Background. The Walter Reed National Military Medical Center (WRNMMC) established a consolidated COVID-19 screening center (CSA) beginning in March 2020 to provide beneficiary and staff testing via a drive-through site. Testing was available to all patients and WRNMMC staff regardless of beneficiary status. Presented is a descriptive analysis of our testing operations and positivity rates within a closed medical system from March 2020 to April 2021.

Methods. For quality and process improvement, we compiled daily testing logs from March 2020 to April 2021 from the CSA. These logs included patient demographics, reason for testing, test result, testing platform, and occupational status at the hospital. We determined positivity rates in various subgroups—asymptomatic, symptomatic, pre-operative, in order to track testing use and access. Additionally, we compared the overall positivity rate to the surrounding civilian community by pulling data from the Maryland Department of Health’s COVID database.

Results. Over the course of nearly 14 months of testing availability, 34,694 beneficiaries were screened with 41,582 individual tests. After May 2020, the monthly overall positivity rate varied from 1.99% to 11.92%, peaking in December 2020 (with high rates in November 2020, 7.52% and January 2021, 9.33%), correlating with or exceeding elevated positivity rates in Montgomery County (November 2020: 4.91%; December 2020: 6.48%; January 2021: 6.51%). When examining only symptomatic individuals, the positivity rate is notably much higher, with monthly rates varying from 6.40% to 21.10%, with a similar peak in December 2020. After full implementation of pre-operative screening for procedures with aerosolization potential in June 2020, the range of positivity rates was 0.28%-1.66%. Since vaccination for COVID-19 became widely available in February 2021, the preoperative positivity rate has remained below 0.05%.

Conclusion. Our institutional experience is unique in its ability to offer universal access to COVID-19 testing for beneficiaries and staff of the DoD under direction of the ID service. Our process serves as a model for public and occupational health response, and may guide lab resource and real-time staffing management in support of COVID-19 diagnostics at a medical center.

Disclosures. All Authors: No reported disclosures

146. Intact Sense of Taste and Smell During COVID-19 Infection Is Associated with Absence of of SARS-CoV-2 Spike Protein Antibody Responses within 3 Months of Symptomatic Illness

James M. Wilson, DO; Sheena Gillani, MD MPH; Robert Bencshop, PhD; Josh Poorbaugh, PhD; Ajay Nirula, MD PhD; Lin Zhang, PhD; Kody Keckler, BA; Kathleen Weber, BSN RN; Ralph Morack, Masters; Stephanie Beasley, BA; Jennifer Brothers, MPH; Gregory Huhn, MD; Rush University Medical Center / Cook County Health System, Chicago, IL; Rush University Medical Center, Chicago, Illinois; Eli Lilly, Indianapolis, Indiana; Cook County Health System, Chicago, Illinois; Cook County Health Systems, Chicago, Illinois; Hektoen Labs, Chicago, Illinois; John H Stroger Jr. Hospital of Cook County, Chicago, Illinois

Session: O-30. Research in COVID-19 Diagnostics

Background. Although studies show most COVID-19 survivors have post-infection immunity against SARS-CoV-2 that could prevent re-infection, there is still a need to identify the breadth of antibody (Ab) responses associated with clinical phenotypes. We characterized Ab profiles at the estimated peak of Ab diversity among adults with recovered SARS-CoV-2 infections and determined their relationships with clinical factors.

Methods. From April-June 2020, 41 health system employees with PCR-confirmed symptomatic COVID-19 infection enrolled 8-10 weeks after symptom onset. Symptom questionnaires including baseline demographics, COVID-19 symptoms, disease severity, and disease duration were collected and plasma samples were assayed using a custom Luminex Multiplex platform (Figure 1) to measure the antibody response against 20 COVID-19 related antigens (Figure 2). Differences in Ab profile titers among different groups were tested using nonparametric t test and Benjamini-Hochberg adjustment for multiplicity. Associations were considered significant at FDR<0.05.

Results. Mean age was 48 years (range 27-68), with 51% female, 37% White, 32% Black, 29% Asian, and 17% Latinx. Ab profiles (Figure 3) showed 100% cross-reactivity with related alpha and beta coronavirus, and 95% with SARS-CoV-1. 78% had Abs against SARS-CoV-2 nucleocapsid protein (NCP). However, 29% of patients had no immune response against the four spike protein epitopes. These participants also reported fewer symptoms, including no cases of anosmia/ageusia, suggesting mild illness. Anosmia/ageusia, fever, and cough associated significantly with higher Ab titers (Figure 4).

