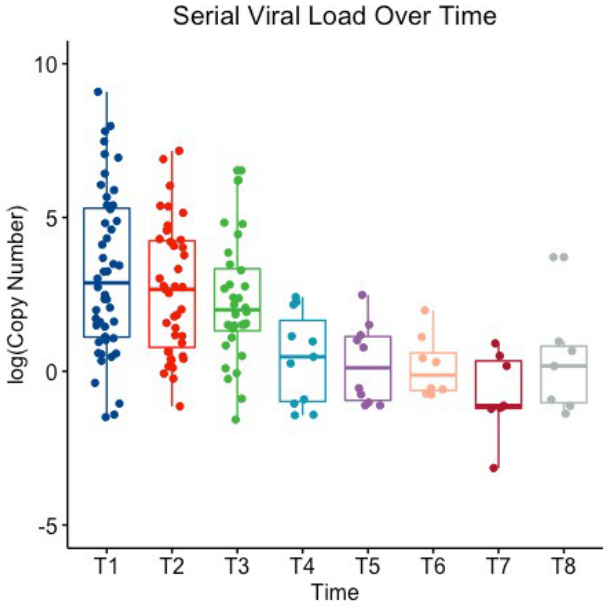
of viral resistance to therapeutic interventions and immune pressure. The goal of this study was to assess the change in viral load and viral genome sequence within patients over time and determine if these changes correlate with clinical and/or demographic parameters.

Methods: Hospitalized patients admitted to Northwestern Memorial Hospital with a positive SARS-CoV-2 test were enrolled in a longitudinal study for the serial collection of nasopharyngeal specimens. Swabs were administered to patients by hospital staff every 4 ± 1 days for up to 32 days or until the patients were discharged. RNA was extracted from each specimen and viral loads were calculated by quantitative reverse transcriptase PCR (qRT-PCR). Specimens with qRT-PCR cycle threshold values less than or equal to 30 were subject to whole viral genome sequencing by reverse transcription, multiplex PCR, and deep sequencing. Variant populations sizes were estimated and subject to phylogenetic analysis relative to publicly available SARS-CoV-2 sequences. Sequence and viral load data were subsequently correlated to available demographic and clinical data.

Results: 60 patients were enrolled from March 26th to June 20th, 2020. We observed an overall decrease in nasopharyngeal viral load over time across all patients. However, the temporal dynamics of viral load differed on a patient-by-patient basis. Several mutations were also observed to have emerged within patients over time.

Distribution of SARS-CoV-2 viral loads in serially collected nasopharyngeal swabs in hospitalized adults as determined by qRT-PCR. Samples were collected every 4 ± 1 days (T#1–8) and viral load is displayed by log(copy number).



Conclusion: These data indicate that SARS-CoV-2 viral loads in the nasopharynx decrease over time and that the virus can accumulate mutations during replication within individual patients. Future studies will examine if some of these mutations may provide fitness advantages in the presence of therapeutic and/or immune selective pressures.

Disclosures: Michael G. Ison, MD MS, AlloVir (Consultant)

521. Similarities and Differences in Transcriptomic Host Response between SARS-CoV-2 and Other Viral Infections

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Background: COVID-19 is a pandemic caused by the SARS-CoV-2 virus that shares and differs in clinical characteristics of known viral infections.

Methods: We obtained RNAseq profiles of 62 prospectively enrolled COVID-19 patients and 24 healthy controls (HC). We collected 23 independent studies profiling 1,855 blood samples from patients covering six viruses (influenza, RSV, HRV, Ebola, Dengue and SARS-CoV-1). We studied host whole-blood transcriptomic responses in COVID-19 compared to non-COVID-19 viral infections to understand similarities and differences in host response. Gene signature threshold was absolute effect size ≥1, FDR ≤ 0.05%.

Results: Differential gene expression of COVID-19 vs HC are highly correlated with non-COVID-19 vs HC (r=0.74, p< 0.001). We discovered two gene signatures: COVID-19 vs HC (2002 genes) (COVIDsig) and non-COVID-19 vs HC (635 genes) (nonCOVIDsig). Pathway analysis of over-expressed signature genes in COVIDsig or nonCOVIDsig identified similar pathways including neutrophil activation, innate immune response, immune response to viral infection and cytokine production. Conversely, for under-expressed genes, pathways indicated repression of lymphocyte differentiation and activation (Fig1).

Intersecting the two gene signatures found two genes significantly oppositely regulated (*ACO1*, *ATL3)*. We derived a third gene signature using COCONUT to compare COVID-19 to non-COVID-19 viral infections (416 genes) (Fig2). Pathway analysis did not result in significant enrichment, suggesting identification of novel biology (Fig1).

