Evaluation of HIV Status as a Risk Factor for COVID-19 Infection: A Combined Cohort Study

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University of Pittsburgh, 2021

Abstract

The HIV/AIDS epidemic in the United States and globally has proved to be a major public health issue and a topic of medical, scientific, and epidemiologic research for almost four decades. The HIV/AIDS pandemic, now considered an ongoing epidemic, changed the way many countries deal with public health associated issues, putting into place prevention measures, surveillance and other practices to prevent the spread of the disease while continuing to educate the public. Human immunodeficiency virus, or HIV, causes impaired immune function and increased susceptibility to opportunistic pathogens, preventing proper immune response, especially in those with advanced stage HIV disease or in those with poor adherence to antiretroviral therapy (ART). As of 2021, coronavirus disease 19 (COVID-19) caused by a novel coronavirus known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is a highly communicable and transmissible respiratory infection responsible for a deadly global pandemic. Immunocompromised individuals, such as those living with HIV, are most susceptible to COVID-19, potentially causing severe disease or death. Data collected by the Multicenter AIDS Cohort Study (MACS) and the Women's Interagency HIV study (WIHS) during the height of the pandemic evaluated risk factors for HIV-positive and HIV-negative participants. This essay assesses the degree to which HIV infected individuals are at a higher risk for disease caused by the novel SARS-CoV-2 and whether a discrepancy exists between HIV-positive and HIV-negative individuals enrolled in the study.

Investigation of potential differences between the groups could determine the relationship between HIV and COVID-19 and if coinfection influences outcomes. Further, susceptibly to COVID-19 and public health infrastructure will be described, and other demographic and geographical relationships will be highlighted.

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Preface

I would like to take the opportunity to thank my essay advisor, Dr. Martinson, for providing the opportunity to work with The Pitt Men's Study and helping me with this project. Thank you to everyone at the Pitt Men's Study, especially William Buchanan and Jeffrey Toth, for helping me gain access to the information collected on the subject and for the great advice they offered during my experience as a student researcher.

I would especially like to thank my committee members, Dr. Elizabeth Felter and Dr. Toan Ha for helping me throughout the project and advising me during the writing process. Special thanks to Dr. Ha for assisting me in working with the data on this project and guiding me in those efforts.

1.0 Introduction

Emergence of SARS-CoV-2 in Wuhan, China, in late 2019 has caused an ongoing global pandemic responsible for over 149 million cases and an estimated 3.14 million deaths worldwide as of mid-2021, although these numbers may be underestimated (Quiros-Roldan, 2020). In the United States alone, 31.2 million cases have been reported with almost 600,000 deaths since January 2020, (1 World Health Organization [WHO], 2021). Rapid spread of the infection and lack of overall understanding of its virulent properties of the disease lead to an increase in pneumonia-like illness throughout the population (Vizcarra, 2020). The sudden increase in cases and deaths due to acute respiratory failure and diminished respiratory function overwhelmed hospital systems, causing employment of significant, widespread public health measures to protect vulnerable populations (Lucas, 2020). Those of advanced age living with diabetes, cardiovascular disease or chronic respiratory conditions such as chronic obstructive pulmonary disease (COPD), asthma, emphysema, as well as immunocompromised individuals are most at risk for severe disease (Mirzaei, 2021). People living with human immunodeficiency virus (PLWH) are considered a vulnerable population, and may be at a higher risk for coinfection due to low immune cell counts or unsuppressed viral loads (Vizcarra, 2020). Factors that may contribute to increased susceptibility include, but are not limited to: age, BMI, male sex, poor adherence to public health guidelines and practices issued by global, federal, and local health agencies and departments, work assignments that increase exposure to others, failure to adhere to antiretroviral therapies as prescribed, educational and language barriers, and lack of resources such as food, transportation, financial support, and shelter (Inciarte, 2020). As of 2019, there are approximately 38 million people living with HIV-positive status worldwide, a cause of concern for a significant

immunocompromised population as COVID-19 continues spread (2 World Health Organization [WHO], 2021). Because information is scarce on HIV as a risk factor for COVID-19 due to its novel properties, initiation of preliminary studies may help to describe any significant association between these diseases. Recent publications vary in conclusive evidence, where, some early observational reports suggest presence of comorbidities and male sex increase overall morbidity of HIV-positive patients (Mirzaei, 2021). However, other studies with small sample sizes do not conclude excess mortality among hospitalized PLWH with COVID-19 infection, specifically in those on ART (Harter, 2020). Other research points to high ART adherence (≥ 95%) have better outcomes than those not taking or with poor adherence (<95%) to ART (Achappa, 2013; Ridgeway, 2020). These results are inconclusive and contradictory, indicating more data collection and larger sample sizes within cohort studies may provide tangible evidence, and help determine potential increased risk or mortality. Implementing further guidelines or defining at risk populations is critical to combatting death due to COVID-19, where consistency in the findings is necessary to addressing morbidity and mortality issues or lack thereof in those with HIV.

1.1 Background of HIV/AIDS Epidemic

Human deficiency virus, or HIV, specifically HIV-1, is a lentivirus responsible for causing acquired immunodeficiency syndrome (AIDS), a disease that has claimed over 33 million deaths since its identification in 1981. HIV-1 is a cross-species retrovirus that resulted from simian immunodeficiency virus in African primates, a direct result of SIVcpz dissemination via chimpanzees (Sharp, 2011). Invasion of host occurs through mucosal sites and most commonly via sexual transmission, especially of rectal surface mucosa. Other sites of entry include genital,

vaginal, gastrointestinal mucosa, as well as blood and placental transmission (Hladik, 2008). HIV targets proteins on immune cells to gain entry, specifically on membranes of CD4+ T lymphocytes or T cells, plasmacytoid dendritic cells (pDCs), myeloid dendritic cells (mDCs), and macrophages, eventually reducing total cell numbers and function of these cells. A decrease in immune cells and function result in low immune function, especially in advanced infection (Martinson, 2007). Thus, AIDS is clinically characterized by a T-cell count <200 uL, where continued depletion describes disease progression (CDC, 2015, Leda, 2020). Pathogenesis of HIV is long-term and persistent and infection effectively causes chronic compromised cell-mediated immunity if antiretroviral therapy (ART) is not employed long-term (Lucas, 2020). Overall weakening of the immune system results in infections by opportunistic pathogens due to decreased or absence of immune functionality, resulting in death (Hladik, 2008). Emergence of HIV has resulted in a public health crisis officially being declared a global epidemic, where major health and global associations such as the World Health Organization and the United Nations have continued work to control and eventually eradicate the disease by 2030 (Lou, 2018). This has proved to be a challenge, though, as many low-income, developing countries have missed targets for testing, therapies, and have failed to promote HIV prevention through public health recommendations (WHO, 2021). Serologic testing and detection for HIV antibodies increases chances for HIV infected individuals to receive early interventions of antiretroviral therapies that increase reportable data and surveillance, while preventing transmission and population incidence. Rates of HIV tend to be higher in those participating in risky sexual behaviors with multiple partners, men who have sex with men (MSM) and injection drug users, and racial minorities especially in urban areas. HIV/AIDS incidence in MSM is higher than the general population, accounting for approximately 40-60% of all cases (Fleming, 2004). Other vulnerable populations include young women and

pregnant and breastfeeding women in Southeast Africa, sex workers, and transgender people, accounting for all other new infections. However, 38 million current and new infections have been reported since 2019, despite new technologies and pharmaceutical advances and introductions, such as pre-exposure prophylaxis (PrEP) and post-exposure prophylaxis (PEP), making headway through ongoing efforts to eradicate the infection. Introduction of ART and combination antiretroviral therapies (cART) remains the most significant means to prevent progression to AIDS and expand life expectancy, where the majority of HIV patients can manage the disease with continued, lifetime ART adherence (WHO, 2021).

