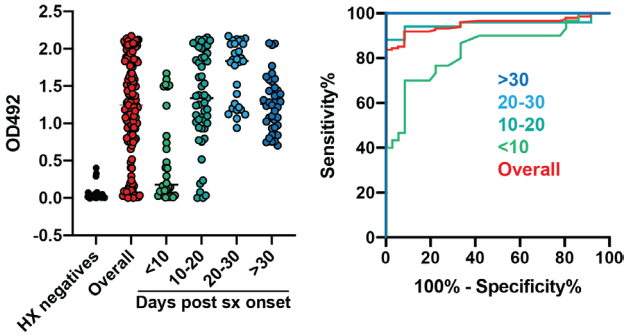
***Methods.*** Blood samples collected for clinical testing and then discarded ("spent samples") were obtained from the clinical laboratory of a medical center in Atlanta. A convenience sample of spent samples from both inpatients (medical/surgical floors, intensive care, obstetrics) and outpatients (clinics and ambulatory surgery) were collected one day per week from January-March 2021. Samples were matched to clinical data from the electronic medical record. In-house single dilution serological assays for SARS-CoV-2 receptor binding domain (RBD) and nucleocapsid (N) antibodies were developed and validated using pre-pandemic and PCR-confirmed COVID-19 patient serum and plasma samples (Figure 1). ELISA optical density (OD) cutoffs for seroconversion were chosen using receiver operating characteristic analysis with areas under the curve for all four assays greater than 0.95 after 14 days post symptom onset. IgG profiles were defined as natural infection (RBD and N positive) or vaccinated (RBD positive, N negative).

Figure 1. Nucleocapsid serology assay validation




Single dilution serological assays for SARS-CoV-2 nucleocapsid antibodies were validated using pre-pandemic and PCR-confirmed COVID-19 patient serum and plasma samples. ELISA optical density (OD) cutoffs for seroconversion were chosen using receiver operating characteristic (ROC) analysis with areas under the curve (AUC) for all four assays greater than 0.95 after 14 days post symptom onset.

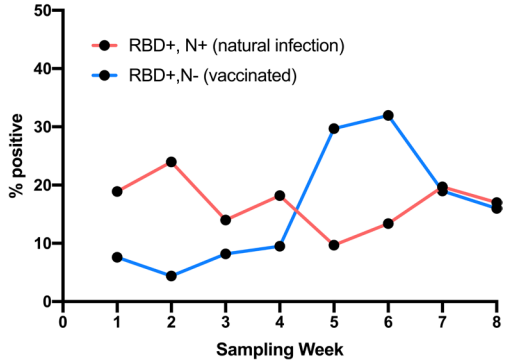
***Results.*** A total of 2406 samples were collected from 2132 unique patients. Median age was 58 years (IQR 40-70), with 766 (36%) ≥ 65 years. The majority were female (1173, 55%), and 1341 (63%) were Black. Median Elixhauser comorbidity index was 5 (IQR 2-9). 210 (9.9%) patients ever had SARS-CoV-2 detected by PCR, and 191 (9.0%) received a COVID-19 vaccine within the health system. Nearly half (1186/2406, 49.3%) of samples were collected from inpatient units, 586 (24.4%) from outpatient labs, 403 (16.8%) from the emergency department, and 231 (9.6%) from infusion centers. Overall, 17.0% had the IgG natural infection profile, while 16.2% had a vaccination profile. Prevalence estimates for IgG due to natural infection ranged from 24.0% in week 2 to 9.7% in week 5, and for IgG due to vaccine from 4.4% in week 2 to 32.0% in week 6 (Table, Figure 2).

