

Outbreak Investigation and Genomic Analysis of Hepatitis C Virus Infection in a Neurosurgical Unit

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Background

Prevalence of HCV infection in Hong Kong: 0.32% from public health survey in 2020-2022.

The commonest genotypes in Hong Kong:

- genotype 1 (48.8%)
- genotype 6 (33.6%), also the commonest genotype in intravenous drug users.

Most common settings of outbreaks:

- Hemodialysis centers, oncohematology clinics, and long-term care facilities
- frequently related to non-adherence to standard precautions among healthcare workers

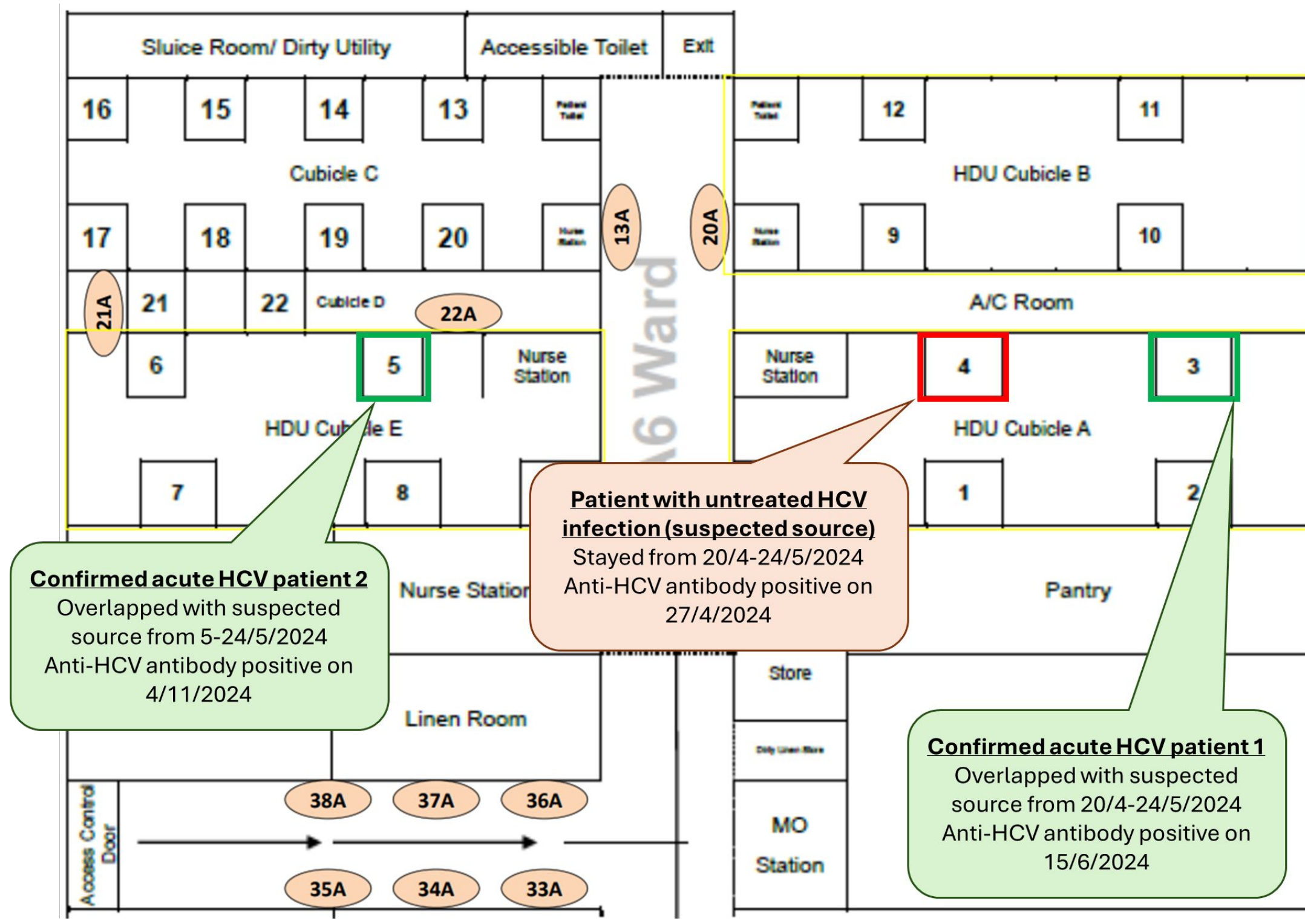
Risk factors for outbreak of blood-borne infections in neurosurgical units:

- multiple traumas, head injuries, or coma, especially in high-dependency unit
- Multiple procedures and drains associated with high risks of nosocomial infections

Summary of the outbreak

In June 2024, an outbreak of nosocomial transmission of HCV infection was identified in a neurosurgical unit in the Princess Margaret Hospital

- One patient was confirmed to have acute hepatitis C infection after admitted for 3 months
- Suspected to be transmitted from a patient with HCV genotype 6a
- Another patient identified as ward contact was found to have deranged liver function and confirmed to have HCV infection

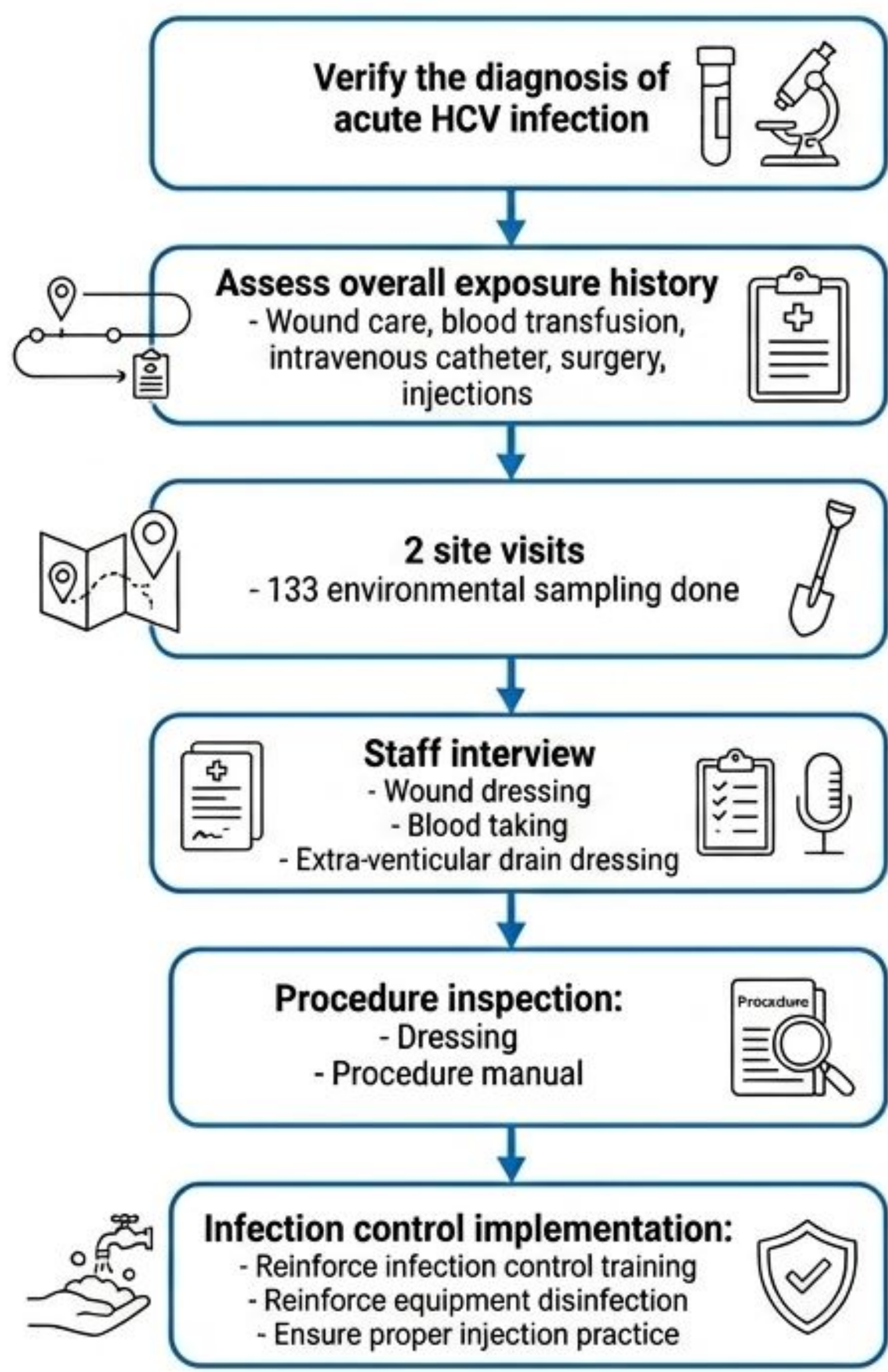


Objective:

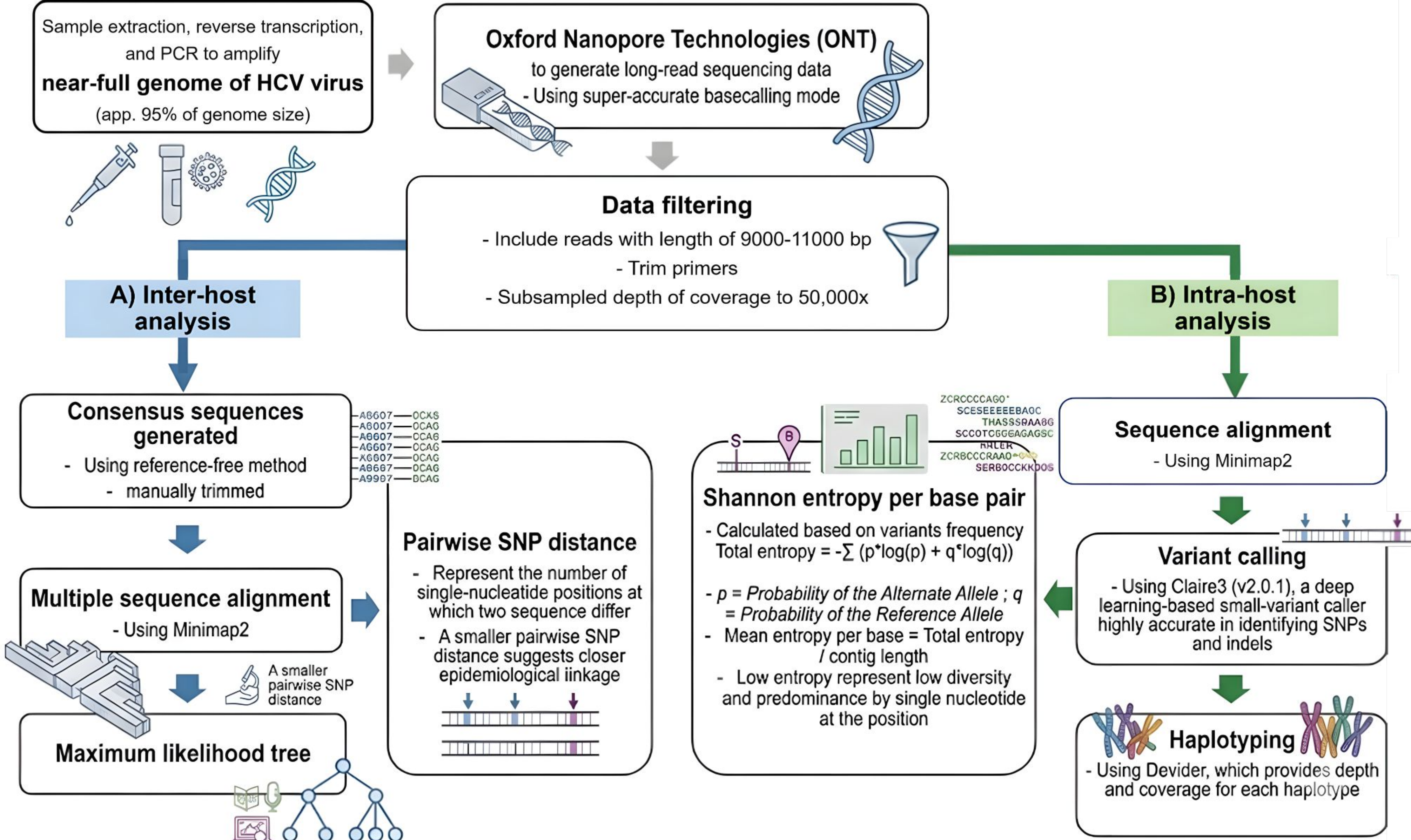
1. Conduct outbreak investigation to identify high risks procedures and practices to interrupt possible transmission route
2. Perform phylogenetic and quasispecies analysis to demonstrate epidemiological linkage