1.2 COVID-19

SARS-CoV-2 is an emergent, novel virus belonging to the family of coronaviruses causing upper and lower respiratory illness that infect humans and the cause of coronavirus disease in 2019 (COVID-19) (Liu, 2020). Isolation and tracing efforts determined the primary infection originated in an outdoor seafood market Wuhan, China. SARS-CoV-2 shows a similar receptor binding domain of the S gene (necessary for viral binding) to a bat betacoronavirus (RaTG13). It is also found that a potential recombination event occurred via Mongolian pangolin which may be the intermediate host reservoir for SARS-CoV-2, causing mutation and human infection. SARS-CoV-2 infects human lung cells by binding to angiotensin converting enzyme 2 (ACE2) on the cell membrane, allowing fusion of the viral envelope (Abdel-Moneim, 2021, Millet, 2018). Although similar novel coronaviruses such as severe acute respiratory syndrome (SARS-CoV) and Middle-Eastern respiratory syndrome (MERS-CoV) caused outbreaks in the past 20 years, with case

fatality rates less than 10% and less than 35%, respectively. Investigational reports show higher affinity (10-20%) ACE2 binding of the S protein in SARS-CoV-2 than in SARS-CoV, which may be a key factor for high transmission and mild to severe illness rates (Varghese, 2020). Thus, the COVID-19 outbreak caused a global pandemic, rapidly disseminating through China, and to the rest of the world within the first 60 days of identification (WHO, 2021).

1.2.1 COVID-19 Transmission and Clinical Characteristics

Viral exposure and transmission is understood to be via respiratory droplets and proximal contact of and with COVID-19 infected patients, both symptomatic and asymptomatic. Respiratory droplets produced through coughing or sneezing can be aerosolized and have the potential to reach up to 1 m if the droplets exceed 5 μm. Contamination of hands through surfaces can cause illness if there is contact with nasal or oral epithelium; droplets may live on surfaces or can be spread through fecal matter or urine in some cases. Transmission may take place most commonly in individuals with advanced age, underlying health issues and comorbidities, immunocompromised patients, and other vulnerable populations, where transmission directly increases with exposure time and proximity to infected individuals (Qu, 2020).

The incubation period for COVID-19 is anywhere from 1-20 days, with 3-14 days being most common. Presentations of COVID-19 are described as pneumonia-like, with mild to severe respiratory illness. Other identifiable characteristics include (at onset): Fever, dry cough, fatigue, shortness of breath, and chills and body aches. Manifestations in more severe cases may include, but are not limited to: acute respiratory distress syndrome (ARDS), septic shock, and multiple organ failure caused by viral sepsis where fever did not present. Severe cases of COVID-19 infection may also result in consolidation lesions in the lower lobes of the lungs and lung fibrosis,

lung tissue infiltration by monocytes and macrophages, and cytokine storm, inducing proinflammatory interleukin 6 (IL-6). Unusual laboratory findings in patients show decreased lymphocyte count at onset of disease (<1.0 x 10^9 /L), where, if levels increase the prognosis for critically ill patients shifts towards recovery. However, CD4+ T cells may determine prognosis, especially in severe cases. If T cell counts reach levels below 400/µL, prognosis and clinical outcome is poor especially in immunocompromised patients (Goyal, 2020, Qu, 2020).

1.2.2 Implications of COVID-19 and Public Health Guidelines

The COVID-19 global pandemic has been, and continues to evolve as a major public health issue. Due to the nature of the disease and almost no existing pharmaceutical treatments, the impacts of the virus are long-lasting, both economically and medically. Considered a health emergency, the COVID-19 pandemic was declared on March 11th, 2020. Negative impacts of the pandemic can be seen in almost all business, economic, and government sectors, damaging a $90 trillion global economy (Jackson, 2020). The responses to the crisis were rapid and employed with hasty decision making by government and public health officials, creating an unclear future and difficult environment to monitor and enforce adherence to changing guidelines (Hartley, 2020). Surveillance of the disease and contact tracing are potential life-saving, effective methods to prevent and contain disease and decrease mortality due to COVID-19 (Qu, 2020). Overall, public health interventions must be employed to vaccinate, eradicate, and reset the global economy.

Prevention and non-pharmaceutical interventions (NPIs) are the easiest, and most cost-effective mode of controlling spread and containing the disease. Notably, quarantine practices, especially in those with increased susceptibility or proximity to infected patients is necessary to reduce risk for transmission. Self-quarantine prevents those potentially exposed to the virus from exposing others

(Qu, 2020). According to CDC recommendations, the length of quarantine is 14 days if close-contact exposure exceeds 15 minutes, or after 10 days without symptoms or test, or after 7 days with a negative test result. These lengths are based off of the incubation period for COVID-19 and the typical onset of symptoms (CDC, 2020). Quarantine, isolation (if diagnosed with COVID-19), and "shelter-at-home" practice is found to be effective in cutting off transmission routes, and prove to be an effective prevention strategy (Pan, 2020).

Other preventative strategies include the use of personal protective equipment (PPE), especially for medical and healthcare staff. PPE for high risk healthcare workers include the use of medical and fitted N-95 masks with optimal filtering efficiency (<95%), surgical masks, goggles, face shields, medical gowns, and gloves (Tcharkhtichi, 2021). Proper use of medical or non-medical masks or other protective face covering by non-healthcare workers in public spaces minimizes potential for infection and community spread by up to 79% (Wang, 2020). Discontinuing all social gatherings and school and work space environments where droplets containing virus can easily spread from person to person, maintaining a safe distance from others where droplets can not be inhaled (CDC recommendation of 6 feet) and continuous hygiene efforts, such as proper handwashing and use of alcohol-based sanitizer when hand washing is not possible are also prevention methods that have shown to decrease widespread disease (CDC, 2020). These strategies are essential to flatten the epidemiological curve of COVID-19, prevent severe disease until the introduction and widespread use of effective vaccinations, and prevent overwhelming healthcare systems.

1.3 HIV and COVID-19

Risk for COVID-19 in relation to outcomes and infection rates among PLWH is not well characterized. Clinical outcomes for COVID-19 have shown to be more severe in those with comorbidities and preexisting conditions, especially for men, those in minority groups, individuals with a history of tobacco use, and high body mass indices (BMI) over 30 (Gervasoni, 2020; Hadi, 2020).

Limited COVID-19 outcomes have been collected specifically in patients with positive HIV status, although the CDC included caution for HIV positive status as a potential risk for severe illness in the COVID-19 risk reports (CDC, 2020). This is contributed to overall compromise in immune function in HIV positive individuals and increased comorbidities or multimorbidity in the identified population. Percentage of heart disease, diabetes, and kidney disease diagnosis is higher in patients with HIV than in other groups (Hadi, 2020; Nagarakanti, 2020). A review article published in January of 2021 reviews the first 6 months of the pandemic. The findings showed there was not a higher risk of mortality in PLWH especially with comorbidities and risk factors, however does not provide data on testing or the prevalence of positive diagnoses in the PLWH group (Johnston, 2021). Other studies have made the characterization that the daily use of class combination antivirals including nucleoside transcriptase inhibitors in addition to protease inhibitors (such as in consistent ART use by PLWH) could reduce the severity of disease, or even prevent illness (Cabello, 2020, Ridgeway, 2020). However, this report is not supported by substantiated inferences, nor are significant studies available to make this conclusive assessment (Patel, 2020). Thus, information on HIV status and COVID-19 diagnoses is insufficient, and further investigation is needed to have true predictors of morbidity and mortality in PLWH.

1.4 MACS/WIHS Cohort Study

The Multicenter AIDS Cohort Study (MACS) started in 1983 at the beginning of the HIV/AIDS pandemic at the Johns Hopkins School of Public Health, expanding to 4 main investigative public health centers by 1986. The MACS continues in collaboration with the Women's Interagency HIV Study (WIHS) to form the MACS/WIHS Combined Cohort Study (MWCCS). The study is funded through National Heart, Lung, and Blood Institute (NHLBI), and partially through other coordinating national institutes contributing to HIV research. As of 2011, the study has expanded to include over 100 investigators contributing to the research and data at the MACS. Investigators and contributors have successfully studied the natural history of AIDS, as well as genetic, behavioral, psychological, biological, virologic, and clinical implications, using quantifiable data and collected specimens from MSM participants. Participation in the MACS is based on MSM status, and surveys individuals with and without HIV positive status (De Jesus, 2020, Detels, 2012). The longitudinal study involves almost 7000 participants nationally, with the largest centers concentrated in Los Angeles, Baltimore, Chicago, and Pittsburgh (De Jesus, 2020). A culmination of research continues to contribute to breakthrough discoveries in the field of HIV/AIDS as well as medicine, pharmaceuticals, sociology, and neuropsychology, and continues to recruit PLWH and reach those most vulnerable or at risk for HIV.

