the cephalosporin and aztreonam groups, respectively (3% vs. 11%, p=0.082, 20% vs. 12%, p=0.451). Because cephalexin has a similar R1 side chain to aminopenicillins, five patients with an aminopenicillin allergy who received cephalexin were evaluated separately; none had an allergic reaction (Table 1, Table 2, Figure 2).

Table 1: Baseline Characteristics

	Aztreonam (n = 81)	Cefazolin/Cephalexin (n = 139)
Age at admission, years*	60 (46 - 77)	49 (33 - 66)
Sex, female	49 (60%)	99 (71%)
Race		
Asian	2 (3%)	0 (0%)
African American	5 (6%)	15 (10%)
Caucasian	61 (75%)	104 (75%)
East Indian	0 (0%)	1 (1%)
Other	13 (16%)	18 (13%)
Unknown	0 (0%)	1 (1%)
Pregnant*	1 (1%)	23 (17%)
Reported allergen**		
Natural Penicillin	76 (94%)	125 (90%)
Aminopenicillin	7 (9%)	14 (10%)
Piperacillin/tazobactam	2 (2%)	1 (1%)
Total number of drug allergies*	3 (1 - 4)	2 (1 - 3)
Antibiotic indication, most prevalent		
Cellulitis	5 (6%)	22 (16%)
Pneumonia	15 (19%)	0 (0%)
Prophylaxis	0 (0%)	13 (9%)
Surgical prophylaxis	0 (0%)	47 (34%)
Sepsis	15 (19%)	0 (0%)
UTI	15 (19%)	23 (17%)
Number of doses received*		
1 Dose	20 (25%)	74 (53%)
> 1 Dose	61 (75%)	65 (47%)
Sulfa allergy*	20 (25%)	17 (12%)
HIV infection	0 (0%)	2 (1%)
Herpes viral infection	1 (1%)	3 (2%)

Data represented as n (%) or median (interquartile range)
*P value < 0.05
**Some patients had anaphylaxis allergies to more than one penicillin

The median age was higher in the aztreonam group, and the majority of patients were female and Caucasian. There were significantly more pregnant females in the cephalosporin group, and the majority of patients reported a natural penicillin allergy.

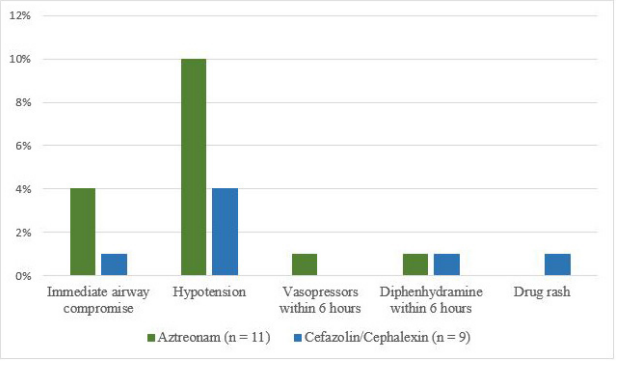
Table 2: Outcomes

Primary Outcome			
	Aztreonam (n = 81)	Cefazolin/Cephalexin (n = 139)	p value
Allergic reactions	11 (14%)	9 (7%)	0.077
Secondary Outcomes			
	Aztreonam (n = 81)	Cefazolin/Cephalexin (n = 139)	p value
IgE-mediated reactions	11 (14%)	8 (6%)	0.046
Antibiotic discontinued	0 (0%)	0 (0%)	
30-day readmission for delayed hypersensitivity reaction	0 (0%)	0 (0%)	
	< 2 Drug Allergies (n = 83)	≥ 2 Drug Allergies (n = 137)	p Value
Allergic reactions	8 (10%)	12 (9%)	0.826
	1 Dose Aztreonam (n = 20)	> 1 Dose Aztreonam (n = 61)	p Value
Allergic reactions	4 (20%)	7 (12%)	0.451
	1 Dose Cephalosporin (n = 74)	> 1 Dose Cephalosporin (n = 65)	p Value
Allergic reactions	2 (3%)	7 (11%)	0.082
	Patients who Received Cephalexin with Aminopenicillin Allergy (n = 5)		
Allergic reactions	0 (0%)		