Methodology

Outbreak investigation



Genomic analysis



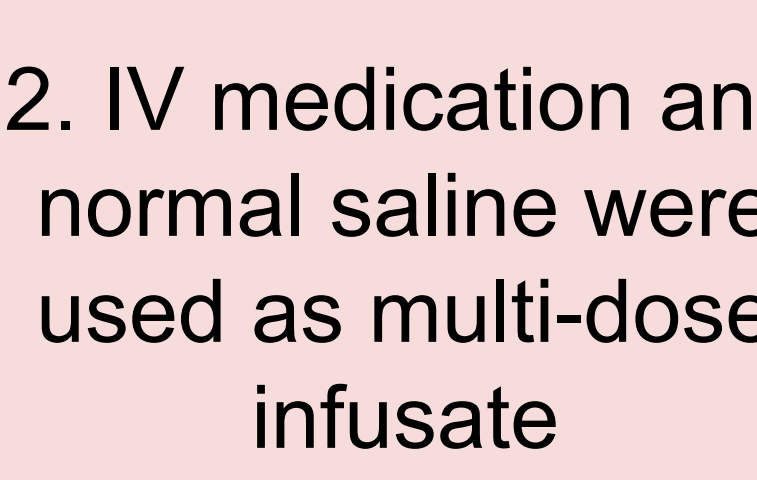
Results

Unpublished data

Infection Control



1. A syringe pump in the equipment room was found to have HCV RNA



2. IV medication and normal saline were used as multi-dose infusate



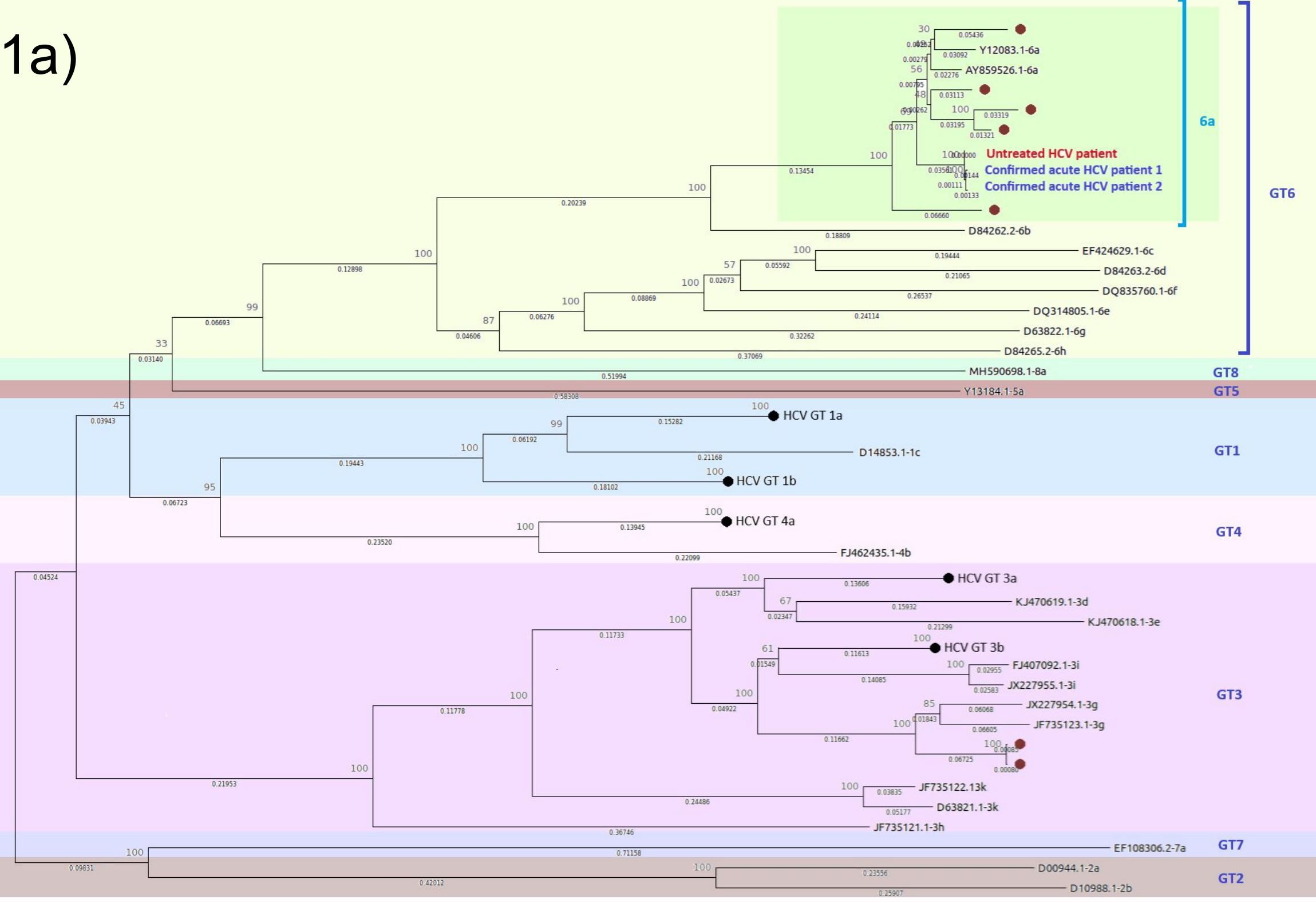
3. Clean dressing materials were noted to be placed in the same trolley with post-procedure items

Follow up actions:

- Increased frequency for disinfecting shared items
- Empty the instrument trolley after each procedure
- Reinforce all staff on hand hygiene, use of personal protective equipment, and safe injection practice