1.4.1 COVID-19 Study

The MWCCS launched a study in April of 2020 to document occurrences of COVID-19 in participants in the MACS and WIHS centers across the United States, concluding in September of 2020. The study aimed to document any changes over time and patterns of COVID-19 testing and

availability, HIV status, adherence to mask use, social distancing, and other public health guidelines, variations in substance use and social behaviors prior to the pandemic, changes in resources or employment status, access to prescription medications, and food insecurity. This study collected qualitative data via phone interviews to investigate causal factors linked to COVID-19 and HIV status, and whether HIV status and outside factors had an impact on COVID-19 infection rates among participants.

1.4.2 Published Article on COVID-19 Study

The article "COVID-19 symptoms and SARS-CoV-2 infection among people living with HIV in the US: the MACS/WIHS combined cohort study" by D'Souza, *et al*. published in *HIV Research & Clinical Practice* in November 2020 analyzes the data from the COVID-19 investigation collected by the MWCCS. The article outlines SARS-CoV-2 infection among participants, as well as the demographic and geographic information collected by the survey, and analyzes positivity rates, associated risks, testing prevalence and reported participant symptoms from April 2020 until June 30, 2020. Using the data collected from the questionnaires, the article reports that 61% PLWH and 39% of seronegative (SN) eligible participants completed the interview. Utilizing collected information from the most recent visit to a site clinic, about 74% of PLWH had undetectable viral loads. The median age of participants was 57 years, where 46% were men and 54% were women. Other identified demographics include race, where 48% were Black non-Hispanic, 36% White non-Hispanic, 13% Hispanic, and 3% were of another racial category.

It is important to note that about 98% of participants reported following stay-at-home orders and physical distancing from others. However, only 62% of participants reported utilization of a mask

in public. PLWH were more likely to report not changing lifestyle than seronegative participants, even after public health guidelines were established.

The publication also focuses on symptom reporting by participants. Over half (53%) of participants experienced at least one symptom consistent with SARS-CoV-2 infection, however, SN participants were more likely to report having at least one symptom since January 2020. Of the 441 participants reporting testing for SARS-CoV-2 infection, 31 PLWH reported positive tests, compared to the 10 SN participants reporting positive tests. Of the PLWH participants, 94% were adhering to prescribed antiviral therapies. The study also highlights that 83% of participants did not seek out testing for a multitude of reasons including not having access to testing if experiencing symptoms before or at the time of the interview or being told by a healthcare provider to self-quarantine instead of getting tested. The results described in the publication also conclude that PLWH had higher positivity rates in high density areas, such as New York City and Chicago. The paper also emphasizes that there was no significant difference between age and/or race and a positive SARS-CoV-2 test result. Thus, the adjusted odds ratio calculated in this paper defines the positivity rate in PLWH as marginally higher (95% CI =1.01-4.85, p=0.046) than in those without HIV diagnosis after adjusting for geographic location and household size.

The article by D'Souza *et al*. is crucial to understanding the background of the study, providing essential information about the MWCCS participant demographic, as well as supplementary data that supports the analysis outlined in this essay. However, the published work reports only on the data collected from baseline interviews, excluding data collected after June 30 2020. This essay continues the analysis of positivity rates among PLWH during all interview waves from April until September 2020, and describes any change in SARS-CoV-2 testing or positivity rates.

2.0 Methods

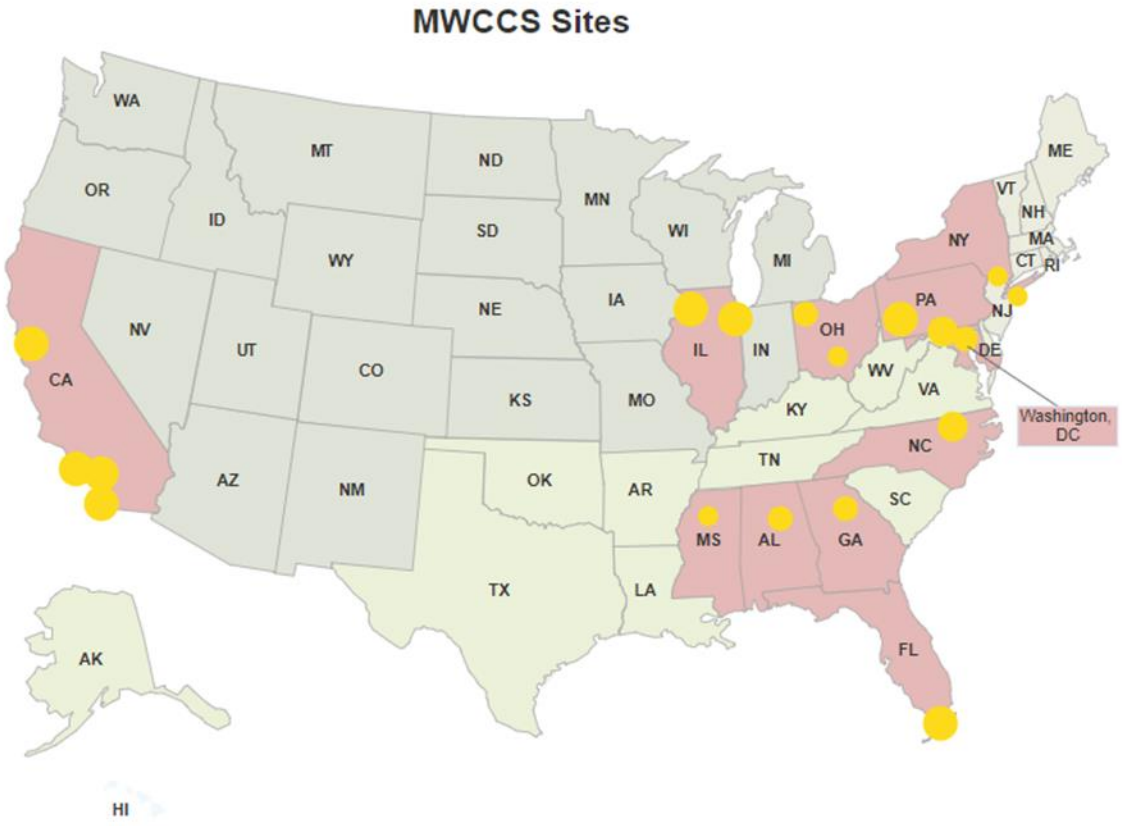


Figure 1: MACS/WIHS (MWCCS) sites participating in the COVID-19 study in the United States.

2.1 Study Design and Participants

A prospective combined cohort study was carried out in the MACS and WIHS centers in the United States as part of a collective MWCCS COVID-19 study. Information was collected from April 2020 until September 2020 in 21 sites across the United States (see fig. 1). The study followed enrolled participants through 3 parts: baseline assessment, follow-up 1 and follow-up 2. Interviews were collected remotely via phone, and data collected was entered into GEMINI systems, the MACS/WIHS CCS data management system. Data collected was stored in the database developed by the MWCCS Data Analysis and Coordinating Center (DACC) managed by Johns Hopkins University School of Public Health. The total participation was for baseline: 3416, follow-up 1: 3389, follow-up 2: 3273. Phone interviews were conducted in 4–6-week intervals, allowing at least 30 days between each questionnaire. All participants were consented before the interview and forms were consistent for all sites in the study. Participants were identified by assigned identification (ID) numbers and were entered into the system by their number. HIV status was designated by ID number, and confirmed during the interview. The duration of each interview was between 15-45 minutes, and additional questionnaires were added to follow-up 1 and follow-up 2 questionnaires. These questionnaires were separate from the COVID forms and were conducted in each follow-up interview to assess food insecurity and substance use changes during the pandemic.