Table. SARS-CoV-2 antibody seropositivity by week of sample collection for spent routine blood chemistry samples.

| | Week 1 (N=301) | Week 2 (N=338) | Week 3 (N=243) | Week 4 (N=336) | Week 5 (N=371) | Week 6 (N=291) | Week 7 (N=426) | Week 8 (N=100) |
|---|---|---|---|---|---|---|---|---|
| IgG RBD | 80 (26.7) | 96 (28.4) | 54 (22.2) | 93 (27.7) | 146 (39.4) | 132 (45.4) | 165 (38.7) | 33 (33.0) |
| IgG N | 64 (21.3) | 140 (41.4) | 44 (18.1) | 94 (27.98) | 38 (10.2) | 49 (16.8) | 96 (22.5) | 23 (23.0) |
| IgG RBD+, N+ | 57 (18.9) | 81 (23.96) | 34 (13.99) | 61 (18.2) | 36 (9.7) | 39 (13.4) | 84 (19.7) | 17 (17.0) |
| IgG RBD+, N- | 23 (7.6) | 15 (4.4) | 20 (8.2) | 32 (9.5) | 110 (29.7) | 93 (31.96) | 81 (19.0) | 16 (16.0) |
| | | | | | | | | |
| IgA | 68 (22.6) | 95 (28.1) | 50 (20.6) | 80 (23.8) | 113 (30.5) | 158 (54.3) | 158 (37.1) | 33 (33.0) |
| IgM | 84 (27.9) | 83 (24.6) | 52 (21.4) | 75 (22.3) | 66 (17.8) | 142 (48.8) | 87 (20.4) | 21 (21.0) |
| | | | | | | | | |
| Any positive | 114 (37.9) | 189 (55.9) | 91 (37.5) | 156 (46.4) | 184 (49.6) | 222 (76.3) | 217 (50.9) | 51 (51.0) |

RBD = receptor binding domain. N = nucleocapsid. Seropositivity defined by enzyme-linked immunoassay (ELISA) optical density cutoffs selected using receiver operating characteristic analysis with areas under the curve (AUC) for all four assays greater than 0.95 after 14 days post symptom onset. IgG defined as positive if both RBD and N seropositive.

Figure 2. RBD and Nucleocapsid seropositivity to differentiate natural infection vs. vaccination by week of sample collection.




RBD = receptor binding domain. N = nucleocapsid. Seropositivity defined by enzyme-linked immunoassay (ELISA) optical density cutoffs selected using receiver operating characteristic analysis with areas under the curve (AUC) for all four assays greater than 0.95 after 14 days post symptom onset.

***Conclusion.*** Estimated SARS-CoV-2 IgG seroprevalence among patients at a medical center from January-March 2021 was 17% by natural infection, and 16% by vaccination. Weekly trends likely reflect community spread and vaccine uptake.

***Disclosures.*** **Daniel Graciaa, MD, MPH, MSc, Critica, Inc** (Consultant)

**372. Detection of SARS-CoV-2 RNAemia in Deceased Tissue Donors**

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**Session:** P-16. COVID-19 Epidemiology and Screening

***Background.*** Tissue donors are evaluated for communicable disease in order to minimize the risk of transmission to recipients. Although there are data suggesting SARS-CoV-2 viremia across a wide spectrum of illness, prevalence in deceased tissue donors and the potential for transplant transmission are unknown.

***Methods.*** Eight tissue banks participated in a retrospective analysis of samples from eligible deceased tissue donors from Oct 2019 through June 2020, one participant in Canada and the remainder located in the United States. All four Census regions of the continental US and all major racial-ethnic groups were represented. EDTA or sodium citrate plasma aliquots were tested in singlicate with the Research Use Only Procleix SARS-CoV-2 Assay on the Procleix Panther System, which uses transcription-mediated nucleic acid amplification (TMA) technology for detection of the SARS-CoV-2 RNA. Plasma (or if unavailable, serum) aliquots were sent to Grifols for an alternate SARS-CoV-2 nucleic acid amplification (NAT) test to verify reactivity and also sent for antibody testing using the emergency use authorization Ortho VITROS Immunodiagnostic Products Anti-SARS-CoV-2 Total test. The VITROS assay uses immunometric technology for qualitative measurement of total antibody (IgG, IgA and IgM) to SARS-CoV-2. The proportion of donors with confirmed RNAemia (i.e., presence of SARS-CoV-2 RNA in plasma or serum) and 95% confidence intervals were computed.