Conclusion. Broad immune responses to various SARS-CoV-2 and related antigens were found among a heterogeneous patient population. However, less than 3 months after symptom onset, protective Ab responses to SARS-CoV-2 spike proteins were not detected in nearly one-third of recovered patients, primarily with mild infection. Intact sense of smell and taste demonstrated the greatest association with loss of seroprotective SARS-CoV-2 Ab responses, which may be clinically useful to predict post-infection immunity. Next steps include comparing the magnitude of Ab responses following full series completion with mRNA vaccination among this cohort.

Disclosures. Robert Bencshop, PhD; Eli Lilly (Employee) Josh Poorbaugh, PhD; Eli Lilly (Employee) Ajay Nirula, MD/PhD; Eli Lilly (Employee) Sheena Gillani, MPH; Eli Lilly (Employee) Stephanie Beasley, BA; Eli Lilly (Employee)

Figure 1: Description of the Luminex Serology Assay

Figure 2: List of the COVID-19 Related Antigens and Controls Measured

Figure 3: Antibody Diversity Profiles

Figure 4: P-values for Variables Associated with High Antibody Titers to Various COVID Antigens

147. Defining the Optimal Serial Testing Interval and Features for Identifying Patients with Early SARS-CoV-2 Infection

Sanjat Kanjilal, MD, MPH; James M. Wilson, DO; Harriet Medical School and Harvard Pilgrim Healthcare Institute, Jamaica Plain, MA

Session: O-30. Research in COVID-19 Diagnostics

Background. Serial testing for SARS-CoV-2 is necessary to prevent spread from patients early in infection. Testing intervals are largely derived from viral kinetic studies performed early in the COVID-19 pandemic. Laboratory and epidemiologic data accrued over the past year present an opportunity to use empirical models to define optimal serial testing intervals and features predictive of early infection.

Conclusion. Laboratory and epidemiologic data accrued over the past year present an opportunity to use empirical models to define optimal serial testing intervals and features predictive of early infection.
Methods. Retrospective analysis of 15,314 inpatients within the Mass General Brigham healthcare system who had two tests within a 36-hour period between May 1, 2020 and May 29, 2021. Early infection was defined as having a negative test followed by a positive test. Patients with prior positive tests were excluded. The primary outcome was the proportion of patients in early infection over the total number tested serially, stratified by 4-hour testing intervals from the timestamp of the first test. Multivariate modeling was used to identify features predictive of early infection. Covariates included demographics, body site, PCR assay, location, community incidence, percent positivity, and median / skew of Ct value distributions.

Results. Of 19,971 test pairs, 193 (0.97%) were characterized as a negative followed by a positive within 36 hours. Bivariate analysis showed a close association between negative to positive test pairs during the first surge in spring 2020 that was not present during the winter surge. Negative to positive test pairs were most common in the 12 to 16 hour time interval (51/193, 26%, Figure 1). After controlling for covariates, the Roche cobas model was used to identify features predictive of early infection. Covariates included demographics, body site, PCR assay, location, community incidence, percent positivity, and median / skew of Ct value distributions. All 4-hour time intervals from 16 to 36 hours were significant for predicting a negative to positive test pair (Table 1).

Conclusion. The likelihood of detecting early infection is dependent on PCR platform and body site of sampling. A range of time intervals between 16 to 36 hours after the initial test were likely to identify positive cases.

Disclosures. Sanjat Kanjilal, MD, MPH, GlaskoSmithKline (Advisor or Review Panel member)

148. Single-amplicon, Multiplex real-time RT-PCR with Tiled Probes to Detect SARS-CoV-2 spike Mutations Associated with Variants of Concern

Maxwell Su1; Katherine S. Immeggluck, n/a2; Samuel Stampfer, MD, PhD3; Anuradha Rao, PhD4; Leda Bassitt, PhD5; Vi Nguyen, BS6; Victoria D. Stiltef, BSc7; Jessica M. Ingerson, MS, MB ASCP8; Colleen S. Kraft, MD, MSc9; Greg S. Martin, MD, MSc2; Anne Piantadosi, MD, PhD3; Wilbur A. Lam, MD, PhD10; Jesse Waggoner, MD11; Ahmed Babiker, MBBS12; Emory University School of Medicine, Atlanta, GA; Emory University School of Medicine, Atlanta, Georgia; Emory University, Atlanta, Georgia

Session: O-30. Research in COVID-19 Diagnostics

Background. Detection and surveillance of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants is of great public health importance. Broadly accessible and inexpensive assays are needed to enhance variant surveillance and detection globally. We developed and validated a single-reaction multiplex real-time RT-PCR (the Spike SNP assay) to detect specific mutations associated with variants of concern (VOC).

