

SARS-COV-2 INFECTION AMONG PERSONS WHO INJECT DRUGS AND THEIR SEXUAL AND INJECTING PARTNERS IN KENYA

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BACKGROUND

- Despite increased vulnerability and barriers to care, there has been a paucity of data on **SARS-CoV-2 infection among key populations** in sub-Saharan Africa.
- A prior seroprevalence study reported SARS-CoV-2 **antibody prevalence** among people who inject drugs (PWID) and their partners of 30.9%.¹
- We seek to **characterize active infections** and define transmission dynamics of SARS-CoV-2 among PWID and their sexual and injecting partners from Nairobi and the coastal region in Kenya.

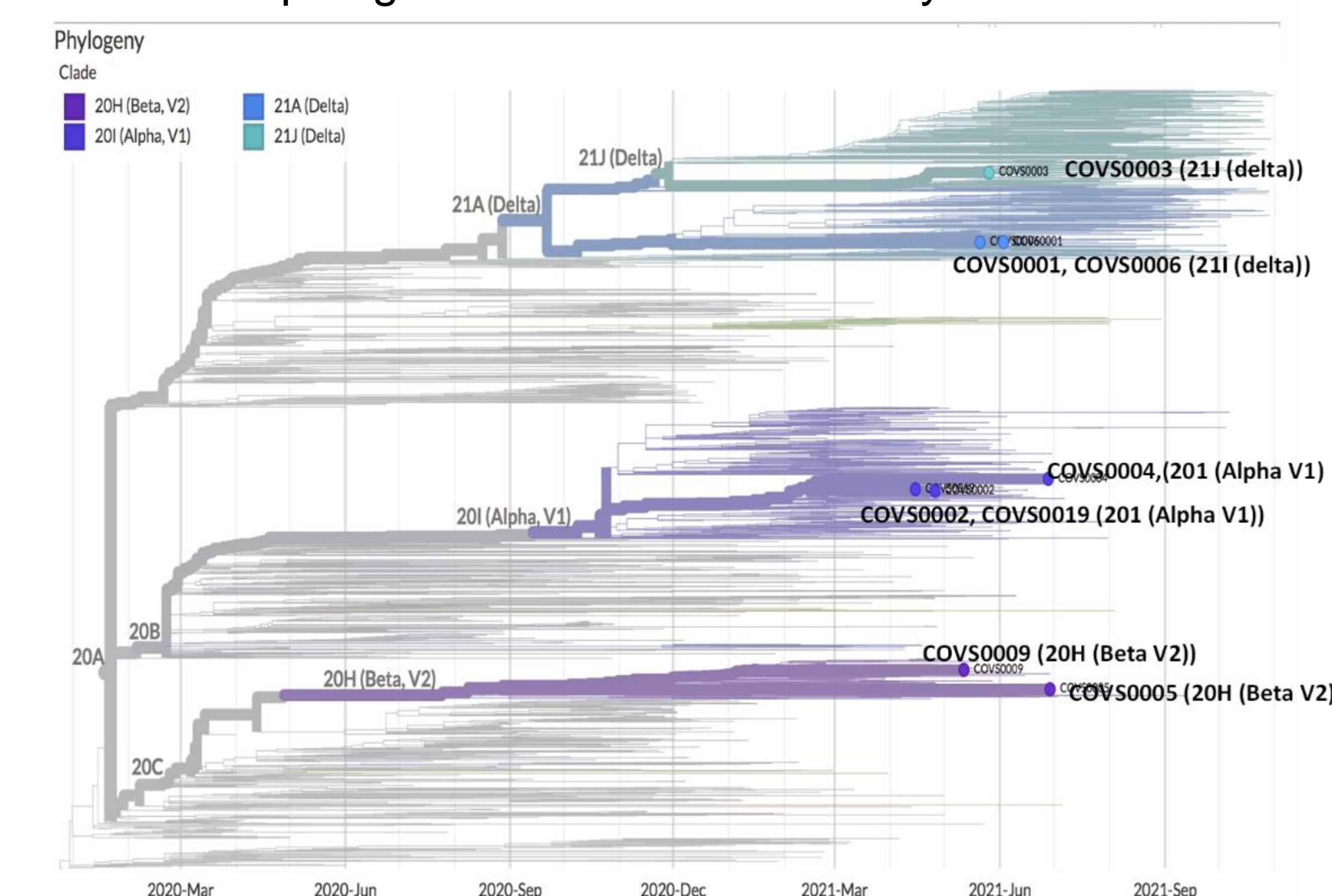
METHODS

- This was a nested **cross-sectional study** of SARS-CoV-2 infection from April to July 2021 within a cohort study of HIV and hepatitis C assisted partner services for PWID in Kenya (NIH R01 DA043409).²
- A total of **1000 PWID and their partners** (500 living with and 500 living without HIV) were recruited for SARS-CoV-2 antibody testing, of whom 440 were randomly selected to provide self-collected nasal swabs for real-time PCR testing.
- Whole genome sequencing (WGS)** was completed on a limited subset of samples (N=23) with CT values ≤ 32.
- Phylogenetic tree construction** and analysis was performed using the Nextstrain pipeline and compared with publicly available SARS-CoV-2 sequences from GenBank.

RESULTS

- A total of **438 participants** (99.5%) provided samples for SARS-CoV-2 PCR testing. Median age was 37 (IQR 32-42); 128 (29.2%) were female; and 222 (50.7%) were living with HIV.
- The **overall prevalence of 19.6%** (86/438) for SARS-CoV-2 infection identified by RT-PCR.
- Table 1 shows the results of the **univariate analyses**, in which there was no increased relative risk of SARS-CoV-2 infection related to positive HIV status or risk factors related to IDU, e.g. frequenting an injection den.

Figure 1. Phylogenetic tree built with Nextstrain. Tree available online at <https://github.com/blab/ncov-kenya>.



Phylogenetic tree of SARS-CoV-2 sequences (WGS) from 8 participants compared with SARS-CoV-2 consensus sequences collected before November 2021 and available on GenBank, with a total of 2441 SARS-CoV2 sequences (from countries outside Africa, and from African countries including 1341 sequences from Kenya)

