Association of SARS-CoV-2 Genomic Load in Nasopharyngeal Samples with Adverse COVID-19 Patient Outcomes: A Retrospective Analysis from an Academic Hospital Center in New York City

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A. BACKGROUND

- SARS-CoV-2 virus has caused more than 37 million cases of Coronavirus Disease 2019 (COVID-19) worldwide and has overwhelmed the healthcare systems.[1]
- Identifying patients who are at high risk for poor outcomes is critically important.[2]
- We aimed to study the association of SARS-CoV-2 genomic load in nasopharyngeal samples at the time of hospital admission with clinical outcomes of patients with COVID-19 infection.
- We used the **Cycle threshold (Ct) value**, the number of amplification cycles needed to yield a positive fluorescent signal in a real-time reverse transcription-polymerase chain reaction test (RT-PCR), as a **surrogate for viral load**.

B. METHODS

Study Design:

- We conducted a retrospective cohort study at the NYU Langone Medical Center.
- **Study period:** March 31st- April 10th 2020.
- We evaluated all patients who presented to the emergency department with clinical and radiographic findings of viral pneumonia and positive SARS-CoV-2 who required hospitalization.
- The **qualitative Cepheid Xpert® Xpress SARS-CoV-2 assay** was used for in-house diagnosis of COVID-19.[3]
- We categorized Ct values into 3 SARS-CoV-2 genomic load groups based on tertiles:
  - Low ≥34.2
  - Intermediate 27.2-34.2
  - High ≤27.7

Outcomes of interest:

- The **main outcome of interest** was the **association of the genomic load** in patients admitted to the hospital with COVID-19 pneumonia with the **composite outcome of death or discharge to hospice care, use of mechanical ventilation or extracorporeal membrane oxygenation (ECMO).**
- Results were adjusted for patient demographics, Body Mass Index (BMI), smoking history, comorbidities, transplant status, Pneumonia Severity Index (PSI), and duration of symptoms.

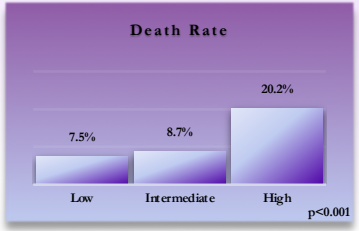
C. RESULTS

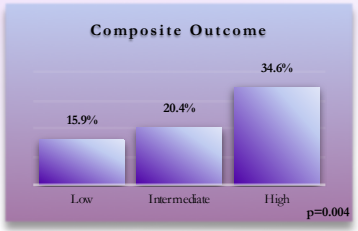
- **314** out of 457 patients who presented to the emergency department with positive swab for SARS-CoV-2 during the study period met the inclusion criteria and were **included in the final analysis**.
- Of the 314 included patients, **107 (34.1%)** were categorized in the **low**, **103 (32.8%)** in the **intermediate**, and **104 (33.1%)** in the **high** SARS-CoV-2 genomic load category.

Patient Characteristics	Low	Intermediate	High
Age (years)			
18-44	14 (13.1%)	10 (9.7%)	13 (9.6%)
45-64	52 (48.6%)	35 (34.0%)	38 (36.5%)
≥65	41 (38.3%)	58 (56.3%)	53 (50.9%)
Race/Ethnicity			
White	44 (41.1%)	54 (52.4%)	42 (40.4%)
Black	11 (10.3%)	12 (11.7%)	18 (17.3%)
Hispanic	11 (10.3%)	10 (9.7%)	14 (13.5%)
Other/Unknown	41 (38.3%)	25 (35.2%)	30 (28.8%)
Gender			
Female	39 (36.4%)	38 (36.9%)	32 (30.8%)
Male	68 (63.6%)	65 (63.1%)	72 (69.2%)
Obesity (BMI≥30)	44 (41.1%)	39 (37.9%)	34 (32.7%)
CCI*			
Low#	**58 (54.2%)**	**41 (39.8%)**	**35 (33.7%)**
Medium	**33 (30.8%)**	**28 (27.2%)**	**36 (34.6%)**
High	**16 (15.0%)**	**34 (33.0%)**	**33 (31.7%)**
Transplant history*	**2 (1.9%)**	**4 (3.9%)**	**15 (14.4%)**
Symptoms for ≤7d*	**47 (43.9%)**	**63 (61.2%)**	**68 (65.4%)**

Footnote: BMI=Body Mass Index, **CCI**= Charlson Comorbidity Index, **#CCI Classification:** Low=1-2, Medium=3-4, High≥5, **d**=days, * Statistically Significant

Figure 1. Association of SARS-CoV-2 genomic load in nasopharyngeal swabs at the time of hospital admission with patient outcomes.

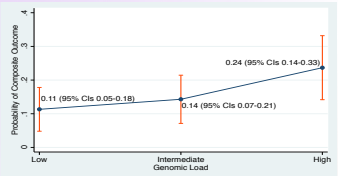




C. RESULTS

- **High genomic load** remained an **independent risk factor for the composite outcome (OR 1.59); p= 0.02)** after **adjusting** for patient **age**, **gender**, **BMI**, **Charlson Comorbidity Index**, **smoking** and **transplant** history, **duration of symptoms**, and **PSI**.
- Duration of symptoms (OR 0.93; p= 0.05) and pneumonia severity index at the time of admission (OR 3.7; p<0.01) were also significantly associated with the composite outcome in multivariate analysis.

Figure 2. Average risk for the composite outcome based on SARS-CoV-2 genomic load if when all the other variables of the multivariate analysis were fixed at their means.



D. CONCLUSIONS

We showed that SARS-CoV-2 genomic load is a predictor of poor outcomes in patients admitted to the hospital with COVID-19 pneumonia, that above and beyond age, comorbidities, and severity of illness on presentation, may be used to risk-stratify patients, in an era where appropriate triaging is of utmost importance

E. REFERENCES

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F. ACKNOWLEDGEMENTS

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