Methods. A single primer was designed to amplify a 348 bp region of spike. Probes were initially designed with locked nucleic acids (LNAs) to increase probe melting temperature, shorten probe length, and specifically detect 417K, E484K, and N501Y (Figure). The assay was optimized and evaluated using characterized variant sample pools. Clinical evaluation was performed on a convenience set of residual nasopharyngeal swabs, and variant calls were confirmed by SARS-CoV-2 genomic sequencing in a subset of samples. Following the initial evaluation, unmodified probes (without LNAs) were designed to detect L452R, L452Q, and E484Q.

Conclusion. Spike SNP distinguishes mutations occurring in different lineages (A-C).

Table 1. Multivariate regression predicting a negative to positive test pair

Table 1. Multivariate regression predicting a negative to positive test pair

| Variable | Subgroup | OR | Lower 95% CI | Upper 95% CI | p value |
|----------|----------|----|--------------|--------------|---------|
| Age      |          | 0.99 | 0.98 | 1.00 | 0.02 |
| Gender (reference: Female) | Male | 1.04 | 0.77 | 1.39 | 0.81 |
| Month    |          | 1.00 | 1.00 | 1.00 | 0.08 |
| Incidence in Boston |          | 1.00 | 1.00 | 1.00 | 0.88 |
| Percent positive across Mass General Brigham |          | 1.10 | 0.97 | 1.25 | 0.15 |
| Median Ct for Mass General Brigham |          | 1.14 | 0.98 | 1.33 | 0.09 |
| Slowed of Ct distribution for Mass General Brigham |          | 4.31 | 0.81 | 23.09 | 0.09 |
| Assay for specimen 1 (reference: Cepheid Xpert) | Holocist Panther | 1.33 | 0.88 | 2.01 | 0.17 |
| Assay for specimen 2 (reference: Cepheid Xpert) | Holocist Panther | 0.99 | 0.66 | 1.52 | 0.95 |
| Body site for specimen 1 (reference: Nasopharynx) | Nasal Lower respiratory tract | 0.67 | 0.16 | 1.94 | 0.52 |
| Body site for specimen 2 (reference: Nasopharynx) | Nasal Lower respiratory tract | 1.78 | 0.29 | 10.00 | 0.43 |
| Location category for specimen 1 (reference: ER) | Inpatient | 1.19 | 0.80 | 1.76 | 0.39 |
| Location category for specimen 2 (reference: ER) | Inpatient | 0.86 | 0.55 | 1.38 | 0.52 |
| Time interval between specimens (reference - 4 to 8 hours) |          | 1.22 | 0.51 | 2.97 | 0.08 |

Representative results of variant detection a single Spike SNP run are shown for mutations in the codons for 417K (A) and mutations that encode 484K (B) and 501Y (C). Curves show 52266 (wild type); pink B.1.1.7; purple, B1.525; and green, B.1.1.7; purple, B1.525; and green, P.1. Variant pools were used for B.1.17, B.1.525, and P.1 strains. Curves are displayed for a given dilution in each channel and result interpretation is shown (D).

Results. The lower limit of 95% detection was 2.46 to 2.48 log₁₀, GE/mL for the three targets (~1-2 GE/reaction). Among 253 nasopharyngeal swabs with detectable SARS-CoV-2 RNA, the Spike SNP assay was positive in 238 (94.1%), including all samples with Ct values < 30 (220/220) for the N2 target and 18/33 samples with N2 Ct values ≥ 30. Results were confirmed by SARS-CoV-2 genomic sequencing in 50/50 samples (100%). Subsequent addition of the 452R probe did not affect performance for the original targets, and probes for 452Q and 484K performed similarly to LNA-modified probes.

Conclusion. The Spike SNP assay provides fast, inexpensive and sensitive detection of specific mutations associated with SARS-CoV-2 VOCs, and the assay can be quickly modified to detect new mutations in the receptor binding domain. Similar analytical performance of LNA-modified and unmodified probes presents options for future assay customization that balance the shorter probe length (LNAs) and increased accessibility (unmodified). The Spike SNP assay, if implemented across laboratories offering SARS-CoV-2 testing, could greatly increase capacity for variant detection and surveillance globally.

Disclosures. Colleen S. Kraft, MD, MSc; Rebiotix (Individual(s) Involved: Self); Advisor or Review Panel member

149. Extraction-free RT-PCR to Detect SARS-CoV-2 Variants of Concern

Brian L. Harry, MD PhD1; Yue Qiu, PhD2; Ling Lu, n/a3; Mara Couto-Rodriguez, MS2; Dorothy Nagy-Szakal, MD PhD3; Niamh B. O’Hara, PhD4; Shi-Long Lu, MD PhD5; Sliman Lu; University of Colorado, Aurora, CO; Biotit, New York, New York

Abstracts • OFID 2021:8 (Suppl 1) • S89