were 759 (12.15%) in COVID-19 patients and 3,465 (2.41%) in controls (P < 0.01). The adjusted incidence of diabetes was 15.34 (95% confidence interval, CI: 14.10 – 16.66) and 11.18 (95% CI: 10.67 – 11.72) per 100 person-year, respectively, with the mean follow-up time as 46.31 (standard deviation: 16.37) days. The adjusted hazard ratio of diabetes in COVID-19 cases was 2.97 (95% CI: 2.44 – 3.63).

Conclusion. Since COVID-19 patients showed a higher incidence of new-onset diabetes in a short-time follow-up, we should consider diabetes as one of the possible complications of COVID-19.

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354. SARS-CoV-2 Viral Viability Culture and Sequencing from Immunocompromised Patients with Persistently Positive SARS-CoV-2 PCR Results

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Session: P-15. COVID-19 Diagnostics

Background. Immunocompromised (IC) patients (pts) can have prolonged SARS-CoV-2 PCR positivity, even after resolution of COVID-19 symptoms. This study aimed to determine if viable virus could be detected in samples collected > 21 days after an initial positive (pos) SARS-CoV-2 PCR in IC pts.

Methods. We obtained 20 remnant SARS-CoV-2 PCR pos nasopharyngeal swabs from IC pts (bone marrow or solid organ transplant, high dose steroids, immunosuppressive medications) with a pos repeat PCR within the previous 30 days. The repeat specimens were cultured on Vero-hACE2-TMPRSS2 cells and incubated for 96 hours to assess viral viability. Viable RNA and infectious virus in the cultured cells were measured by qPCR and infectious plaque assays. RNA sequencing was performed on a HiSeq platform (Illumina). Samples also underwent SARS-CoV-2 antigen (Ag) testing (BD Veritor). Clinical data were extracted from the electronic health record by chart review.

Results. Pt characteristics are in Table 1. Viral cultures from the repeat specimen were negative (neg) for 18 pts and pos for 2 (Table 2). Pt 1 is a 60M treated with obinatuzumab 19 days prior to his first pos PCR test, with repeat specimen collected 21 days later (cycle threshold (Ct) not available). Pt 1 had a low viral titer (27 PFU/mL) & a D614G mutation on sequencing. Pt 2 is a 75M treated with rituximab 10 days prior to his first pos PCR test, with repeat specimen collected 23 days later (Ct 27.56/27.74). Pt 2 had a high viral titer (2e6 PFU/mL) and D614G, S98F, and S813I mutations.

Demographics of Study Population (N=20)

Variable	Viral culture (-) (n=18) N (%) or Median (range)	Viral culture (+) Patient 1	Viral culture (+) Patient 2
Sex			
Male	9 (50)	Yes	Yes
Race*			
White	14 (78)		
African American	4 (22)	Yes	Yes
BMI	26.7 (20.1 – 52.0)	37.0	27.2
Age at date of first positive PCR	64 (20 – 79)	60	75
Time between positive PCRs (days)	22.5 (12 – 62)	23	21
Positive PCR after the initial positive test	6 (33)	7 PCR+ repeated tests total	8 PCR+ tests repeated total
Immunosuppressive condition			
Autologous BMT/HCT in 6 months before positive PCR date	1 (6)		
Hematologic malignancy	3 (17)	Yes	Yes
Solid organ transplant, on immunosuppressive medication	10 (56)		
Receiving high dose steroids	3 (17)		Yes
Prednisone >20mg/day for >14 days at time of positive PCR test	1 (6)*		
Immunosuppressive meds in previous 30 days	12 (67)		
Other comorbidities			
COPD	4 (22)		
Chronic lung disease	6 (33)		
Hypertension	12 (67)		Yes
Heart condition	10 (56)	Pulmonary embolism	Congestive heart failure
Diabetes, Type 2	7 (39)		
Chronic kidney disease	8 (44)	Yes	
Dialysis	3 (17)	Yes	
Autoimmune or rheumatologic disease[b]	3 (17)		
Cancer, active	4 (22)	Chronic lymphocytic leukemia	Marginal zone lymphoma
Other immunosuppressing condition	15 (83)		
Chronic liver disease	1 (6)		
Alcohol abuse	1 (6)		
Current smoker	2 (11)		
Obesity	5 (28)	Yes	