Statistical deconvolution of bulk transcriptomic data found M1 macrophages, plasmacytoid dendritic cells, CD14+ monocytes, CD4+ T cells and total B cells changed in the same direction across COVID-19 and non-COVID-19 infections. Cell types that increased in COVID-19 relative to non-COVID-19 were $CD56^{bright}$ NK cells, M2 macrophages and total NK cells. Those that decreased in non-COVID-19 relative to COVID-19 were $CD56^{dim}$ NK cells & memory B cells and eosinophils (Fig3).

Figure 1

Fig1. Heatmap of the significance level in each gene set of interest including COVID-19 vs HC (+) and (-), non-COVID-19 viral vs HC (+) and (-), and COVID-19 vs non-COVID-19 viral (+) and (-) and combinations of the intersect of COVID-19 vs HC with non-COVID-19 viral. Scale in heatmap is from 1 to 10 for the significance level.

Figure 2

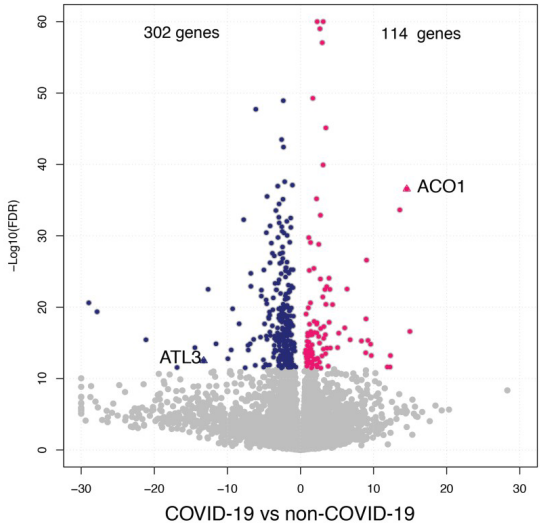

Fig2. Using COCONUT conormalized data, we compared head-to-head COVID-19 versus non-COVID-19 viral infections . Significance score [defined as -log10(FDR)] vs mean difference of co-normalized log2-transformed expression data between COVID-19 patients (n = 62) vs other viral infections (n = 652). The chosen cutoff of ES ≥ 1 or ≤ -1 with FDR ≤ 0.05% yields 416 COVID-19 specific signature, including 114 positively regulated genes and 302 negatively regulated genes.

Figure 3

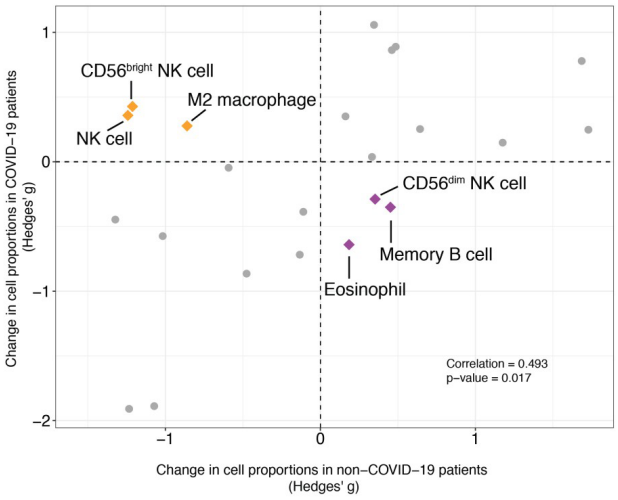

Fig3. Concordant and discordant changes in cellular proportions estimated with statistical deconvolution of bulk transcriptomic data comparing COVID-19 to non-COVID-19 viral infections. Cell types that increased in COVID-19 (hence decreased in non-COVID-19) were CD56^{bright} NK cells, M2 macrophages, and total NK cells. Those that decreased in non-COVID-19 but increased in COVID-19 were CD56^{dim} NK cells, memory B cells, and eosinophils. c) Concordant and discordant changes in cellular proportions comparing COVID-19 to non-COVID-19 viral infections. Cell types that increased in COVID-19 (hence decreased in non-COVID-19) were CD56^{bright} NK cells, M2 macrophages, and total NK cells. Those that decreased in non-COVID-19 but increased in COVID-19 were CD56^{dim} NK cells, memory B cells, and eosinophils.

Conclusion: The concordant and discordant responses mapped here provide a window to explore the pathophysiology of COVID-19 vs other viral infections and show clear differences in signaling pathways and cellularity as part of the host response to SARS-CoV-2.