***Results.*** Of 3,455 donor samples with valid final results, 26 (0.76%) were initially positive for SARS-CoV-2 RNA; of these, 3 were confirmed by alternate NAT. Of donor samples collected in 2019 0.00% (95% CI: 0.00%,0.43%) were confirmed RNAemic, while of those collected in 2020, 0.12% (0.04%,0.34%) were confirmed RNAemic. One of 26 initial positive, and none of the three samples confirmed by alternate NAT, tested positive for anti-SARS-CoV-2 Spike antibodies by serology. Infectivity studies are pending on one sample with sufficient available volume.

***Conclusion.*** The rate of SARS-CoV-2 RNAemia in deceased tissue donors is approximately 1 per 1,000, and it is unknown whether this RNAemia reflects the presence of infectious virus. Given these results, the risk of transmission through tissue is most likely to be low.

***Disclosures.*** **Melissa Greenwald, MD**, **Alamo Biologics** (Consultant)**Eurofins VRL Laboratories** (Consultant)**Right Cell Biologics** (Consultant, Consultant Medical Director) **Eduard Grebe, PhD**, **Gilead Sciences** (Consultant)**Sedia Biosciences Corporation** (Consultant, Grant/Research Support)**Vitalant** (Employee) **Alyce Linthurst Jones, PhD**, **LifeNet Health** (Employee) **Matthew Kuehnert, MD**, **American Association of Tissue Banks** (Board Member)**ICCBBA** (Board Member)**Musculoskeletal Transplant Foundation** (Employee)

**373. Household transmission of SARS-CoV-2 B.1.1.7 lineage –2 U.S. States, 2021**

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**Session:** P-16. COVID-19 Epidemiology and Screening

***Background.*** In December 2020, B.1.1.7 lineage of SARS-CoV-2 was first detected in the United States and has since become the dominant lineage. Previous investigations involving B.1.1.7 suggested higher rates of transmission relative to non-B.1.1.7 lineages. We conducted a household transmission investigation to determine the secondary infection rates (SIR) of B.1.1.7 and non-B.1.1.7 SARS-CoV-2 lineages.

***Methods.*** From January–April 2021, we enrolled members of households in San Diego County, CA, and Denver, CO metropolitan area (Tri-County), with a confirmed SARS-CoV-2 infection in a household member with illness onset date in the previous 10 days. CDC investigators visited households at enrollment and 14 days later at closeout to obtain demographic and clinical data and nasopharyngeal (NP) samples on all consenting household members. Interim visits, with collection of NP swabs, occurred if a participant became symptomatic during follow-up. NP samples were tested for SARS-CoV-2 using TaqPath™ RT-PCR test, where failure to amplify the spike protein results in S-Gene target failure (SGTF) may indicate B.1.1.7 lineage. Demographic characteristics and SIR were compared among SGTF and non-SGTF households using two-sided p-values with chi-square tests; 95% confidence intervals (CI) were calculated with Wilson score intervals.

***Results.*** 552 persons from 151 households were enrolled. 91 (60%) households were classified as SGTF, 57 (38%) non-SGTF, and 3 (2%) indeterminant. SGTF and non-SGTF households had similar sex distribution (49% female and 52% female, respectively; P=0.54) and age (median 30 years, interquartile range (IQR 14–47) and 31 years (IQR 15–45), respectively). Hispanic people accounted for 24% and 32% of enrolled members of SGTF and non-SGTF households, respectively (p=0.04). At least one secondary case occurred in 61% of SGTF and 58% of non-SGTF households (P=0.66). SIR was 52% (95%[CI] 46%-59%) for SGTF and 45% (95% CI 37%-53%) for non-SGTF households (P=0.18).