*All patients were non-Hispanic

[b]Prednisone status unknown for 1 patient; autoimmune diseases status unknown for one patient

Characteristics of patients with a positive SARS-CoV-2 viral culture

Variable	Patient #1	Patient #2
History at time of first + PCR	60 year old male with chronic lymphocytic leukemia on obinutuzumab and venetoclax presented with a cough for several weeks, and acute on chronic diarrhea.	75 year old male with marginal zone lymphoma with treatment with bendamustine and rituxan presented with 2 weeks of cough.
Other medical conditions	Fibromyalgia Acute encephalopathy Hyperlipidemia Anemia	Hyperlipidemia Deep vein thrombosis Methemoglobinemia Acute hemolytic anemia
Dates and results of SARS-CoV-2 PCR tests (study specimens in **bold**)	3/23/20 + **4/15/20 +** 5/07/20 + 5/28/20 + 6/12/20 + 7/13/20 + 7/22/20 +	4/05/20 + 4/27/20 + 5/04/20 + 5/11/20 + **5/18/20 +** 6/01/20 + 6/11/20 + 6/23/20 + 7/07/20 -
Any other respiratory viruses?	No	No
Cause of death	COVID-19	Alive as of June 2021
Viral culture results from the repeat test	27 PFU/mL	2e6 PFU/mL
Spike protein mutations from the repeat test	D614G	D614G, S98F, S813I

Conclusion. 90% of specimens collected > 21 days after an initial pos SARS-CoV-2 PCR did not have viable virus detected on their repeat specimen. The 2 pts with pos viral cultures had active hematologic malignancies treated with an anti-CD20 mAb at the time of COVID-19 diagnosis. One pt had a high concentration of active, viable virus. No known variants of concern were noted in this cohort, collected in Q2 2020, though prolonged replication is a risk for variant development. Further data are needed about risk factors for persistent viable viral shedding & methods to prevent transmission of viable virus from IC hosts.

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355. A Novel Likelihood-Based Model to Estimate SARS-CoV-2 Viral Titer from Next-Generation Sequencing Data

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Session: P-15. COVID-19 Diagnostics

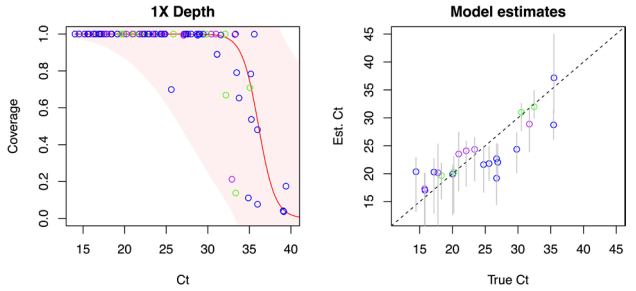
Background. The quantitative level of pathogens present in a host is a major driver of infectious disease (ID) state and outcome. However, the majority of ID diagnostics are qualitative. Next-generation sequencing (NGS) is an emerging ID diagnostics and research tool to provide insights, including tracking transmission, evolution, and identifying novel strains.

Methods. We built a novel likelihood-based computational method to leverage pathogen-specific genome-wide NGS data to detect SARS-CoV-2, profile genetic variants, and furthermore quantify levels of these pathogens. We used de-identified clinical specimens tested for SARS-CoV-2 using RT-PCR, SARS-CoV-2 NGS Assay (hybrid capture, Twist Bioscience), or ARTIC (amplicon-based) platform, and COVID-DX software. A training (n=87) and validation (n=22) set was selected to establish the strength of our quantification model. We fit non-uniform probabilistic error profiles

to a deterministic sigmoidal equation that more realistically represents observed data and used likelihood maximized over several different read depths to improve accuracy over a wide range of values of viral load. Given the proportion of the genome covered at varying depths for a single sample as input data, our model estimated the Ct of that sample as the value that produces the maximum likelihood of generating the observed genome coverage data.

