

SARS-CoV-2 Exhibits Clade-Specific Differences in Nasopharyngeal Viral Loads

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Background

- The rapid spread of **SARS-CoV-2**, the causative agent of **COVID-19**, has been accompanied with the emergence of distinct viral clades
- Viral diversity has been identified through whole genome sequencing efforts
- Less is known about the viral kinetics affecting viral loads amongst different clades

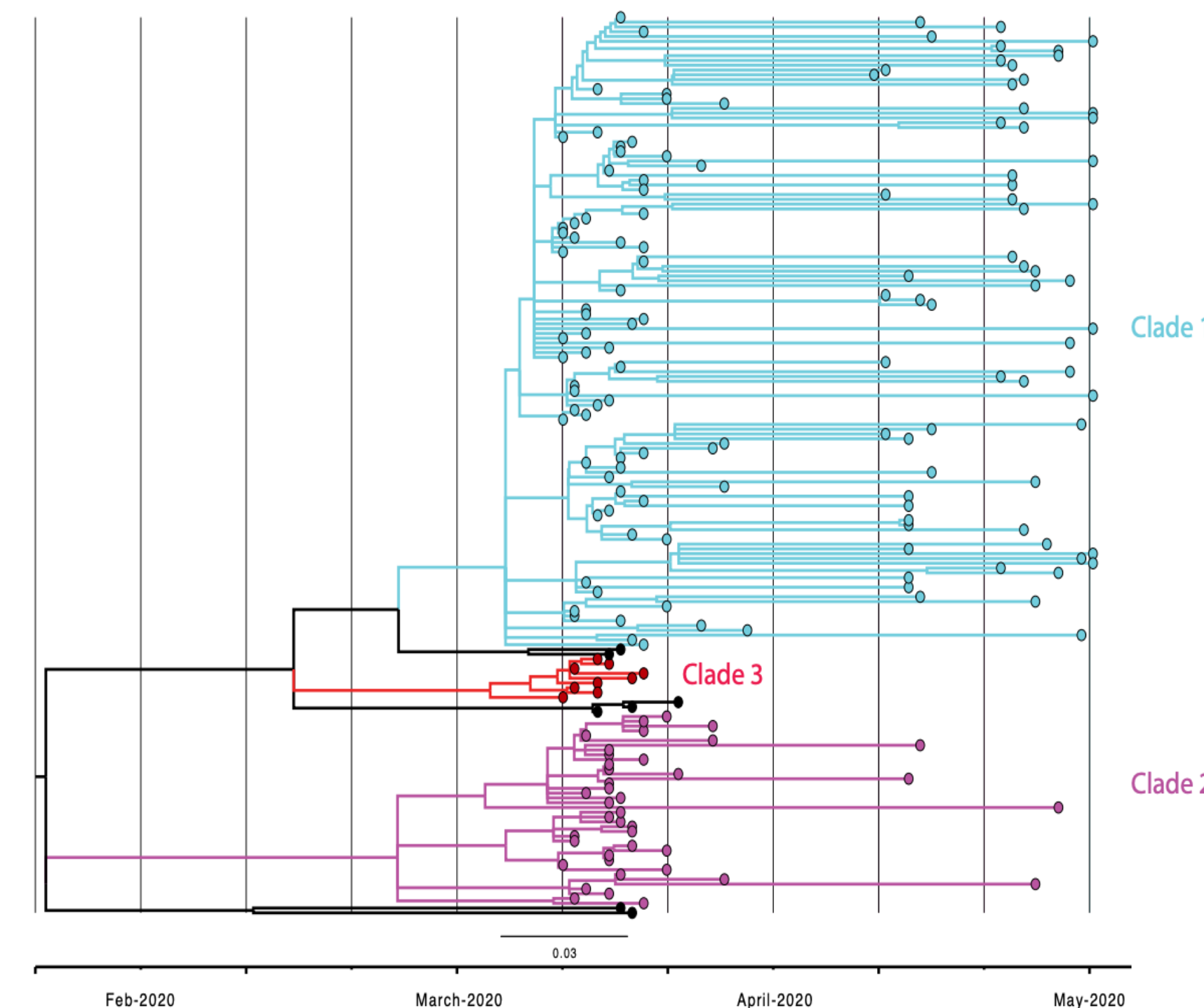
Objectives

- To assess the phylogenetics of SARS-CoV-2 over a limited period
- To determine if separate clades of SARS-CoV-2 display differences in viral replication and in turn
- To determine if differences in Ct value lead to differences in disease severity

