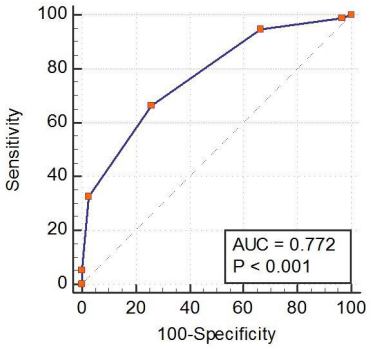
Figure 2. Receiver Operating Characteristic (ROC) Curve for Intensive Care Unit Admission



Criterion	No ICU	ICU
0	7 (3.3%)	1 (1%)
1	65 (30.2%)	4 (4.1%)
2	87 (40.5%)	28 (28.6%)
3	50 (23.3%)	33 (33.7%)
4	6 (2.8%)	27 (27.6%)
5	0	5 (5.1%)
Total	215	98

Data are presented as absolute value (percentage).
Abbreviations: AUC, area under the curve; ICU, intensive care unit

Disclosures: **All Authors**: No reported disclosures

62. Association Between Influenza Co-infection and Poor Outcomes in Patients Hospitalized with COVID-19

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Session: O-12. COVID-19 Clinical Calls and Indicators 2

Background: In December 2019, a novel coronavirus (COVID-19) infection emerged in Wuhan, China, establishing itself as a deadly pathogen leading to an ongoing pandemic. The incidence of co-infection of COVID-19 and Influenza has not been widely reported. Both infections have been known to share similar mechanisms of transmission, however currently, there is no evidence regarding the relationship between co-infection between this viruses and worsening outcomes. Once social distancing measures are eased, and daily activities resumed, there is a possibility for a second wave of cases. Given the incidence of influenza is higher during winter, a higher co-infection rate is expected in these months.

Methods: In this study, the aim was to assess the association of influenza co-infection with outcomes in patients diagnosed with COVID-19 in a hospital-based case-control study in Bronx, New York. 19 patients with Influenza co-infection were found in total. 1 patient did not meet inclusion/exclusion criteria. Charts were reviewed from 18 confirmed cases of influenza and COVID-19 patients. Controls were selected from the remaining pool of patients with COVID-19 in the same period. Cases were matched for age, sex and underlying comorbidities (Hypertension, Diabetes Mellitus, liver disease, cardiovascular disease, HIV status, immunocompromised state other than HIV). The measured outcomes were: in-hospital mortality, need for mechanical ventilation, need for vasopressors and need for renal replacement therapy. For each outcome, Chi Square test and Odds ratio were obtained.

Results: After statistical analysis, no significative difference was found in the following variables: in-hospital mortality [Odds ratio (OR) 0.769; 95% confidence interval (CI): 0.185–3.191; p value= 0.717], need for mechanical ventilation (OR 1.3; 95% CI: 0.313–5.393; p value= 0.717), need for vasopressors (OR 1.923; 95% CI: 0.383–9.646; p value= 0.423), need for renal replacement therapy (OR 1.0; 95% CI: 0.208–4.814; p value= 1.0).

Conclusion: There was no difference in the outcome in COVID-19 patients co-infected with influenza compared to non co-infected patients, however, a larger sample of cases will be needed for further assessment of these outcomes.

Disclosures: **All Authors**: No reported disclosures

63. Prognosis of COVID-19 Patients with Diabetic Ketoacidosis with or Without Hyperosmolar Hyperglycemic State

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Session: O-12. COVID-19 Clinical Calls and Indicators 2

Background: One of the risk factors for poor outcome with SARS-CoV-2 infection is diabetes mellitus; diabetic ketoacidosis (DKA) and hyperosmolar hyperglycemic state (HHS) are the most serious complications of diabetes mellitus. We aimed to explore the clinical characteristics and outcomes of COVID-19 patients presenting with isolated DKA or combined DKA/HHS to our institution.

Methods: A retrospective, hospital based observation case series was performed on patients with SARS-CoV-2 admitted to Intensive Care Unit between 03/20/20 and 04/20/20. Inclusion criteria were: 1) Blood Glucose >250mg/dL; 2) Serum bicarbonate < 18 mmol/L; 3) Anion Gap >10; 4) serum pH < 7.3; 4) ketonemia or ketonuria; and 5) positive SARS-CoV-2 RT-PCR. Hyperosmolality, on the other hand, was defined as an effective/calculated plasma osmolality >304 mOsm/kg.

Results: A total of 87 patients with COVID-19 were admitted to the ICU during the study period, 12 of them had either isolated DKA or DKA/HHS. Baseline demographics, lab values and outcome are summarized in Table 1. Six of the patients had isolated DKA and six had combined DKA and HHS. The median age for the patient was 49.5 years old (range from 19 to 62 years old). The male to female ratio was 5:1. Of the 12 patients, 10 patients (83%) had a history of DM, nine were type 2 and only one type 1; two patients were newly diagnosed DM, presenting as DKA, presumptively precipitated by COVID-19. Five patients (42%) had a BMI >30 kg/m2. As for ethnicity; seven were Hispanic (59%), four African American (33%), and one Caucasian (8%).

Patients with combined DKA/HHS, higher BMI, higher HbA1c, severe acidosis tended to have higher mortality. The striking feature was that isolated DKA or combined DKA/HHS was the initial presentation for COVID-19 for most of the cases.

Table 1: Demographic characteristic, inflammatory markers and outcome.