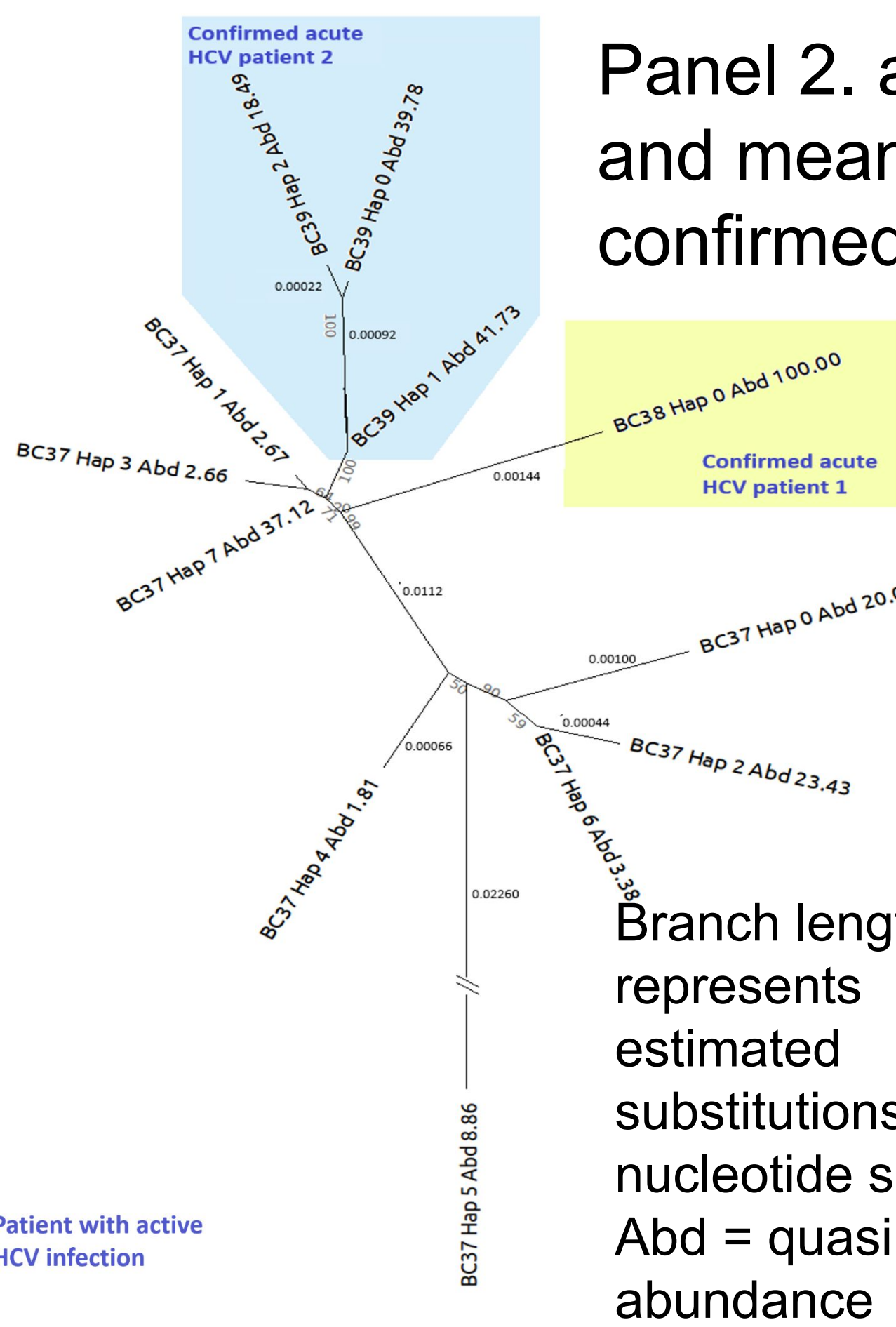
Genomic analysis

Panel 1. a) Phylogenetic tree of near full genome analysis and b) Pairwise distance matrix by number of SNPs from patients investigated in the outbreak and unrelated patients with HCV infection.



Branch length are drawn to scale. Number at the branch represents bootstrap proportions in support of the adjacent node based on 1000 resampling iterations.

Panel 2. a) Haplotype analysis and b) number of SNVs among haplotypes and mean entropy per base of the patient with active HCV infection and two confirmed acute HCV infected patients.



Branch length scale represents estimated substitutions per nucleotide site
Abd = quasi species abundance

Patient	Genotype	Approximate duration of infection from clinical data	SNVs	Number of haplotypes	Mean entropy per base
Patient with active HCV infection (source)	6a	unknown	25	8	0.001742
Patient 1 with acute HCV infection	6a	26-59 days	0	1	0
Patient 2 with acute HCV infection	6a	164-183 days	4	3	0.000269
Unrelated controlled cases	6a	>10 years	71	6	0.005092
Unrelated controlled cases	6a	>5 years	72	3	0.005082
Unrelated controlled cases	1b	>10 years	194	22	0.013965
Unrelated case of needle stick injury (source)	3g	unknown	10	10	0.000642
Unrelated case of needle stick injury (victim)	3g	41 days	2	3	0.00014

Quasi species analysis showed that the patients with acute HCV infection shared highly similar sequences as the major haplotype of the source, and only have 1-3 haplotypes with low mean entropy per base.

Conclusions

1. All patients involved in the outbreak were treated with direct acting antivirals and achieve sustained virological response at 12 weeks.
2. Site visits identified opportunities to enhance safe injection practice and optimize segregation of trolley items.
3. Phylogenetic study confirmed high sequence similarity among the HCV patients in this outbreak, with haplotype analysis indicating that the transmitted strains in both individuals derived from the dominant haplotype of the patient with active HCV infection.

Reference

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This study is approved by Central Institutional Review Board of the Hospital Authority.

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