The population of participants were divided into HIV- and HIV+ groupings. Baseline interviews included questions related to clinical symptoms, concurrently existing symptoms, severity of reported symptoms, potential exposures, reasons for testing, HIV status, any current antiretroviral therapies and adherence, access to healthcare, tobacco use or exposure to tobacco use, physical, sexual, or emotional abuse, and psychosocial impacts of the pandemic. The baseline

questionnaire asked participants to recall any symptoms as well as the duration of those symptoms since January 2020. The interviews asked participants to divulge information about adherence to public health guidelines, social distancing, and specific actions taken to prevent spread of COVID-19. If participant answered “yes” to diagnostic testing for COVID-19, further inquiry into type of collection (mouth or throat swab, nasal swab, blood test, or saliva collection) proceeded. The test result was confirmed with the reported testing site in most cases. Follow-up interviews were similar in structure but did not include questions about antiretroviral therapies and date in which they were prescribed, if any, for PLWH, blood pressure medications ending in “-pril” or “-sartan” or of living situations and homelessness. Both follow-up interviews asked participants to recall symptoms since the previous interview, anywhere from 6 to 8 weeks before. Provider information was collected for participants tested for COVID-19, prescribed treatment, and/or were hospitalized for severe illness.

3.0 Results

Testing and SARS-CoV-2 positivity levels of HIV negative and HIV positive groups were identified in each interview category (baseline, follow-up 1, and follow-up 2). A total of 3416 (N=3416) baseline interviews were conducted in all sites. 3389 (N=3389) interviews were conducted in the first "wave" of follow-ups and 3273 (N=3273) were conducted in the "second" wave of follow-up interviews among all sites. 2082 HIV+ (60.9%) and 1334 HIV- (39.1%) participant interviews were reported for the initial wave of baseline interviews. A total of 2064 and 1962 of HIV+ participants were interviewed for follow-ups 1 and 2 respectively. 1325 and 1311 interviews for HIV- participants were conducted for follow-ups 1 and 2 respectively. Other demographic information such as age, BMI, known comorbidity, occupation, tobacco use, living arrangements, and other information is independent of this data, and was inaccessible at the time of this analysis.

Of interviews conducted in all sites during baseline questionnaire administration, 280 (N=280) HIV+ and 171 (N=171) HIV- participants were tested for COVID-19. After the first follow-up "wave", 403 (N=403) HIV+ and 240 (N=240) HIV- participants were tested. Finally, during the second follow-up "wave", 470 (N=470) HIV+ and 299 (N=299) HIV- were tested. Among the participants with HIV diagnosis, 31 participants had a positive test for COVID-19 during baseline interviews, while 10 participants without HIV diagnosis tested positive for COVID-19. In the follow-up interviews, those with HIV diagnosis tested for COVID-19, 26 tested positive during the first "wave" of follow-ups while 25 tested positive during the second "wave" of follow-ups. In those without HIV diagnosis tested for COVID-19, 10 participants tested positive in the first "wave", and 9 tested positive in the second "wave".

During baseline interviews, 37 HIV+ and 21 HIV- participants reported hospitalization for COVID-19 related illness. Twenty-seven HIV+ and 12 HIV- participants reported hospitalizations for COVID-19 diagnosis during follow-up interviews.

Table 1: Baseline, follow-up 1 and follow-up 2 interviews and COVID-19 testing data collected based on HIV status.

All sites	HIV status	Interviews conducted	Not tested for COVID-19	Tested for COVID-19	Negative test	positive test
Baseline	HIV+	2082	1802	280	248	31
	HIV-	1334	1163	171	159	10
Follow-up 1	HIV+	2064	1661	403	367	26
	HIV-	1325	1085	240	227	10
Follow-up 2	HIV+	1962	2365	470	440	25
	HIV-	1311	1551	299	282	9

3.1 Comparison of COVID-19 Diagnosis

Figure 2 presents the analysis of COVID-19 rates among those that tested positive. Rates were calculated as percentages, where: 7% of HIV+ and 2% of HIV- rate of infection in the baseline assessment, 4 % of HIV+ and 2% rate in follow-up 1, and 3% of HIV+ and 1% of HIV- rate in follow-up 2.

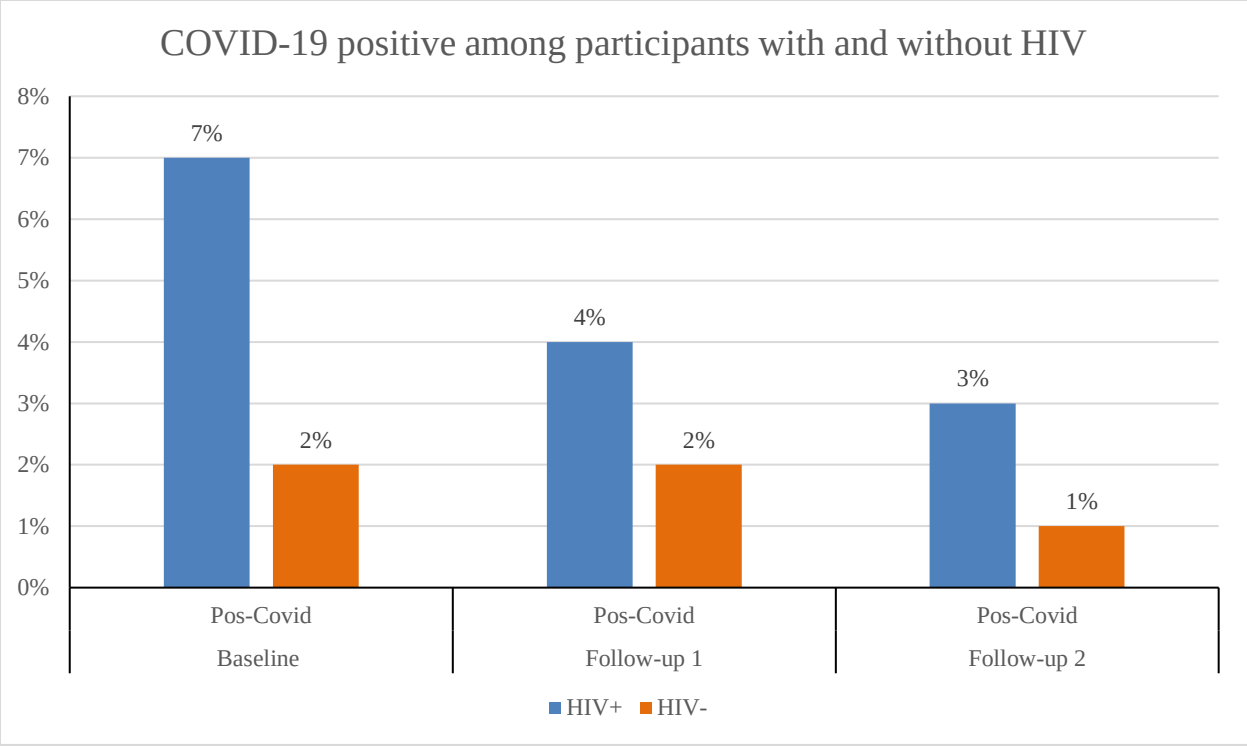


Figure 2: Positivity rates among HIV+ and HIV- participants during each interview phase confirmed and reported by each site.

Figure 3 presents the analysis of COVID-19 infection rates in all participants that were tested for COVID-19. This graph shows the percent of positive and negative test results among HIV+ and HIV- groups, however it is necessary to point out the rate of testing is higher in the HIV+ group than in the HIV- group.

A Chi squared test was performed for the categorical group analysis to determine whether there is a significant correlation between HIV+ status and COVID-19 positive rates, and if these rates change in each "wave" of interviews (Tables 2-4). The analysis performed resulted in these statistical conclusions at $p < .05$. X^2 (1, N=448) = 3.415, p=.065 at baseline, X^2 (1, N=630) = 1.576, p=.209 at follow-up 1, and X^2 (1, N=756) = 2.173, p=.140. For each interview, a chi-squared test

of independence indicated there was no significant association between HIV+ individuals and COVID-19 diagnosis in any category.

A Chi squared test was then performed to determine if overall, correlation existed among each wave if considered collectively (Table 5). The results of the analysis determined, at $p<.05$, X^2 (1, N=1834) =7.075, p=.0078. For all interviews, a chi-squared test of independence showed that there was significance between HIV+ individuals and COVID-19 diagnosis overall.

Table 2: Chi squared calculation and significnace level at p < 0.05 for baseline interviews.

		Covid-19 +	Covid-19 -	X^2	P value
Baseline	HIV+	31	248	3.145	.065
	HIV-	10	159		

Table 3: Chi squared calculation and significance level at p<0.05 for follow-up 1 interviews.