Cases	Age	Sex	Ethnicity	BMI	HbA1c	Admitting BG	pH	Bicarb	Anion gap	BHOB	Calculated serum osmolarity	CRP	LDH	D-dimer	Ferritin	Outcome
1	24	F	Hispanic	28.9	11.4	319	7.11	18	15	3.64	282	4.5	181	N/A	313	Stable
2	51	M	Hispanic	24	13.5	901	6.9	2.2	>29	>4.5	302	5.6	469	3820	1322	Stable
3	45	F	Caucasian	28.1	9.2	324	6.8	1.6	24	N/A	298	6.5	201	19300	320	Stable
4	33	M	AA	40.7	13.5	404	7.3	9.4	24	>4.5	282	1.7	253	346	389	Stable
5	48	M	AA	25.2	13.6	1130	7.2	9.1	33	>4.5	365	8.3	263	4120	909	Stable
6	52	M	AA	23.6	12.1	683	7.24	11	21	>4.5	318	11.2	691	1220	1650	Stable
7	52	M	Hispanic	33	>16	454	7.12	13	28	>4.5	289	16.8	753	63735	848	MV
8	19	M	AA	58.9	10.9	1112	7.1	8	32	>4.5	307	8.1	695	1234	1628	Expired
9	38	M	Hispanic	24.2	N/A	1070	6.77	<5	>29	>4.5	347	2.6	275	834	807	Expired
10	62	M	Hispanic	34.5	12	326	7.29	16	18	3.27	287	17	396	578	396	Expired
11	62	M	Hispanic	24.1	13.3	604	7	6	29	N/A	323	13.2	397	1060	6671	Expired
12	62	M	Hispanic	30.5	N/A	959	6.86	6.6	>29	>4.5	358	N/A	N/A	N/A	3400	Expired
Average	**45.7**			**31.3**	**12.2**	**690.5**	**7.06**	**9.2**	**24.9**		**313**	**8.7**	**415.8**	**9624.7**	**1554.4**	
Median	**49.5**			**28.5**	**12.1**	**643.5**	**7.105**	**9.1**	**24**		**304.5**	**8.1**	**396**	**1227**	**878.5**	

Table 1: Demographic characteristic, inflammatory markers and outcome.

F (Female), M (Male), BMI (Body Mass Index), HbA1c (Hemoglobin A1c, normal range 4-5.6%), BG (blood glucose, normal range 70-140 mg/dL), pH (normal range 7.34-7.44), Bicarb (Bicarbonate, normal range 20-31 mmol/L), CRP (C-reactive protein, normal range 0-0.8 mg/dL), LDH (lactate dehydrogenase, normal range 122-222 U/L), D-dimer (0-500 ng/mL), Ferritin (24-336 ng/mL), Anion gap (5-15 mmol/L), BHOB (beta-hydroxybutyrate, normal range 0.02-027 mmol/L), Serum osmolality (278-305 mOsm/kg), MV (Mechanical Ventilation), N/A (not available)

Conclusion: Our observational retrospective case series reinforces the need to watch for new onset DM and monitor blood sugar closely in those with known diabetes mellitus during SARS-CoV-2 infection, in order to avoid such serious complications as DKA and HHS.

Disclosures: **Jihad Slim, MD**, **Abbvie** (Speaker's Bureau)**Gilead** (Speaker's Bureau)**Jansen** (Speaker's Bureau)**Merck** (Speaker's Bureau)**ViiV** (Speaker's Bureau)

64. Metagenomic Sequencing to Identify Alternative Infections and Co-infections in Persons Under Investigation for covid-19

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Background: Broad testing for respiratory viruses among persons under investigation (PUI) for SARS-CoV-2 is performed inconsistently, limiting our understanding of alternative infections and co-infections in these patients. Here, we used unbiased metagenomic next-generation sequencing (mNGS) to assess the frequencies of 1) alternative viral infections in SARS-CoV-2 RT-PCR negative PUIs and 2) viral co-infections in SARS-CoV-2 RT-PCR positive PUIs.

Methods: A convenience sample set was selected from PUIs who were tested for SARS-CoV-2 in the Emory Healthcare system during the first 2 months of the pandemic from 02/26-04/23/20. Laboratory results were extracted by chart review; Flu/RSV and multiplex respiratory pathogen PCRs had been performed at the discretion of treating physicians. Excess nasopharyngeal swab samples were retrieved within 72 hours of collection and underwent RNA extraction and SARS-CoV-2 testing by triplex RT-PCR. mNGS was performed by DNAse treatment, random primer cDNA synthesis, Nextera XT tagmentation, and high-depth Illumina sequencing. Reads underwent taxonomic classification by KrakenUniq, as implemented in viral-ngs.

Results: 53 PUIs were included, 30 negative and 23 positive for SARS-CoV-2 by RT-PCR. Among SARS-CoV-2 negative PUIs, 28 (93%) underwent clinical testing for alternative infections, and 8 (29%) tested positive for another respiratory virus. In all cases, mNGS identified the same virus (**Table 1**). In another 3 PUIs, mNGS identified two viruses that were not tested for and one that was missed by routine testing. No SARS-CoV-2 was detected by mNGS among RT-PCR negative PUIs. Among SARS-CoV-2 RT-PCR positive PUIs, 18 (69%) underwent clinical testing for co-infections, and none were detected. mNGS did not identify any viral co-infections but did detect SARS-CoV-2 in all 23 PUIs.