Results. The model fit on 87 SARS-CoV-2 NGS Assay training samples produced a good fit to the 22 validation samples, with a coefficient of correlation (r2) of ~0.8. The accuracy of the model was high (mean absolute % error of ~10%, meaning our model is able to predict the Ct value of each sample within a margin of ±10% on average). Because of the nature of the commonly used ARTIC protocol, we found that all quantitative signals in this data were lost during PCR amplification and the model is not applicable for quantification of samples captured this way. The ability to model quantification is a major advantage of the SARS-CoV-2 NGS assay protocol.

The likelihood-based model to estimate SARS-CoV-2 viral titer



Left. Observed genome coverage (y-axis) plotted against Ct value (x-axis). The best-fitting logistic curve is demonstrated with a red line with shaded areas above and below representing the fitted error profile. RIGHT: Model-estimated Ct values (y-axis) compared to laboratory Ct values (x-axis) with grey bars representing estimated confidence intervals. The 1:1 diagonal is shown as a dotted line.

Conclusion. To our knowledge, this is the first model to incorporate sequence data mapped across the genome of a pathogen to quantify the level of that pathogen in a clinical specimen. This has implications in ID diagnostics, research, and metagenomics.

Disclosures. **Heather L. Wells, MPH**, **Biotia, Inc.** (Consultant) **Joseph Barrows, MS**, **Biotia** (Employee) **Mara Couto-Rodriguez, MS**, **Biotia** (Employee) **Xavier O. Jirau Serrano, B.S.**, **Biotia** (Employee) **Marilyne Debieu, PhD**, **Biotia** (Employee) **Karen Wessel, PhD**, **Labor Zotz/Klimas** (Employee) **Christopher Mason, PhD**, **Biotia** (Board Member, Advisor or Review Panel member, Shareholder) **Dorottya Nagy-Szakal, MD PhD**, **Biotia Inc** (Employee, Shareholder) **Niamh B. O'Hara, PhD**, **Biotia** (Board Member, Employee, Shareholder)

356. The Role of Procalcitonin in Antimicrobial Stewardship Among Cancer Patients Admitted with COVID-19

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Session: P-15. COVID-19 Diagnostics

Background. Procalcitonin (PCT) has been used to guide antimicrobial therapy in bacterial infections. With the wide spread use of empiric use of antibiotics in cancer patients admitted with COVID-19 disease, we aimed to evaluate the role of PCT in decreasing the duration of empiric antimicrobial therapy among cancer patients admitted with COVID-19.

Methods. We conducted a retrospective study of cancer patients admitted to MD Anderson Cancer Center who had a PCT test done within 72 hours of admission following their COVID-19 diagnosis between March 1, 2020 and June 6, 2021. Patients were divided into 2 groups of PCT < 0.25 ng/mL and PCT >=0.25 ng/mL. We assessed pertinent cultures including blood and respiratory, as well as antibacterial use and duration of empiric antibacterial therapy.

Results. We identified 544 patients with a median age of 62 years (range, 14-93). There were 312 (57%) patients that had at least one culture obtained from a sterile or infected site within 7 days following admission. None of the patients who had PCT< 0.25 had a positive culture whereas 41/111 (37%) patients with PCT >= 0.25 had at least one positive culture [P< 0.0001]. Among the 373 patients who had a PCT < 0.25, 129 (35%) patients received more than 72 hours of IV antibiotics compared to 87/171 (51%) among patients with PCT >=0.25 [P= 0.0003].

Conclusion. These results confirm the correlation between a PCT level greater than 0.25 and a documented bacterial infection. Furthermore, procalcitonin could be useful in enhancing antimicrobial stewardship in cancer patients with COVID-19 by reducing the duration of antimicrobial therapy beyond the initial empiric 72 hours until PCT results become available.

Disclosures. **Natalie J Dailey Garnes, MD, MPH**, **AlloVir** (Other Financial or Material Support, collaborator on research protocol)

357. A Comparison of Chest CT Findings in Cancer and Non-Cancer Patients with COVID-19

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Session: P-15. COVID-19 Diagnostics

Background. The purpose of this study was to compare chest computed tomography (CT) scan findings in cancer versus non-cancer patients with COVID-19 infection. We sought to assess the correlation between radiologic patterns of COVID-19 pneumonia, clinical course, and outcomes.

