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[a]			
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)[a]		
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	

[a]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