Prevalence of SARS-CoV-2 infection (identified by PCR) among PWID and their partners in Kenya was 19.6%.

No significant association with HIV or risk factors related to injection drug use.

Table 1. Predictors of positive SARS-CoV-2 PCR among PWID and their partners in Kenya

	Positive PCR (N = 86)	Negative PCR (N = 352)	Relative risk	p-value
Living with HIV (at enrollment)	49 (57.0)	173 (49.2)	1.29 (0.88-1.89)	0.196
Virally suppressed (n=148)	31 (70.5)	117 (72.2)	0.93 (0.53-1.66)	0.817
Currently on ART (n=214)	47 (95.9)	67 (97.1)	0.77 (0.23-2.55)	0.668
Frequented an injection den in the past week	76 (88.4)	289 (82.1)	1.52 (0.83-2.80)	0.179
Currently taking methadone	46 (53.5)	157 (44.6)	1.33 (0.91-1.95)	0.140
Reported stable housing	76 (88.4)	315 (89.5)	0.91 (0.51-1.64)	0.763
High-risk exposure in past 2 weeks?	5 (5.8)	15 (4.3)	1.29 (0.59-2.83)	0.525
Any sexual or injecting partners diagnosed with COVID-19?	6 (7.0)	12 (3.4)	1.75 (0.88-3.47)	0.108
Any sexual or injecting partners died from COVID-19 or flu-like illness since March 2020?	8 (9.3)	18 (5.1)	1.63 (0.88-2.99)	0.119
Any housing partners diagnosed with COVID-19?	3 (3.5)	8 (2.3)	1.40 (0.52-3.76)	0.501
Any housing partners died from COVID-19 or flu-like illness since March 2020?	1 (1.2)	12 (3.4)	0.38 (0.06-2.56)	0.323

RESULTS (cont.)

- Eight samples were successfully sequenced** via WGS and classified as WHO variants of concern: 3 Delta, 3 Alpha, and 2 Beta.
- Seven were classified into clades** predominantly circulating in Kenya during 2021.
- Notably, **two sequences were identical** and matched identically to another Kenyan sequence, which is consistent with, though not inductive of, a transmission linkage.

CONCLUSIONS

- Overall, the risk of SARS-CoV-2 infection in this population of PWID and their partners was **not significantly associated** with risk factors related to injection drug use.
- At a genomic level, the SARS-CoV-2 strains in this study were **consistent with contemporary Kenyan lineages** circulating during the time and not unique to PWID.
- Prevention efforts**, therefore, must also focus on marginalized groups for control given the substantial amount of mixing that likely occurs between populations.

REFERENCES

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