		Covid-19 +	Covid-19 -	X^2	P value
Follow-1	HIV+	26	367	1.576	.209
	HIV-	10	227		

Table 4: Chi squared calculation and significance level at p<0.05 for follow up 2 interviews.

		Covid-19 +	Covid-19 -	X^2	P value
Follow-2	HIV+	25	440	2.173	.140
	HIV-	9	282		

Table 5: Chi sqared calculation and significance level at p<0.05 for all categories of interviews.

		Covid-19 +	Covid-19 -	X^2	P value
Overall (all 3 interview "waves")	HIV+	82	1055	7.075	.0078
	HIV-	29	668		

The proportion of participants reporting positive COVID-19 tests did not vary by HIV status in each interview wave, nor did it differ by the timeframe of interview during early and middle stages of the pandemic. Based on the collected data, there is no significant evidence to suggest that correlation exists between the subgroups, and other potential confounding factors should be considered. However, if all interview waves are considered, there is a significant relationship between HIV positive status and COVID-19 positive diagnosis compared to the seronegative group. This is a considerable correlation, and concludes that overall, there is significance in the analysis. This could be due to the larger sample size in each category and higher effect size than in the other calculations.

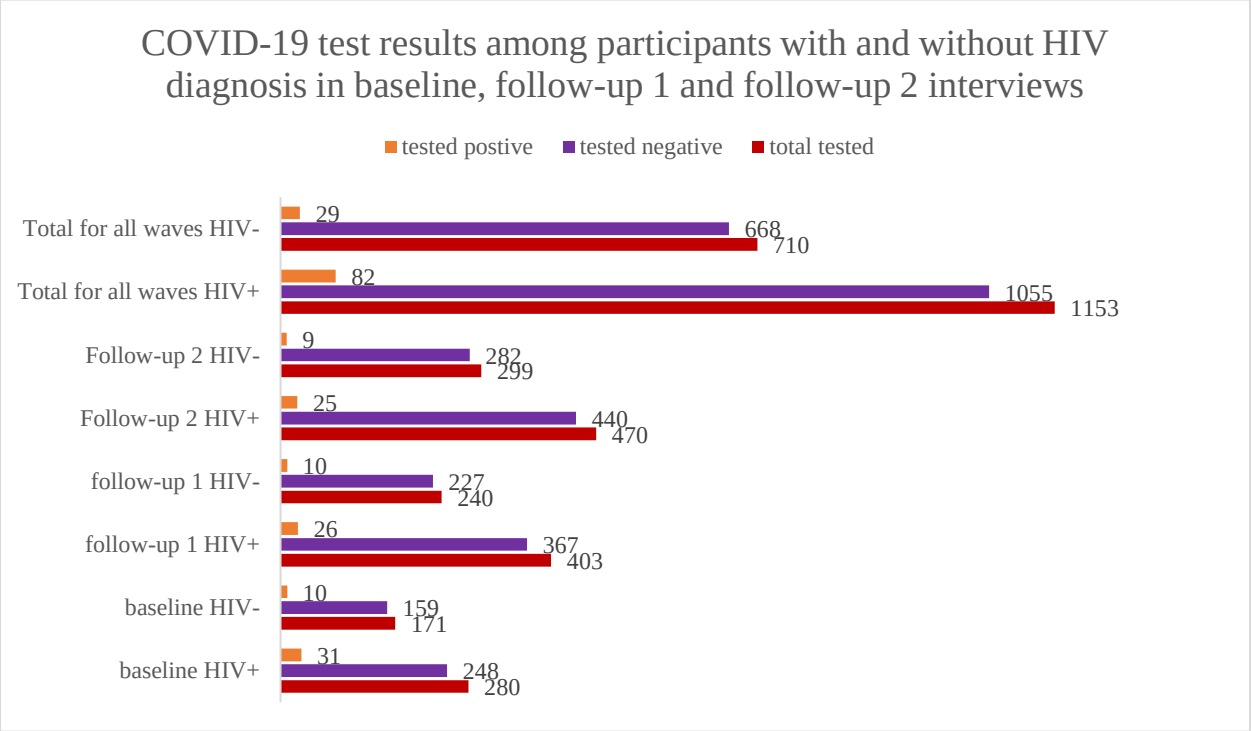


Figure 3: Results of all three "waves" of interviews and final total. Participants with and without HIV diagnosis and total number, negative results, and positive results of COVID-19 diagnostic tests.

4.0 Discussion

The goal of this analysis was to look at the overall correlation between HIV status and COVID-19 diagnosis. The study was able to isolate PLWH and those without HIV diagnosis participants to provide indication of possible coinfection or heightened risk for coinfection during peak COVID-19 transmission rates throughout the United States, despite stringent public health regulations put into place by federal, state, and local departments. This analysis showed that there was no significant relationship between HIV+ and HIV- groups and lab diagnosed SARS-CoV-2 infection reported by participants and confirmed by reported testing site during each interview wave. Overall, there is a significant association between HIV positive status and COVID-19 diagnosis between April and September 2020 when reported diagnoses were considered collectively. Therefore, the study points to a greater impact over the course of the pandemic, or while interviews were taking place, demonstrating potential for PLWH to be at an increased risk for SARS-CoV-2 infection. However, this analysis looks primarily at HIV status and COVID-19 test results, separate from other factors such as accessibility to testing, geographical location, or other demographics that may represent potential differences in outcomes. Adjustments can be made for these factors, resulting in more accurate identification of independent predictors (Etienne, 2020).

Diagnostic testing of SARS-CoV-2 infection via nasopharyngeal or oral swab are the most common and effective methods of testing, especially for active infections. However, availability of diagnostic kits utilizing reverse transcription polymerase chain reaction (RT-PCR) for viral RNA detection were widely unavailable during the first months of the COVID-19 pandemic (Beeching, 2020). Less than 0.01 per 1000 people were tested each day in early March 2020, compared to 2.57 per 1000 people that were tested at the end of August 2020 (Hasell, 2020).

Asymptomatic carriers or those without severe symptoms were frequently turned away from testing to ultimately preserve diagnostic tests for individuals with more severe symptoms. This increased the frequency of infections, while the delay in availability both promoted transmissions and decreased possible diagnoses (WHO, 2020). Long wait times for results, potential for false negative readings, inaccuracy and low sensitivity of "rapid" testing, and significant stress on healthcare and medical lab workers increased potential exposure time to others, especially those with mild symptoms. The demand for testing kits continues to outweigh the supply, causing healthcare prioritizing to those working directly with compromised hospital or long-term facility patients, vulnerable individuals in hospitals or long-term facilities, and those with active symptoms consistent with SAR-CoV-2 infection. To compensate for lack of available tests, especially in areas of high demand, strict public health guidelines were put in place to prevent unnecessary testing, thwart further community spread, and to help control overwhelmed hospital systems (WHO, 2021). Thus, discouragement from public health and healthcare authority to utilize testing unless experiencing severe illness or have known contact with another with confirmed positive test result and overall lack of testing in general may be a contributing factor to low rates of testing in these groups, and could be an indication of potentially undocumented rates of positivity in the study.

To monitor the progression of the pandemic, it is incredibly important to determine the positivity rate as it reflects the number of tests being performed in the community, but also could indicate who is prioritized for testing dependent on available tests. High positivity rates may indicate more testing patients with severe illness in a population, leaving out those who may be tested without symptoms. However, lower positivity rates may reflect a population where insufficient testing is being performed, or that testing is available to those who want to be tested with mild or no symptoms. If testing is sufficient, then positivity rates should hover in the 4-5% range for at least

14 days but should not be the determinant factor for lifting or changing public health guidelines (Johns Hopkins University of Medicine, 2021). The United States population positivity rates of COVID-19 during mid-April of 2020 was around 21.3%, compared to 6% mid-May, 3.9% mid-June, 6.8% mid-July, and 6.10% mid-August (Hassell, 2020). This sudden decrease can be attributed to increase in public information about the virus, public health mitigations such as stay-at-home orders, mask mandates, and closure of public and private gathering spaces nationally by April 2020. The jump in positivity rates from June to July reflect loosening of state and local laws during periods of low incidence rates, which ultimately caused spikes in reported COVID-19 cases across the United States. However, the positivity rate for PLWH study participants is comparatively similar to that of the general public during the first and second wave of interviews (about 9% higher), but is almost half the rate in the third wave of interviews (between July and August 2020). The rate for participants without HIV diagnosis is about 70-80% less than the general population, which may explain the need to control for other factors in each group.