***Conclusion.*** SIRs were high in both SGTF and non-SGTF households; our findings did not support an increase in SIR for SGTF relative to non-SGTF households in this setting. Sequence confirmed SARS-CoV-2 samples will provide further information on lineage specific SIRs.

***Disclosures.*** **All Authors**: No reported disclosures

### 374. Need to Improve Minority Representation through COVID-19 Community Research Partnership

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**Session:** P-16. COVID-19 Epidemiology and Screening

***Background.*** Minorities are often unrepresented in research, which limits equity in healthcare advances. The racial and ethnic disparities in outcomes of individuals infected with COVID-19 highlight the importance of inclusivity in research to improve public health measures.

***Methods.*** We performed a descriptive analysis of the racial and ethnic distribution of children enrolled in our COVID-19 Community Research Partnership (CRP) study, a syndromic and serological surveillance study of children aged 2 – 17 years receiving care at three healthcare systems spanning North and South Carolina. Syndromic surveillance involved daily symptom reporting using a web-based monitoring application. Participants consenting to serological surveillance were mailed at-home tests sampling finger prick capillary blood. In-person and electronic recruitment efforts were conducted in English and Spanish. At one of the study sites, we compared the racial/ethnic distribution of enrolled children to the racial/ethnic distribution of all children who received care at the same site during the same timeframe. We compared the racial/ethnic distribution of participants who ultimately submitted samples for serological testing compared to those who consented to serologic testing.

***Results.*** At total of1630 children were enrolled from April 2, 2021 – June 8, 2021. Most children were > 5 years old, 50.2% were female, and 88.5% were from mostly urban counties (Table 1). Of enrolled children, 4.2% were Hispanic, 8.2% were black, and 81.6% were white (Table 2). Among 135,355 unique children who received care at the institution during the same time, 12.4% were Hispanic, 23.0% were black, and 63.1% were white. Of 1552 participants who consented to serologic testing, 4.4% were Hispanic, 8.1% were black, and 81.8% were white (Table 3). To date, 242 children submitted serologic samples; 4.1% were Hispanic, 5.0% were black, and 85.5% were white.

Table 1. Characteristics of enrolled children in COVID-19 surveillance study

| Characteristics | N (%) |
|---|---|
| Number of Atrium enrollees (N) | 1630 |
| **Age (years):** | |
| ≥2 – ≤ 5 | 343 (21.0%) |
| >5 – ≤10 | 518 (31.8%) |
| >10 – ≤15 | 590 (36.2%) |
| >15 – ≤18 | 179 (11.0%) |
| | |
| **Sex at Birth:** | |
| Female | 818 (50.2%) |
| Male | 812 (49.8%) |
| | |
| **Rurality of County of Residence:** | |
| Mostly urban | 1443 (88.5%) |
| Mostly rural | 187 (11.5%) |
| Completely rural | 0 (0%) |

Table 2. Racial and Ethnic distribution of children enrolled in the study compared to target population

| | Enrolled study population (N = 1630) | Enrolled healthcare system patient population (N = 135355) |
|---|---|---|
| **Race:** | | |
| White, n (%) | 1330 (81.6%) | 85433 (63.1%) |
| Black, n (%) | 133 (8.2%) | 31116 (23.0%) |
| Native Hawaiian/Pacific Islander, n (%) | 2 (0.1%) | 186 (0.1%) |
| Asian, n (%) | 54 (3.3%) | 4822 (3.6%) |
| American Indian/Alaska Native, n (%) | 7 (0.4%) | 1025 (0.8%) |
| Middle Eastern/North African, n (%) | 1 (0.1%) | 260 (0.2%) |
| 2+ Races, n (%) | 33 (2.0%) | 2901 (2.1%) |
| Do not wish to specify, n (%) | 70 (4.3%) | 9612 (7.1%) |
| | | |
| **Ethnicity:** | | |
| Hispanic/Latino | 69 (4.2%) | 16834 (12.4%) |
| Not Hispanic/Latino | 1472 (90.3%) | 111492 (82.4%) |
| Not Specified | 89 (5.4%) | 7029 (5.2%) |