Data are n (%); P value: <0.05 is statistically significant

There were less allergic reactions (IgE or non-IgE mediated) in the first-generation cephalosporin group compared to the aztreonam group, but this was not statistically significant. Also, there were fewer IgE-mediated reactions in the cephalosporin group. There was no difference in allergic reactions in patients with two or more reported drug allergies compared to less than two drug allergies. No difference in allergic reactions was observed when comparing those who received a single antibiotic dose versus multiple doses within the cephalosporin and aztreonam groups. Of the five patients who received cephalexin and reported an aminopenicillin anaphylactic allergy, none had an allergic reaction. Additionally, there were not any patients readmitted within 30 days for delayed hypersensitivity reactions and no antibiotics were discontinued due to other documented adverse reactions.

Figure 2: Occurrence of Allergic Reactions



Of the patients who had allergic reactions in the cephalosporin and aztreonam groups, these included immediate airway compromise, hypotension with one patient in the aztreonam group receiving vasopressors within the pre-defined time frame, receipt of the non-standing rescue medication of diphenhydramine, and drug rash.

Conclusion. There was no difference in the incidence of allergic reactions between the aztreonam and first-generation cephalosporin group, and fewer serious allergic reactions occurred in the cephalosporin group. This study suggests that cefazolin and cephalexin can safely be used in patients who report anaphylaxis to an agent in the penicillin class.

Disclosures. **Janessa Smith, PharmD**, **Merck & Co.** (Employee)

144. Clinical Validation and Performance of a T-cell Immunosequencing Assay to Identify Past SARS-CoV-2 Infection

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

Background. Our understanding of the SARS-CoV-2 immune response has critical gaps that are inadequately addressed with available tools. We report the clinical performance of T-Detect COVID, the first T-cell assay to identify prior SARS-CoV-2 infection using T-cell receptor (TCR) sequencing and repertoire profiling from whole blood samples.

Methods. The T-Detect COVID assay combines high-throughput immunosequencing of the TCRß gene from blood samples with a statistical classifier demonstrating 99.8% specificity for identifying prior SARS-CoV-2 infection. The assay was employed in several retrospective and prospective cohorts to assess primary and secondary Positive Percent Agreement (PPA) with SARS-CoV-2 RT-PCR (N=205; N=77); primary and secondary Negative Percent Agreement (NPA; N=87; N=79); PPA compared to SARS-CoV-2 serology (N=55); and pathogen cross-reactivity (N=38). The real-world performance of the test was also evaluated in a retrospective review of test ordering (N=69) at a single primary care clinic in Park City, Utah.

Results. In validation studies, T-Detect COVID demonstrated high PPA (97.1% ≥15 days from diagnosis) in subjects with prior PCR-confirmed SARS-CoV-2 infection; high NPA (~100%) in SARS-CoV-2 negative cases; equivalent or higher PPA with RT-PCR compared to two commercial EUA antibody tests; and no evidence of pathogen cross-reactivity. Review of assay use in a single clinic showed 100% PPA with RT-PCR in individuals with past confirmed SARS-CoV-2 vs. 85.7% for antibody testing, 100% agreement with positive antibody results, and positive results in 2/4 convalescent subjects with seroreversion to a negative antibody. In addition, 12/69 (17.3%) individuals with absent or negative RT-PCR tested positive by T-Detect COVID, nearly all of whom had compatible symptoms and/or exposure. TCR positivity was observed up to 12+ months (median 118 days) from the date of positive RT-PCR.

Conclusion. A T-cell immunosequencing assay shows high clinical performance for identifying past SARS-CoV-2 infection from whole blood samples. This assay can provide additional insights on the SARS-CoV-2 immune response, with practical implications for clinical management, risk stratification, surveillance, assessing vaccine immunity, and understanding long-term sequelae.

