drinking water DS is typical of many large cities in the U.S.; there are older sections, water loss via leaks, and maintenance challenges associated with aging infrastructure. Our previous studies in metro Atlanta indicated modestly increased risks of emergency department visit for gastrointestinal illness associated with longer water residence times (estimated by a hydraulic model) and with source water turbidity. We report on preliminary results of an ongoing study in which we determine the vulnerability to microbial risk for the COA's drinking water DS using our previous work on longer water residence times, as well as available data on pipe breaks and pressure loss events to assess potential contaminant intrusion and microbial regrowth in the COA DS using an Automated Monitoring & Sampling (AMS) device. The AMS continuously monitors physical and chemical measurements of DS water quality, and collects routine large volume water samples (90L) for microbiological analyses. All samples are concentrated by ultrafiltration and tested for indicators of intrusion (E. coli and Clostridium perfringens), indicators of regrowth (Total coliforms, heterotrophic plate count bacteria, Pseudomonas aeruginosa and Aeromonas hydrophila), and coliphages (MS2 and somatic) as models of enteric viruses. Our preliminary results indicate sporadic positive detection of low concentrations of total coliforms, E. coli, C. perfringens, A. hydrophila, P. aeruginosa, and HPC, in routine large-volume samples.