4.1 Limitations

Some issues arising in this study are in part due to the lack of demographic, geographic, and medical information to address potential confounding variables. Although appropriate controls were used, a deeper analysis may explain the possible low positivity rate, testing availability issues at the beginning of the pandemic, and behavior changes according to changing public health response and concern for those with underlying health conditions. Understanding of COVID-19 and the manifestation of the disease itself is an important yet limiting factor of the study. Although some participants mentioned experiencing mild symptoms consistent with COVID-19 diagnosis,

most were not tested during the symptomatic period. Lack of apparent knowledge of where to receive testing and lack of testing in general may also factor into the low testing rate among participants especially during baseline interviews. Also, consideration of ART adherence and overall use of ART could also be an important factor in determining if positivity rates were higher or lower among those on ART or cART. Thus, actual disease prevalence may have gone untraced during the interview stage, and could be much higher than confirmed by this cohort study.

4.2 Conclusion and Further Direction

This preliminary analysis concluded that there is not significant association between COVID-19 infection rates and HIV positive status for participants in any discrete timeframe that the interviews were administered, however, if considered collectively, an association between HIV positive status and COVID-19 diagnosis can be determined in this combined cohort study. There is not enough evidence to conclude that COVID-19 infections are higher in the HIV+ group compared to the HIV- group when isolated from other confounding factors in each wave of interview administration. It is important to clarify that other factors identified through this study may have an effect on overall interpretations of this data, and could give a more refined explanation for the findings of this research. Factors such as age, sex, race, geographic location, underlying conditions, and adherence to ART should be considered in further analyses of this data, and could describe the risk factors for SARS-CoV-2 infection. Further direction of this study could identify these potential risk factors for those with HIV diagnosis and whether HIV positive individuals are more or less likely to adhere to public health guidelines, receive vaccinations when available, and voluntarily receive testing for COVID-19. Inclusion of these variables could shed light on the

COVID-19 pandemic, increase knowledge and understanding of the disease, and ultimately improve the quality of life for people living with HIV. Overall, the public health impact of this study can aid in understanding the implications of global pandemics and epidemics, assist medical professionals in diagnosing and understanding the risk factors of SARS-CoV-2 infection in individuals with HIV diagnoses, and help to avoid future outbreaks that affect the most vulnerable populations.

Appendix A D'Souza et al. supplementary figures

Appendix Table 1: MWCCS partcipant characteristic completing COVID-19 survey by sex and HIV serostatus (D'Souza et al., 2020).

Characteristics	N	Percent				
			Men		Women	
	All	All	PLWH	SN	PLWH	SN
	N=3411	N=3411	N=788	N=798	N=1290	N=535
Date of survey administration						
April 8-30	791	23	7	13	36	31
May 1-31	2157	63	68	72	56	61
June 1-30	463	14	25	15	8	8
Race and Ethnicity						
Black, non-Hispanic	1637	48	26	15	71	74
Hispanic, any race	454	13	17	7	14	15
White, non-Hispanic	1224	36	55	77	11	6
Other, non-Hispanic	96	3	2	1	3	5
Region of US						
West (California)	824	24	38	38	12	13
Northeast (New York)[&]	524	15	0	0	28	31
Mid-Atlantic (Washington DC, Maryland, Pennsylvania)	965	28	41	50	13	14
South (Alabama, Florida, Georgia, Mississippi, and North Carolina)[&]	624	18	0	0	36	31
Midwest (Illinois, Ohio)	474	14	21	11	12	11
Where are you living now?						
In your own house/apartment	2979	87	87	93	87	81
At parent's/someone else's house/apartment	344	10	10	5	10	16
Other living arrangement+	87	3	3	2	3	3
Number of people who live with you						
0	1132	33	39	41	30	20
1	1244	36	42	48	30	27
2	467	14	11	7	17	19
≥3	566	17	8	4	23	34
Current tobacco and marijuana use						
Smoke tobacco	808	24	19	11	30	35
Vape tobacco	55	2	2	2	2	2
Use marijuana (smoke, vape or dab)	738	22	29	20	18	23
Anyone who smokes tobacco in your shared living space	533	16	14	9	18	23
Age in years: median (IQR)	3411	57 (49,64)	59 (52,66)	65 (59,71)	54 (47,60)	52 (44,58)
Current CD4 cells/mm³*: median (IQR)	1926	682 (478,911)	657 (483,858)	NA	695 (475,936)	NA
Current HIV RNA copies/ml*: median (IQR)	1923	<20 (<20,<20)	<20 (<20, 23)	NA	<20 (<20, 22)	NA
Currently taking any antiretroviral medications*	2078	95	95	NA	95	NA

Appendix Table 2. Social distancing practices and other public health guideline following reported by partcipants (D'Souza, et al, 2020).

Practices used to prevent the spread of SARS-CoV-2 infection	Percent			P-value
	All N=3411	PLWH N=2078	SN N=1333	
Staying home as much as possible	97	97	97	0.32
Social distancing (6 ft)	98	98	98	0.98
Self-isolating due to symptoms or positive test	2	3	2	0.10
Self- isolating due to exposure to infected person	2	2	2	0.38
Self- isolating due to being unsure of infection status	5	5	6	0.67
Not making changes to daily life and routine~	13	15	11	0.003
Taking other steps (additional self-reported answers)	75	73	79	<.001
Other*: gloves	22	23	22	0.69
Other*: masks	62	60	66	<.001
Other*: using disinfectant, washing hands and surfaces	34	33	35	0.27
Other*: no visitors, not going out, ordering food, ordering grocery delivery	2	3	2	0.35

Appendix Table 3: Social distancing mandates in place during interviews from April-June 2020 at each site (D'Souza et al., 2020).

Study Site	Date range (year=2020)		Date Started (year=2020)			
	Collected survey data	Shelter in place mandate	Social distancing mandate	Re-opening Start Date^		
				Phase 1	Phase 2	Phase 3
WEST						
Los Angeles, CA	04/24-06/19	3/20-5/7	3/16	5/8	6/12	TBD
San Francisco, CA	04/23-06/18	3/19-5/16	3/17	5/17	6/1	TBD
NORTHEAST						
Bronx, NY	04/21-06/16	3/20-5/15	3/20	6/8	6/22	7/6
Brooklyn, NY	04/22-06/11	3/20-5/15	3/20	6/8	6/22	7/6
MID-ATLANTIC						
Baltimore, MD	05/01-06/25	3/30-5/15	3/16	5/15	6/5	TBD
Washington D.C.	04/30-06/18	04/01- 06/08	3/16	5/29	6/22	TBD
SOUTH						
Miami, FL	04/16-06/10	4/1-4/30	3/24	5/4	6/5	7/13
Atlanta, GA	04/23-06/18	4/2-4/30	4/23	5/1	5/27	6/11
Chapel Hill, NC	04/21-06/22	3/27-5/8	3/12	5/8	5/22	TBD
Birmingham, AL	04/20-05/22	3/16-4/30	3/16	5/22	7/3	TBD
Jackson, MS	05/01-05/29	4/1-5/3	4/1	5/4	6/1	TBD
MIDWEST						
Chicago, IL	05/11-06/30 (men) 04/08-06/05(women)	3/20-5/29	3/26	6/3	6/26	TBD
Pittsburgh, PA	04/20-06/30	4/1-5/8	3/12	5/8	5/12	TBD
Columbus, OH	04/20-06/30	3/22-5/1	3/10	5/4	6/5	TBD

Appendix B Interview Questionnaire Examples

SECTION B. COVID-19 TESTING AND TREATMENT

As we have at prior visits, I will need to ask you numerous questions about your health history. I will be asking you a series of questions about diseases and symptoms you may have had. I am going to use the words "health care provider" to mean any doctor, nurse practitioner, or physician assistant you may go to for medical care.

B.1 Since January have you had any of the following symptoms...