Disclosures. **Sudeb C. Dalai, MD, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Jennifer N. Dines, MD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Thomas M. Snyder, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Rachel M. Gittelman, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Tera Eerkes, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Pashmi Vaney, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Sally Howard, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Kipp Akers, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Lynell Skewis, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Anthony Monteforte, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Pamela R. Witte, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Cristina Wolf, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Hans Nesse, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Jia Qadeer, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Sarah Duffy, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Emily Svejnoha, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Caroline Taromino, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Ian M. Kaplan, PhD**, **Adaptive Biotechnologies** (Employee, Shareholder) **John Alsobrook, MD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Thomas Manley, MD**, **Adaptive Biotechnologies** (Employee, Shareholder) **Lance Baldo, MD**, **Adaptive Biotechnologies** (Employee, Shareholder, Leadership Interest)

145. SARS-CoV-2 (COVID-19) Testing Experience within a Military Treatment Facility

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

Background. The Walter Reed National Military Medical Center (WRNMMC) established a consolidated COVID-19 screening area (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, 9.53%), 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 beginning in Feb 2021, the preoperative positivity rate has remained below 0.85%.

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

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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.

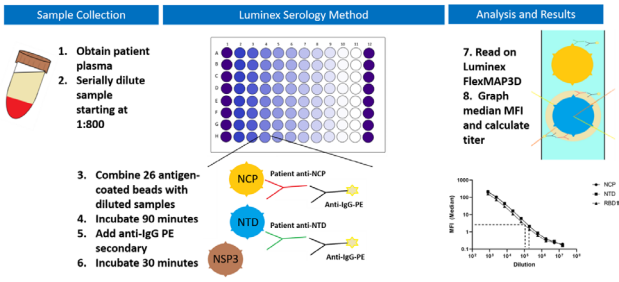


Figure 1: Description of the Luminex Serology Assay

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

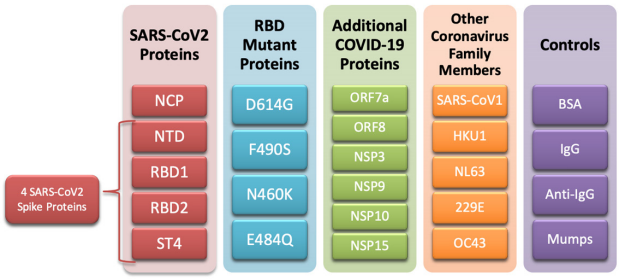
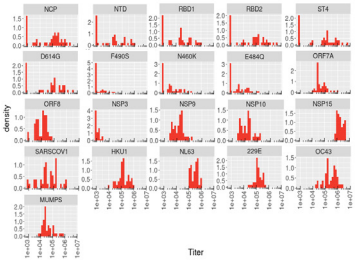


Figure 2: List of the COVID-19 Related Antigens and Controls Measured

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).

Figure 3: Antibody Diversity Profiles



Antigens and Controls		N of Patients	%Titer>MRD	%Titer>MRD	Median of Titer
SARS-CoV2 Proteins	NCP	41	22%	78%	121,840
	NTD	41	32%	68%	19,932
	RBD1	41	29%	71%	24,696
	RBD2	41	27%	73%	71,529
	ST4	41	29%	71%	98,591
RBD Mutant Proteins	D614G	41	29%	71%	108,678
	F490S	41	66%	34%	800
	N460K	41	39%	61%	2,655
	E484Q	41	41%	59%	2,759
Additional COVID-19 Proteins	ORF7a	41	0%	100%	33,121
	ORF8	41	2%	98%	13,604
	NSP3	41	49%	51%	845
	NSP9	41	0%	100%	15,849
	NSP10	41	0%	100%	16,452
	NSP15	41	0%	100%	1,640,505
Other Coronavirus Family Members	SARS-COV-1	41	5%	95%	27,834
	HKU1	41	0%	100%	143,098
	NL63	41	0%	100%	333,323
	229E	41	0%	100%	134,673
	OC43	41	0%	100%	298,107
Controls	Mumps	41	0%	100%	27,157

Figure 3: The minimal required dilution (MRD) for the antibody diversity profiles was 1:800. Any signal lower than the MRD was reported as 800.