Disclosures: Simone A. Thair, PhD, Inflammatix, Inc. (Employee, Shareholder) Yudong He, PhD, Inflammatix Inc. (Employee) Yehudit Hasin-Brumshtein, PhD, Inflammatix (Employee, Shareholder) Suraj Sakaram, MS in Biochemistry and Molecular Biology, Inflammatix (Employee, Other Financial or Material Support, stock options) Rushika R. Pandya, MS, Inflammatix Inc. (Employee, Shareholder) David C. Rawling, PhD, Inflammatix Inc. (Employee, Shareholder) Purvesh Khatri, PhD, Inflammatix Inc. (Shareholder) Timothy Sweeney, MD, PHD, Inflammatix, Inc. (Employee, Shareholder)

522. The Simple and Novel SAS Score to Predict Mortality at Presentation in 2541 Hospitalized COVID-19 Patients

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Background: The clinical spectrum of the novel corona virus disease 2019 (COVID-19) ranges from mild to severe disease and death. We aim to construct a simple and novel scoring model that will predict mortality events in hospitalized COVID-19 patients.

Methods: We established a retrospective cohort of 2541 patients admitted with COVID-19 from February 19, 2020 to April 28, 2020 to Henry Ford Health System, MI. Sociodemographic data, comorbidities, and clinical data were collected. Our novel SAS score was constructed using 3 easily available parameters, namely **S**ex, **A**ge, and Oxygen **S**aturation at presentation (Table 1 and 2). Primary endpoint was mortality. Multivariate analysis with logistic regression was done and the model was assessed using receiver operating characteristic (ROC) with area under ROC (AUROC) to determine the optimal cutoff for sensitivity, specificity, and positive and negative predictive values.

Table 1. The SAS score points calculator

Variable	Points
Sex	
Female	0
Male	1
Age in years	
≤60	0
61-70	1
71-80	2
>80	3
SpO2 %	
>94	0
90-94	1
<90	2

Abbreviations: SpO2, oxygen saturation

Table 2. Clinical characteristics of 2541 hospitalized patients with COVID-19

Characteristic	Survivors N=2081	Non-Survivors N=460	*P* Value
Age Mean (SD)	61.2 (16.0)	75 (13.8)	<0.0001
Age ≥65 N (%)	892 (42.86)	371 (80.65)	<0.0001
Male gender N (%)	1036 (49.78)	262 (56.96)	0.005
Race N (%)			
Black	1198 (57.57)	213 (46.3)	<0.0001
White	645 (31)	207 (45)	
Asian	43 (2.1)	4 (0.87)	
Other	195 (9.37)	36 (7.83)	
	N=1966	N=424	
BMI Median (IQR)	31 (26.5-36.7)	27.6 (23.4-32.5)	<0.0001
BMI ≥30 N(%)	1099 (52.81)	151(32.83)	<0.0001
Comorbidities N (%)			
Lung	1330 (63.91)	289 (62.83)	0.661
Immunodeficiency	24 (1.15)	6 (1.30)	0.786
Cardiac disease	156 (7.5)	66 (14.35)	<0.0001
CKD	800 (38.44)	299 (65)	<0.0001
COPD	299 (11)	96 (20.87)	<0.0001
Hypertension	1343 (64.54)	320 (69.57)	0.040
Asthma	216 (10.38)	35 (7.61)	0.072
Cancer	285 (13.7)	95 (20.65)	0.0002
Diabetes	771 (37.1)	184 (40)	0.237
Max mSOFA score Median (IQR)	2 (1-4)	7 (5-9)	<0.0001
SOFA Category N (%)			
0-1	488 (32.38)	9 (2.41)	<0.0001
2-4	715 (47.45)	84 (22.52)	
≥5	304 (20.17)	280 (75.1)	
Maximum pulse oximetry Median (IQR)	92 (90-94)	89 (82-92)	<0.0001
Saturation categories N (%)			
≥95			<0.0001
90-94	463 (22.25)	41 (8.91)	
86-89	1099 (52.81)	176 (38.26)	
≤85	232 (15.52)	85 (18.48)	
	196 (9.42)	158 (34.35)	
Treatments N (%)			
Hydroxychloroquine	1666 (80.1)	319 (69.35)	<0.0001
Azithromycin	740 (35.56)	190 (41.3)	0.021
Methylprednisolone	1135 (54.54)	321 (69.78)	<0.0001
Prednisone	547 (26.3)	85 (18.48)	0.001
Tocilizumab	62 (2.98)	52 (11.3)	<0.0001
ICU admission N (%)	333 (16)	281 (61.1)	<0.0001
ICU days Median (IQR)	7 (4-12)	9 (5-14)	0.001
Mechanical ventilation N (%)	193 (9.27)	255 (55.43)	<0.0001
Ventilator days N (%)	8 (4-12)	9 (4-13)	0.207

Abbreviations: SD, standard deviation; BMI, body mass index; IQR, interquartile range; CKD, chronic kidney disease; COPD, chronic obstructive pulmonary disease; mSOFA, modified SOFA (Sequential organ failure assessment) score; ICU, intensive care unit.

Results: The mean age of survivors was 61 compared to 75 years for non-survivors (standard deviation 16 vs 13.8, p< 0.0001), and 1298 (51.1%) were men. Multivariate