HCV PHYLOGENETIC NETWORKS AMONG PEOPLE WHO INJECT DRUGS IN KENYA

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Background: Hepatitis C virus (HCV) is a global health problem especially among people who inject drugs (PWID). Low-and-middle income countries (LMICs) carry a high burden of HCV, but little is known about HCV transmission dynamics in these settings.

Methods: We recruited PWID in Nairobi, coastal, and western Kenya at needle and syringe programs using respondent-driven sampling. Next-generation sequencing (NGS) data from HCV hypervariable region 1 (HVR1) were analyzed using Global Hepatitis Outbreak and Surveillance Technology to identify transmission clusters.

Results: Out of 141 cases, n=65 (46%) were genotype 1A, n=72 (51%) 4A, and n=4 (3%) mixed 1A/4A (n=3), 1A/2B (n=1). There were 12 transmission clusters involving 79 cases (56%). The largest cluster had n=33 members; genotype 4A was predominant with 4 cases of genotype 1A linked through one mixed 4A/1A case. The other clusters ranged in size from 2-18. Additionally, there were 24 cases of endemic HCV strains (strains that are not linked by transmission but evolved recently in high-risk communities). In total, n=102 (72%) of all tested case had transmission or endemic links. The participant with the most linked cases was infected with genotype 4A, had 20 links by transmission, and clustered with 27 cases infected with endemic strains. Only 12 pairs of cases were likely linked by direct transmission suggesting the majority of linked cases are probably from incompletely sampled transmission chains.

Conclusion: Transmission clusters involving >50% of cases indicate sampling from high-risk populations of PWID. Although evolutionary history of genotypes 1A and 4A are different, the HCV strains sampled from these populations have likely experienced recent expansions. Genotype 2B was found only in a mixed infection with genotype 1A, which may indicate replacement by genotype 1A. Future directions include analyzing these data in terms of geography, duration of drug use, injection practices, community size, and linkage in respondent-driven sampling chains.

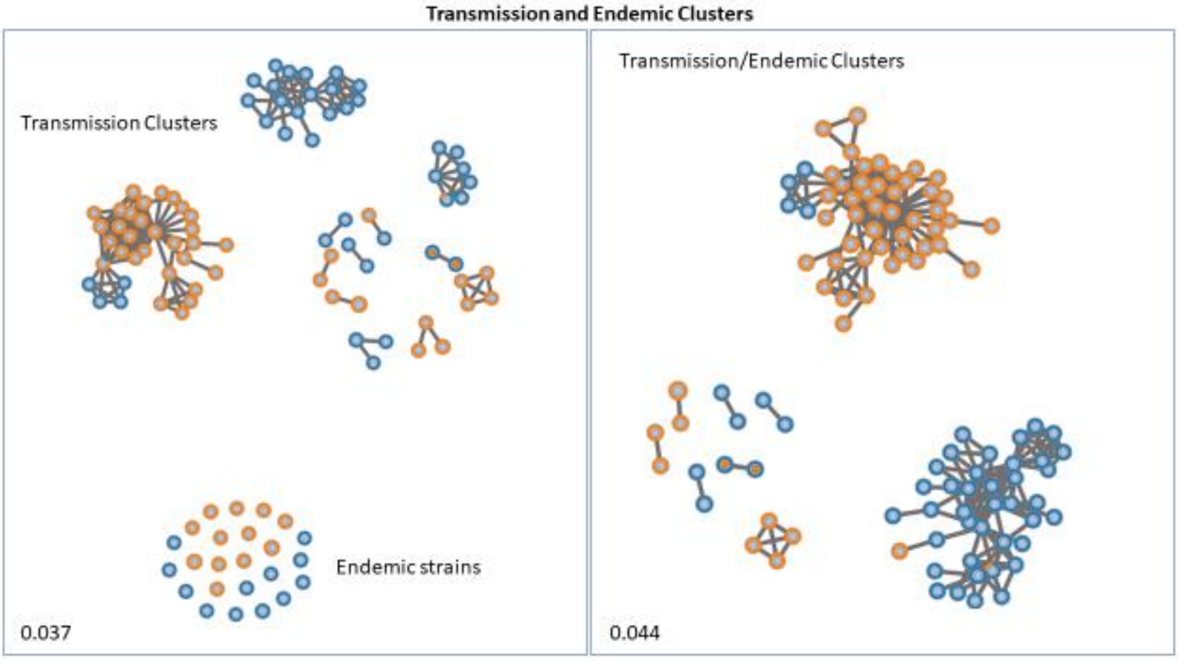

Figure Legend: GHOST transmission networks. Orange node – genotype 4A case; Blue node – genotype 1A case.

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