Methods. We performed a retrospective study of COVID-19 positive cancer and non-cancer pts who had chest CT scans at the time of diagnosis, at our hospital and 16 other centers in Asia, Australia, Europe, North America and South America, between March, 2020 and November, 2020. Patients' age, underlying diseases, symptoms, laboratory studies, and radiologic findings consisting of bilateral ground-glass opacities (GGOs), multifocal organizing pneumonia (MOP) were collected in association with clinical outcomes.

Results. We identified 426 pts with cancer and 622 non-cancer pts. Thereafter, cancer pts were analyzed into 3 distinct groups and similar to non-cancer pts: GGOs group (n=224, 54%), GGOs+MOP group (n=61, 14.6%), and a third group of neither GGOs or MOP (n=131, 31.4%) in cancer pts, and in non-cancer pts: GGOs group (n=387, 62.8%), GGOs +MOP group (n=100, 16.2%), and a third group of neither GGOs or MOP (n=129, 21%). The median patients' age was 54 in non-cancer pts vs 62 in cancer pts (p< 0.001) and there were more males in the non-cancer group 57% vs 47% (p=0.001). Cough was more prevalent in non-cancer pts, 71% vs 59% (p< 0.001) and similar to fever (73% vs 57%, p< 0.001). Neutropenia < 0.5 k/μL and lymphocytopenia < 1 k/μL were more frequent in cancer pts (p< 0.001). In cancer pts, there was no statistically significance difference between the 3 groups (hospital admission, mechanical ventilation, readmission within 30 days, and mortality), except pts who required non-invasive (NI) ventilation were more frequent in the GGOs group, 55% (p=0.005). In non-cancer, pts with GGOs +MOP have higher hospital admission, ICU transfer, NI- and mechanical ventilation compared to the 2 other groups (p< 0.001). While readmission to hospital or mortality rate within 30 days were similar between the 3 groups.

Conclusion. This study reveals that non-cancer pts tended to have more radiologic findings on chest CT scan compared to cancer pts at the time of COVID-19 diagnosis and were associated with more worrisome COVID-19-related clinical outcomes.

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358. Early Cardiac Marker of Mortality in COVID-19

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Session: P-15. COVID-19 Diagnostics

Background. Epicardial adipose tissue (EAT) is a highly inflammatory depot of fat, with high concentrations of IL-6 and macrophages, which can directly reach the myo-pericardium via the vasa vasorum or paracrine pathways. TNF-α and IL-6 diminish cardiac inotropic function, making EAT inflammation a potential cause of cardiac dysfunction.

Methods. A retrospective cohort study assessing EAT Thickness and Density from CT scans, without contrast, from adult patients during index admission for COVID-19 infection at Mount Sinai Medical Center from March 2020 to January 2021. A total of 1,644 patients were screened, of which 148 patients were included. Follow-up completed until death or discharge. The descriptive analysis was applied to the general population, parametric test of normality for comparisons between groups. Kaplan survival analysis was conducted after survival distribution was confirmed significant. It was followed by the assumption of normality by Q-Q Plot, prior to performing a multiple regression analysis in the vulnerable group using a K-Matrix input for cofounders. A log-rank test was conducted to determine differences in the survival distributions for the different ranges of EAT thickness.

Results. A total of 148 Participants were assigned to two groups based on epicardial adipose tissue in order to classify them as increased or decreased risk of cardiovascular risk: >5mm (n = 99), < 5mm (n = 49). The survival percentage was higher in the group with no EAT inflammation compared to the group with EAT inflammation (95.0% and 65%, respectively). Participants with EAT >5mm had a median day of hospital stay of 18 (95% CI, 16.86 to 29.92). The survival distributions for the two categories were statistically significantly different, $\chi2(2) = 6.9$, $p < 0.01$. A Bonferroni correction was made with statistical significance accepted at the $p < 0.025$ level. There was a statistically significant difference in survival distributions for the EAT >5 mm vs EAT < 5 mm, $\chi2(1) = 6.953$, $p = 0.008$.