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

COVID Antigens		Anosmia/ Ageusia (n=21)	Chills (n=23)	Cough (n=21)	Diarrhea (n=17)	Dyspnea (n=16)	Emesis (n=5)	Fever (n=23)	Headache (n=27)	Male (n=20)	Myalgias (n=28)	Nausea (n=8)	Pneumonia (n=4)	Rigor (n=6)	Sore Throat (n=18)	Wheezing (n=7)
SARS-CoV2 Proteins	NCP	0.0084*	0.3950	0.0886	0.3385	0.4901	0.8028	0.1644	0.8920	0.3317	0.0886	0.9346	0.2239	0.1838	0.9350	0.2239
	NTD	0.0064*	0.3279	0.0462*	0.5827	0.4748	0.7600	0.0568	0.8920	0.2629	0.0886	0.8414	0.3950	0.1248	0.8414	0.1589
	RBD1	0.0064*	0.3268	0.0462*	0.6343	0.3624	0.7416	0.0462*	0.8224	0.3086	0.0886	0.8414	0.2800	0.1707	0.9239	0.0886
	RBD2	0.0064*	0.2800	0.0275*	0.6501	0.3331	0.6773	0.0540	0.8168	0.3159	0.0886	0.7674	0.2759	0.1707	0.9707	0.0886
	ST4	0.0064*	0.3086	0.0338*	0.6501	0.3385	0.7416	0.0462*	0.8386	0.2700	0.0886	0.8405	0.2800	0.1048	0.9085	0.0887
RBD Mutant Proteins	D614G	0.0064*	0.2239	0.0338*	0.7416	0.3317	0.7854	0.0315*	0.9085	0.2239	0.0886	0.8414	0.3017	0.1185	0.8695	0.0886
	F490S	0.0963	0.3969	0.0540	0.8414	0.4744	0.3385	0.0945	0.9467	0.7416	0.3086	0.7416	0.1735	0.4901	0.7559	0.2239
	N460K	0.0064*	0.3385	0.0462*	0.5629	0.5370	0.6663	0.0886	0.8168	0.3317	0.0886	0.7874	0.3317	0.1631	0.8405	0.1016
	E484Q	0.0064*	0.3317	0.0462*	0.5258	0.5629	0.6782	0.1345	0.8414	0.3573	0.1185	0.7416	0.3385	0.1992	0.8744	0.1350
Additional COVID-19 Proteins	ORF7a	0.4748	0.7922	0.6773	0.8414	0.5437	0.4415	0.9707	0.5274	0.6969	1.000	0.8211	0.7874	0.1531	0.2800	0.8116
	ORF8	0.9027	0.8828	0.5165	0.8414	0.3844	0.4901	0.8347	1.0000	0.8224	0.6969	1.0000	0.4179	0.2800	0.3317	0.7416
	NSP3	1.0000	0.5069	0.8740	1.0000	0.7135	0.4901	0.7416	0.8224	0.6969	0.7432	0.9085	0.6501	0.6969	0.6187	0.8224
	NSP9	0.3858	0.4317	0.1185	0.9707	0.2239	0.4646	0.1324	0.6782	0.8224	0.6343	1.0000	0.8414	0.9914	0.4643	0.1992
	NSP10	0.7416	0.9350	0.9426	0.8876	0.8876	0.3317	0.9914	0.8871	0.8414	0.9667	0.9914	0.5069	0.4901	0.3385	0.8695
	NSP15	0.6773	0.6192	0.7697	0.9952	0.2573	0.3317	0.3934	0.7922	0.8414	0.5444	0.8414	0.4995	0.9596	0.6192	0.4901

Analyses of COVID related proteins were unable to be completed.
* Denotes p <0.05

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, Shareholder) **Lin Zhang, PhD**, **Eli Lilly and Company** (Employee, Shareholder) **Stephanie Beasley, BA**, **Eli Lilly** (Employee)

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

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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 empiric models to define optimal serial testing intervals and features predictive of early infection.