Early Detection of Potential Hepatitis A and Norovirus Outbreaks in Detroit, MI
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BACKGROUND

Water-related disease burden has been an increasing area of concern worldwide. It is estimated that the leading cause of water-related diarrheal illnesses globally is of viral origin. Viruses pose a major threat to human health due to their high mutation rates, low infectivity dose, and lack of medications to treat viral infections. These agents can be particularly difficult to manage in urban settings since high population density promotes the rapid spread of communicable diseases. Methods for early detection of disease outbreaks are needed to protect public health.

In this study a wastewater-based-epidemiology method is applied for early detection and surveillance of water-related viral outbreaks in urban communities serviced by the Detroit Water and Sewerage Department (DWSD). The central premise of the proposed approach is that community wastewater represents a snapshot of the status of public health. Analyzing wastewater is equivalent to obtaining and analyzing a community urine and fecal sample. Monitoring temporal changes in virus concentration and diversity excreted in community wastewater, in combination with monitoring metabolites and biomarkers for population adjustments, allows early detection of outbreaks.

STUDY AREA

Influent wastewater samples were collected from three sampling stations located within the Detroit Wastewater Treatment Plant. Each station pulls raw sewage from one of the three main sewers (interceptors): North Interceptor—East Arm (NI-EA), Detroit River (DRH), and Oakwood-Northwest-Wayne County (O-NWI). These interceptors collect sewage from most municipalities situated in the three largest counties in Michigan: Oakland, Wayne, and Macomb.

METHODS

Viruses were isolated, quantified, and characterized in wastewater samples using standard molecular methods and whole-genome shotgun (WGS) sequencing.

RESULTS

Data used to plot graphs were extracted from Michigan Department of Health and Human Services weekly disease surveillance reports. Sampling window shown in graphs denotes months in which wastewater was collected for virus analysis. Preliminary laboratory analysis of wastewater samples indicates that associations may exist between virus concentrations in wastewater and frequency of reported disease cases.

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Figure 1. Hepatitis A cases in Wayne, Oakland, and Macomb counties.

Figure 2. Norovirus and gastrointestinal illness (Gi) cases in Wayne, Oakland, and Macomb counties.

Figure 3. Estimated temporal correlation between reported hepatitis A cases in service counties and average measured hepatitis A virus (HAV) concentrations in wastewater samples. Data suggest associations exist between measured HAV concentrations in wastewater collected one week prior to reported disease cases.

Figure 4. Estimated temporal correlation between reported norovirus and gastrointestinal illness (Gi) cases in service counties and average measured norovirus (NoV) GII concentrations in wastewater samples. Disparities between clinical cases (reported the week of and post sampling) and concentration measurements could be due to the short incubation period of norovirus, un- or misdiagnosed cases, prolonged periods between sampling dates, and uncertainty in clinical data.

Figure 5. Viral group composition in sample metagenomes. Biological replicates were pooled to form 18 samples (3 interceptors sampled on 6 dates) that were sequenced on an Illumina HiSeq 4000 platform.

Figure 6. Heat map of virus genus diversity and abundance of select ssRNA viral families in wastewater samples per sampling date. Abundance is defined as the number of genus-specific contigs normalized by the total number of affiliated sequences assigned to the ssRNA root in MEGAN for each sample.

Figure 7. Viral Metagenomics

Figure 8. Conceptual correlation models for estimating parallels between hepatitis A (top) and norovirus (bottom) clinical case counts and their viral concentrations in wastewater. Dotted lines represent the duration in days or hours of the associated event.

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