

Oral Session:

Clusters of Hepatitis C Virus Infection among Patients Receiving Chronic Hemodialysis in Three Hemodialysis Facilities – Northern Region, Taiwan, 2019–2020

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Background:

Hepatitis C virus (HCV) transmission in hemodialysis facilities has been reported. However, the transmission route of sporadic cases is difficult to clarify. Taiwan CDC received reports of 4 patients with acute HCV infection from facility A in May 2019, and a patient from facility B in March 2020. Preliminary investigation revealed that three of them had been hospitalized in hospital C during their incubation periods. To prevent further transmission, we conducted an investigation to identify possible cause for infection.

Methods:

We defined cases as hemodialysis patients with anti-HCV antibody seroconversion within 12 months. Facilities with cases were required to screen anti-HCV antibody of all HCV negative patients every 3 months until 6 months after identified the last case. We checked HCV RNA for case patients then used gene sequencing and phylogenetic analysis to evaluate the similarity between patients' viral genomes. Public health authorities interviewed patients and staff, reviewed medical records, and made multiple on-site observations to identify possible epidemiological link and infection control lapses.

Results:

Facility A identified additional five cases (AR 1.2%) during August 2019–November 2020. Two of nine cases of facility A were linked with a case in facility B because their RNA similarity was > 95%. They had been hospitalized and dialyzed in the same inpatient hemodialysis facility of hospital C during their incubation periods.

Facility B identified two additional cases (AR 3.5%) on June 2020. Viral sequencing revealed that these two cases were genetically linked (RNA similarity > 97%) to a patient with chronic hepatitis C on the same shift. On-site inspections found nonadherence to safe injection practices, hand hygiene, and environmental cleaning protocols.

Conclusions:

The investigation confirmed two different sources of infection among patients from three facilities. Gene sequencing for patients with acute HCV infection in hemodialysis facilities can help identify transmission linkage and recognize potential outbreaks.