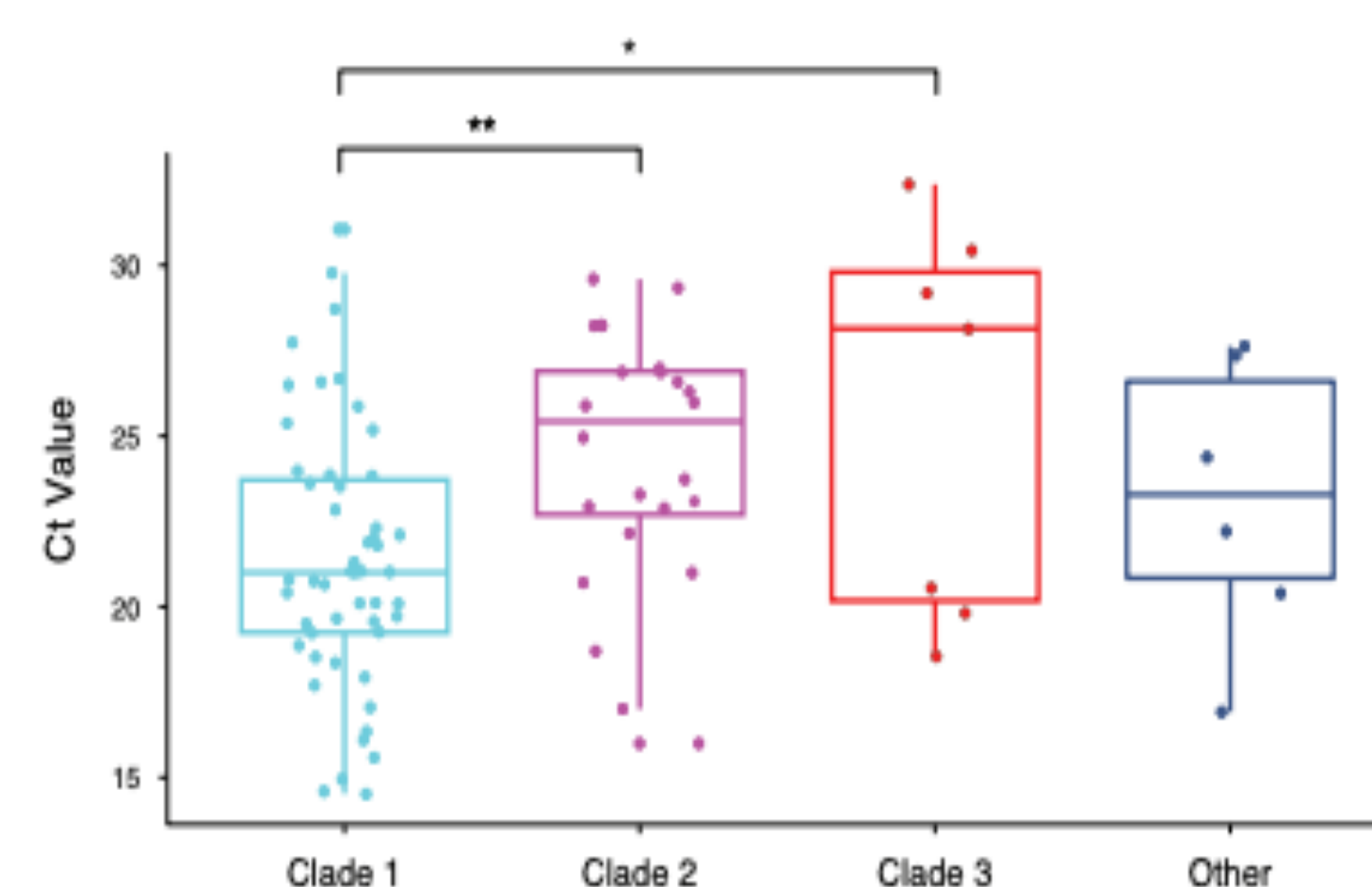
Methods

- **Sample Collection:** 88 total samples were collected from patients presenting to Northwestern Memorial Hospital from March 14, 2020 through May 1, 2020 with positive SARS-CoV-2 from nasopharyngeal swabs.
- **Sequencing:** Cycle threshold (Ct) values less than 35 were considered positive and whole genome sequencing was performed by reverse transcription, multiplex PCR, and deep sequencing.
- **Phylogenetic analysis:** Phylogenetic analysis was conducted relative to publicly available SARS-CoV-2 sequences. Sequence and viral load data were correlated to each clade.