Table 3. Racial and ethnic distribution of children who participated in serology testing

| | Serology Completed (N = 242) | Consented to serology testing (N = 1552) |
|---|---|---|
| **Race:** | | |
| White, n (%) | 207 (85.5%) | 1270 (81.8%) |
| Black, n (%) | 12 (5.0%) | 125 (8.1%) |
| Native Hawaiian/Pacific Islander, n (%) | 2 (0.8%) | 2 (0.1%) |
| Asian, n (%) | 9 (3.7%) | 50 (3.2%) |
| American Indian/Alaska Native, n (%) | 1 (0.4%) | 7 (0.5%) |
| Middle Eastern/North African, n (%) | 0 (0%) | 0 (0%) |
| 2+ Races, n (%) | 3 (1.2%) | 32 (2.1%) |
| Do not wish to specify, n (%) | 8 (3.3%) | 66 (4.3%) |
| | | |
| **Ethnicity**: | | |
| Hispanic/Latino | 10 (4.1%) | 68 (4.4%) |
| Not Hispanic/Latino | 218 (90.1%) | 1405 (90.5%) |
| Not Specified | 14 (5.8%) | 79 (5.1%) |

***Conclusion.*** Despite efforts to recruit a diverse group of children, the proportion of minorities enrolled in our COVID-19 surveillance study underrepresents the targeted population. Ongoing efforts will work to identify barriers and facilitators to research participation among minority families.

***Disclosures.*** **Amina Ahmed, MD**, Nothing to disclose

### 375. High Laboratory-confirmed SARS-CoV-2 Attack Rate in Lima Health Care Personnel During August 2020-March 2021 Suggests Role for Improved Infection Control

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**Session:** P-16. COVID-19 Epidemiology and Screening

***Background.*** Peru has one of the highest per capita SARS-CoV-2 death rates in Latin America. Healthcare workers (HCW) are a critical workforce during the COVID-19 pandemic but are themselves often at increased risk of infection. We evaluated SARS-CoV-2 attack rate and risk factors among frontline HCWs.

***Methods.*** We performed a prospective cohort study of HCW serving two acute care hospitals in Lima, Peru from Aug 2020 to Mar 2021. Participants had baseline SARS-CoV-2 serology using the CDC ELISA, active symptom monitoring, and weekly respiratory specimen collection with COVID-19 exposure/risk assessment for 16-weeks regardless of symptoms. Respiratory specimens were tested by real-time reverse transcriptase PCR (rRT-PCR).

***Results.*** Of 783 eligible, 667 (85%) HCW were enrolled (33% nurse assistants, 29% non-clinical staff, 26% nurses, 7% physicians, and 6% other). At baseline and prior to COVID-19 vaccine introduction, 214 (32.1%; 214/667) were reactive for SARS-CoV-2 antibodies. In total, 72 (10.8%; 72/667) HCWs were found to be rRT-PCR positive during weekly follow-up. Of the rRT-PCR positive HCWs, 37.5% (27/72) did not report symptoms within 1-week of specimen collection. During follow up, HCW without detectable SARS-CoV-2 antibodies at baseline were significantly more likely to be rRT-PCR positive (65/453, 14.3%) compared to those with SARS-CoV-2 antibodies at baseline (4/214, 1.9%) (p-value: < 0.001). Three HCW were both serologically reactive and rRT-PCR positive at baseline. Looking only at HCW without SARS-CoV-2 antibodies, nurse assistants (rRT-PCR positive: 18.6%; 27/141) and non-clinical healthcare workers (16.5%; 21/127) were at greater risk of infection compared to nurses (8.5%; 10/118), physicians (7.9%; 3/38), and other staff (10.3%; 4/29) (RR 1.95;95%CI 1.2,3.3; p-value: 0.01).