HCV Phylogenetic Networks Among People Who Inject Drugs in Kenya

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Disclosures

- No relevant financial disclosures

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Background/Aims

- HCV is a global health problem among people who inject drugs (PWID)
- Low- and middle-income countries (LMICs)
  - 80% of the global burden of HCV infection and mortality[1]
- More data may be needed on HCV transmission dynamics in these settings to inform interventions to curb transmission of HCV and other blood borne infections

1. Graham & Swan. Antiviral Research. 2015.

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Methods

- We recruited PWID in Nairobi, coastal, and western Kenya at needle and syringe programs using respondent-driven sampling
- Collected serum samples sent to CDC (Atlanta)
- Next-generation sequencing (NGS) of the HCV hypervariable region 1 (HVR1)
- NGS data analyzed using Global Hepatitis Outbreak and Surveillance Technology[1]

1. Khudyakov et al. Antiviral Therapy. 2012. Campo et al. J Infect Dis. 2016. Longmire et al. BMC Genomics. 2017. Ramachandran et al. EBioMedicine. 2018.

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Results

- Out of 140 cases
  - 65 (46%) genotype 1A
  - 72 (51%) genotype 4A
  - 3 (3%) mixed 1A/4A (n=2), 1b/2b (n=1)
- Clusters
  - 2 large clusters (n=70)
    - Cluster 1 - HCV strains of genotype 4a (n=34) and 1a (n=4)
    - Cluster 2 - HCV strains of genotype 1a (n=32)
  - 9 small clusters (n=20)
    - 1 small cluster of 4 members
    - 8 small clusters of 2 members
  - Unlinked (n=50)

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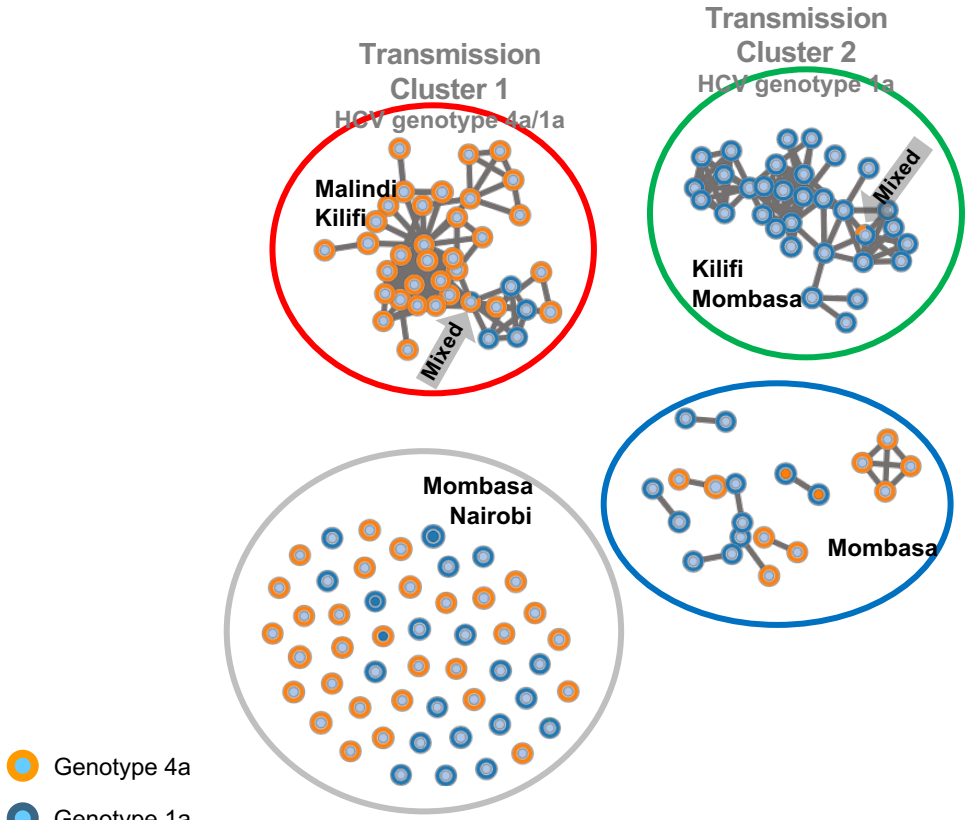
Transmission Networks

GHOST Transmission network, 0.038



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Conclusions/Implications

- Transmission clusters involving >50% of cases indicate sampling from high-risk populations of PWID
- Genotype 1A and 4A strains have likely experienced recent expansions
- Future directions:
  - Analyzing these data in terms of geography, injection practices, community size
  - Inform targeted case finding and interventions to improve outcomes among PWID in Kenya

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Acknowledgments

Study participants & their families

Kenya National Blood Transfusion Services (Nairobi, Mombasa, Malindi, and Kisumu, Kenya) for assistance in plasma separation; Kenya Medical Research Institute (Kisumu, Kenya) for assistance with HCV RNA confirmatory tests; National AIDS & STI Control Program (Kenya) for their contributions and support; Centers for Disease Control and Prevention, Division of Viral Hepatitis (Atlanta, GA, USA)

Funders

National Institute On Drug Abuse

- R01DA032080 (PIs Ann Kurth, Peter Cherutich)
- K99/R00 DA043011 and DP2 DA053730 (PI Matthew Akiyama)

Albert Einstein Global Health Center pilot grant (PI Matthew Akiyama)

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