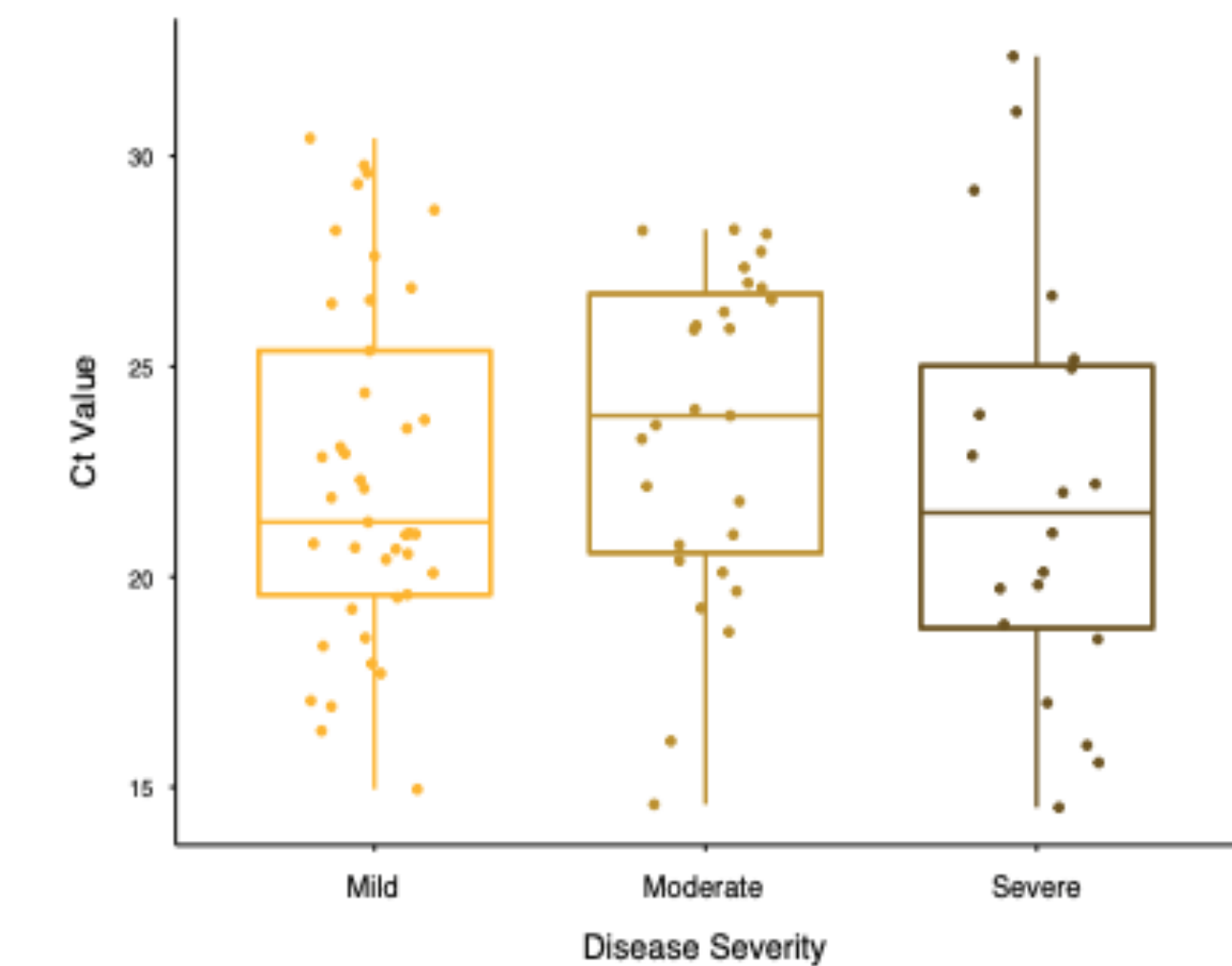
Phylogenetic Analyses of SARS-CoV-2 (Chicago)



Viral Clade and Ct Values



Ct Value and Disease Severity



Results

- Clade 1 viruses were shown to be rapidly expanding
- Clade 2 was uniquely predominant in Chicago with limited global distribution
- Clade 1 demonstrated significantly lower Ct values ($p=0.0062$) than both Clade 2 and Clade 3 despite no significant difference in time from symptom onset to specimen collection
- There was no significant differences in disease severity amongst the three clades

Conclusions

- SARS-CoV-2 genotype may impact viral load, which may in turn influence transmission and overall viral spread