DETECTING HEPATITIS C VIRUS TRANSMISSION CLUSTERS USING REMNANT SERUM SPECIMENS FROM KEY AFFECTED POPULATIONS TESTED IN PUBLIC HEALTH SETTINGS

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Background: Recent outbreaks of hepatitis C virus (HCV) among people who inject drugs demonstrate the failure to implement evidence-based prevention and treatment strategies appropriately in communities where they are needed. Expanded use of Global Hepatitis Outbreak Surveillance Technology (GHOST), an automated cloud-based system that uses next-generation sequencing data to conduct molecular surveillance, strain characterization and identify HCV transmission clusters, may advance prevention efforts by enhancing the ability of health departments to efficiently target resources.

Methods: Serum specimens from individuals who undergo fee-exempt confirmatory HCV RNA testing at sites supported by the Wisconsin Department of Health Services (DHS) are routinely analyzed and stored at the state's public health laboratory. These instances reflect testing done in public health settings such as syringe exchange programs and correctional facilities, and not traditional healthcare settings, resulting in a sample enriched with younger persons with a history of injection drug use. We retrospectively identified individuals who tested HCV RNA-positive at sites supported by DHS from 2016 to 2017. Frozen residual serum specimens corresponding to these individuals were removed from storage and shipped to the GHOST center where a novel amplicon-based Illumina MiSeq sequencing protocol that targets the hypervariable region of the HCV genome was implemented. Sequence data was uploaded to the GHOST portal where HCV transmission networks were inferred and visualized.

Preliminary Results: Between 2016 and 2017, 459 individuals tested HCV RNA-positive in public health settings in Wisconsin. Of these, 10% of samples failed PCR amplification and sequencing. Among the first 110 specimens processed, transmission network analysis showed that 22 individuals were linked into 9 clusters for an overall clustering rate of 20%. Genotype 1a (63%) was the most common circulating strain, followed by 3a (26%), 3b (5%), 1b (3%), 2a (1%) and mixed genotypes (2%).

Conclusion: Capitalizing on scientific innovations in genomic sequencing and an existing laboratory infrastructure that processes specimens collected in public health settings provides an opportunity to conduct an epidemiologic investigation of transmission networks involving populations' key to the spread of HCV.

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