		How many days did you have this symptom?	Do you have this symptom now?	How severe [IS/WAS] this symptom??
a. A fever >100.4 F	NO... 0 **(b)** YES.. 1 SFEVRCV	DAYS FEVDYSCV	NO... 0 YES.. 1 FEVNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 FEVSEVCV
b. Felt feverish	NO... 0 **(c)** YES.. 1 SFFVRCV	DAYS FFVDYSCV	NO... 0 YES.. 1 FFVNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 FFVSEVCV
c. Chills	NO... 0 **(d)** YES.. 1 SCHLSCV	DAYS CHLDYSCV	NO... 0 YES.. 1 CHLNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 CHLSEVCV
d. Muscle aches	NO... 0 **(e)** YES.. 1 SMUSCCV	DAYS MUSDYSCV	NO... 0 YES.. 1 MUSNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 MUSSEVCV
e. Runny nose	NO... 0 **(f)** YES.. 1 SRNSECV	DAYS RNSDYSCV	NO... 0 YES.. 1 RNSNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 RNSSEVCV
f. Sore throat	NO... 0 **(g)** YES.. 1 SSTHRCV	DAYS STHDYSCV	NO... 0 YES.. 1 STHNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 STHSEVCV
g. Cough (new onset or worsening of chronic cough)	NO... 0 **(h)** YES.. 1 SCOGHCV	DAYS COGDYSCV	NO... 0 YES.. 1 COGNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 COGSEVCV
h. Shortness of breath (dyspnea)	NO... 0 **(i)** YES.. 1 SDYSPCV	DAYS DYSDYSCV	NO... 0 YES.. 1 DYSNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 DYSSEVCV
i. Nausea or vomiting	NO... 0 **(j)** YES.. 1 SNVOMCV	DAYS NVODYSCV	NO... 0 YES.. 1 NVONOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 NVOSEVCV
j. Headache	NO... 0 **(k)** YES.. 1 SHDACCV	DAYS HDADYSCV	NO... 0 YES.. 1 HDANOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 HDASEVCV
k. Abdominal pain	NO... 0 **(l)** YES.. 1 SABPNCV	DAYS ABPDYSCV	NO... 0 YES.. 1 ABPNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 ABPSEVCV
l. Diarrhea (3 loose stools or looser than normal stools in a 24hr period)	NO... 0 **(m)** YES.. 1 SDIARCV	DAYS DIADYSCV	NO... 0 YES.. 1 DIANOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 DIASEVCV
m. Loss of taste	NO... 0 **(n)** YES.. 1 SLTSTCV	DAYS TSTDYSCV	NO... 0 YES.. 1 TSTNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 TSTSEVCV
n. Loss of smell	NO... 0 **(o)** YES.. 1 SLSMLCV	DAYS SMLDYSCV	NO... 0 YES.. 1 SMLNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 SMLSEVCV

o. Other	NO... 0 **(p)** YES.. 1 SOTHRCV			
	SPECIFY:_____ SSPOTCV	DAYS OTHDYSCV	NO... 0 YES.. 1 OTHNOWCV	MILD..... 1 MODERATE.. 2 SEVERE.... 3 OTHSEVCV

B.2. Did any of these symptoms happen at the same time?

NO... 0 **(B.3 INTRODUCTION)**
YES.. 1 SSTIMCV

a. Which ones?
[INTERVIEWER: RESTATE SYMPTOMS FROM B1 AND ASK PARTICIPANT TO SELECT ONLY THOSE THAT HAPPENNED CONCURRENTLY. CIRCLE "YES" RESPONSE BELOW FOR THOSE SYMPTOMS THAT PARTICIPANT LISTS.]

		NO	YES	
i.	Fever > than 100.4 F	0	1	CFEVRCV
ii.	Felt feverish	0	1	CFFVRCV
iii.	Chills	0	1	CCHLSCV
iv.	Muscle aches	0	1	CMUSCCV
v.	Runny nose	0	1	CRNSECV
vi.	Sore throat	0	1	CSTHRCV
vii.	Cough (new onset or worsening of chronic cough)	0	1	CCOGHCV
viii.	Shortness of breath (dyspnea)	0	1	CDYSPCV
ix.	Nausea or vomiting	0	1	CNVOMCV
x.	Headache	0	1	CHDACCV
xi.	Abdominal pain	0	1	CABPNCV
xii.	Diarrhea (3 loose stools or looser than normal stools in a 24-hour period)	0	1	CDIARCV
xiii.	Loss of taste or loss of smell	0	1	CTSMLCV
xiv.	Other	0	1	COTHRCV

The next few questions ask about a respiratory illness that has been affecting people called coronavirus. We want to understand what people are doing to try and prevent the spread of this infection.

B3. Are you currently:

	NO	YES	
a. Staying home as much as you can?	0	1	PHOMECV
b. Practicing social distancing by maintaining 6 feet from others when in a public space?	0	1	PSD6FCV
c. In self-quarantine (not leaving the house at all) because you have symptoms or tested positive for coronavirus?	0	1	PSQSPCV
d. In self-quarantine (not leaving the house at all) because you were in contact with someone who was infected with coronavirus?	0	1	PSQCICV
e. In self-quarantine (not leaving the house at all) because you are unsure of your infection status?	0	1	PSQUICV
f. Taking other steps	0 **(g)**	1	POTHRCV

SPECIFY: PSPOTCV

g. Not making any changes to your daily life and routine?	0	1	PNCHGCV

B.4. Have you been tested for coronavirus?

NO... 0 **(B.6)**
YES.. 1 **(COLLECT MEDICAL RECORDS RELEASE)** TESTDCV

a. What was the date of that test? MM TSTDTMCV DD TSTDTDCV YYYY TSTDTYCV

b. **INTERVIEWER INSTRUCTIONS:** Collect all available information about coronavirus testing.
[INTERVIEWER: ENTER ".9" FOR ANY MISSING DATA IN THIS QUESTION.]

PROVIDER NAME: TPNAMCV

PROVIDER INSTITUTION: TPINSCV

PROVIDER ADDRESS: TPADDCV

B.5. What was the result of that test?

NEGATIVE.. 1
POSITIVE.. 2
PENDING... 3 TRESLCV

B.9 Why haven't you been tested for coronavirus, is it because...

	NO	YES	
a. You haven't felt sick	0	1	NTNSKCV
b. Testing was not available	0	1	NTAVLCV
c. You haven't had transportation to get to or from a testing location	0	1	NTTRNCV
d. You were worried about not being able to pay	0	1	NTPAYCV
e. You didn't know where to go for testing	0	1	NTWTGCV
f. You didn't have someone to watch your children or other people in your care while you went for testing	0	1	NTCRECV
g. You haven't been able to take time off from work	0	1	NTWRKCV
h. You were told by a healthcare provider to self-quarantine instead of getting tested	0	1	NTTSQCV
i. Other	0 **(B.10)**	1	NTOTHCV

SPECIFY: NTSPOCV

B.7. Since January, have you been hospitalized because you had coronavirus or because you had difficulty breathing or a respiratory infection?

NO... 0 **(IF B4=0 GO TO B9. IF B4=1 GO TO B10.)**
YES.. **1 (COLLECT MEDICAL RECORDS RELEASE)** HOSPICV

a. **INTERVIEWER INSTRUCTIONS:** Collect all available information for hospitalization.
[INTERVIEWER: ENTER "-9" FOR ANY MISSING DATA IN THIS QUESTION.]

PROVIDER NAME: HPNAMCV

HOSPITAL NAME: HHNAMCV

HOSPITAL ADDRESS: HHADDCV

b. On what date were you admitted into the hospital? MM HADDTMCV DD HADDTDCV YYYY HADDTYCV

c. On what date were you discharged from the hospital? MM HDSDTMCV DD HDSDTDCV YYYY HDSDTYCV

B.8. Would you say that...

You have recovered and are symptom free..... 1 **(B.10)**
You are feeling better but not completely recovered.. 2 **(B.10)**
You are not feeling better..... 3 **(B.10)** RCOVRCV

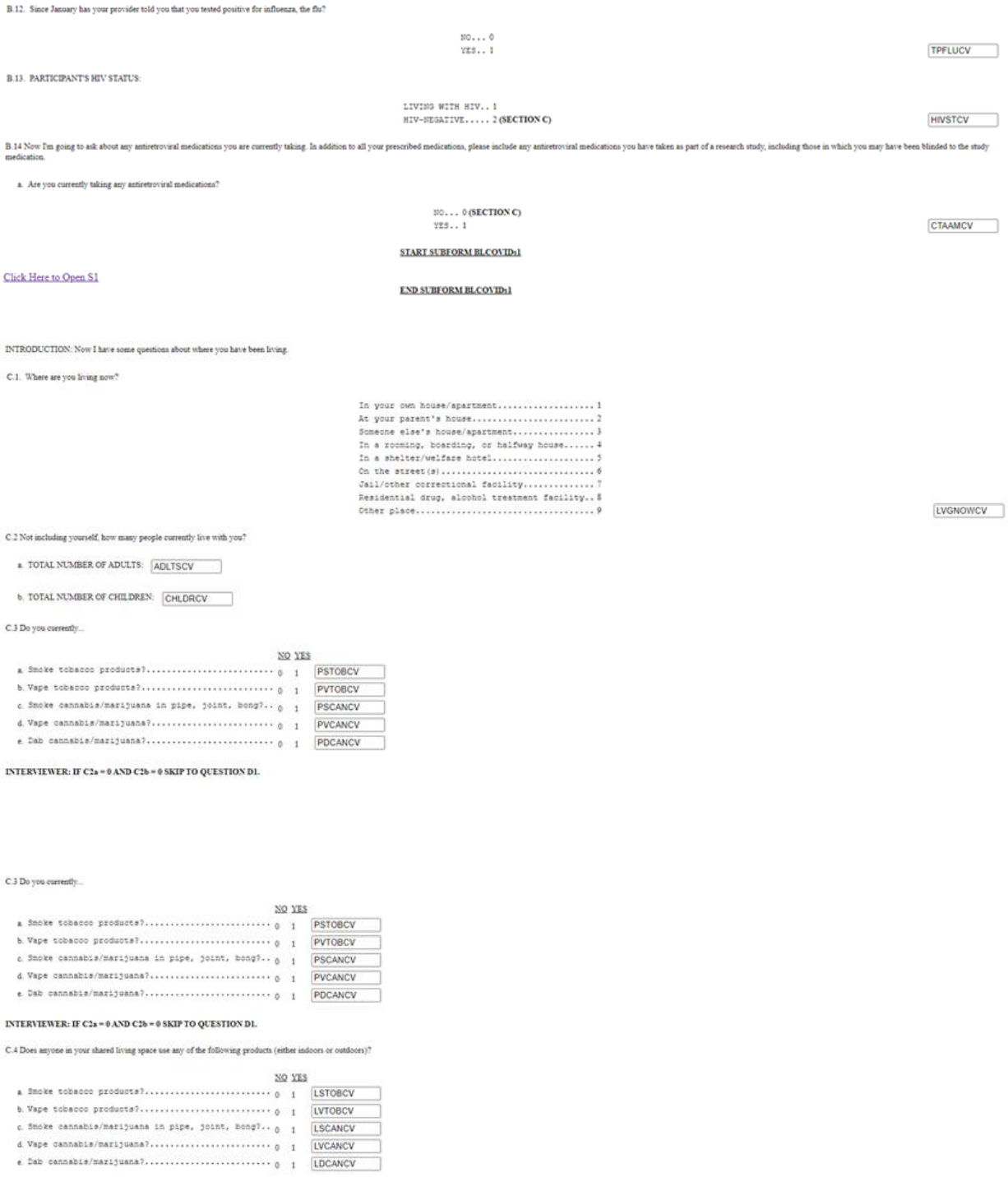
B.10. Do any of your medications have a generic name that ends in "-pril" or "-sartan"? These drugs are often taken by people with high blood pressure, diabetes, and heart disease.

NO... 0 **(B.12)**
YES.. 1 MGNAMCV

B.11 Which one?

Name of Medication

	NO	YES	
a. benazepril (Lotensin)	0	1	MBENACV
b. Captopril	0	1	MCAPTCV
c. enalapril (Vasotec, Epaned)	0	1	MENALCV
d. Fosinopril	0	1	MFOSICV
e. lisinopril (Prinivil, Zestril, Qbrelis)	0	1	MLISICV
f. Moexipril	0	1	MMOEXCV
g. perindopril (Aceon)	0	1	MPERICV
h. quinapril (Accupril)	0	1	MQUINCV
i. ramipril (Altace)	0	1	MRAMICV
j. trandolapril (Mavik)	0	1	MTRANCV
k. azilsartan (Edarbi)	0	1	MAZILCV
l. candesartan (Atacand)	0	1	MCANDCV
m. eprosartan (Teveten)	0	1	MEPROCV
n. irbesartan (Avapro)	0	1	MIRBECV
o. telmisartan (Micardis)	0	1	MTELMCV
p. valsartan (Diovan, Prexxartan)	0	1	MVALSCV
q. losartan (Cozaar)	0	1	MLOSACV
r. olmesartan (Benicar)	0	1	MOLMECV
s. sacubitril/valsartan (Entresto)	0	1	MENTRCV
t. nebivolol/valsartan (Byvalson)	0	1	MBYVACV



B.12. Since January has your provider told you that you tested positive for influenza, the flu?

NO... 0
YES.. 1 — TPFLUCV

B.13. PARTICIPANT'S HIV STATUS:

LIVING WITH HIV.. 1
HIV-NEGATIVE..... 2 **(SECTION C)** — HIVSTCV

B.14 Now I'm going to ask about any antiretroviral medications you are currently taking. In addition to all your prescribed medications, please include any antiretroviral medications you have taken as part of a research study, including those in which you may have been blinded to the study medication.

a. Are you currently taking any antiretroviral medications?

NO... 0 **(SECTION C)**
YES.. 1 — CTAAMCV

START SUBFORM BLCOVIDs1

Click Here to Open S1

END SUBFORM BLCOVIDs1

INTRODUCTION: Now I have some questions about where you have been living.

C.1. Where are you living now?

In your own house/apartment..... 1
At your parent's house..... 2
Someone else's house/apartment..... 3
In a rooming, boarding, or halfway house..... 4
In a shelter/welfare hotel..... 5
On the street(s)..... 6
Jail/other correctional facility..... 7
Residential drug, alcohol treatment facility.. 8
Other place..... 9 — LVGNOWCV

C.2 Not including yourself, how many people currently live with you?

a. TOTAL NUMBER OF ADULTS: ADLTSCV

b. TOTAL NUMBER OF CHILDREN: CHLDRCV

C.3 Do you currently...

	NO	YES	
a. Smoke tobacco products?	0	1	PSTOBCV
b. Vape tobacco products?	0	1	PVTOBCV
c. Smoke cannabis/marijuana in pipe, joint, bong?	0	1	PSCANCV
d. Vape cannabis/marijuana?	0	1	PVCANCV
e. Dab cannabis/marijuana?	0	1	PDCANCV

INTERVIEWER: IF C2a = 0 AND C2b = 0 SKIP TO QUESTION D1.

C.3 Do you currently...

	NO	YES	
a. Smoke tobacco products?	0	1	PSTOBCV
b. Vape tobacco products?	0	1	PVTOBCV
c. Smoke cannabis/marijuana in pipe, joint, bong?	0	1	PSCANCV
d. Vape cannabis/marijuana?	0	1	PVCANCV
e. Dab cannabis/marijuana?	0	1	PDCANCV

INTERVIEWER: IF C2a = 0 AND C2b = 0 SKIP TO QUESTION D1.

C.4 Does anyone in your shared living space use any of the following products (either indoors or outdoors)?

	NO	YES	
a. Smoke tobacco products?	0	1	LSTOBCV
b. Vape tobacco products?	0	1	LVTOBCV
c. Smoke cannabis/marijuana in pipe, joint, bong?	0	1	LSCANCV
d. Vape cannabis/marijuana?	0	1	LVCANCV
e. Dab cannabis/marijuana?	0	1	LDCANCV

Appendix Figure 1: Interview questionnaire examples from baseline interview. Interviewer markered "0" for no, "1" for yes, and completed other survey questions based on reported answers from participants. Participants were asked questions about symptoms and duration, testing, public health guidelines and practice, ART adherence, household density, smoking habits, and prescribed blood pressure medications.

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