Statewide Genomic Surveillance of SARS-CoV-2 Variants in Rhode Island

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INTRODUCTION

Background

- SARS-CoV-2, responsible for the COVID-19 pandemic, has caused significant global morbidity and mortality.
- Enhanced genomic surveillance efforts since 2020 have noted the continued emergence of novel SARS-CoV-2 variants with mutations that confer selective advantage in hosts.
- CDC categorizes circulating variants as variants being monitored (VBM), variants of interest (VOI), variants of concern (VOC), and variants of high consequence (VOHC).
- Changing variant landscape is concerning and highlights the need for continued molecular monitoring of SARS-CoV-2 variants in order to understand the clinical and public health impact of COVID-19.

Objective

- To describe statewide genomic surveillance efforts and characterize circulating SARS-CoV-2 variants in Rhode Island (RI) from the start of the COVID-19 pandemic.
- (See QR codes at the lower right of the poster for published reports of the presented data).

METHODS

- Deidentified RI SARS-CoV-2 sequences since the first case in the state in 2/2020, generated at authors, other academic settings, CDC, and commercial laboratories, were extracted from https://www.gisaid.org.
- Genomic and phylogenetic analyses including quality control were conducted with standard tools and custom python scripts. Sequences were classified per CDC definitions.
- Specific mutations that are characteristic of the most recent VBM Delta and VOC Omicron were explored outside of their designated lineages.

RESULTS

- 17,340 SARS-CoV-2 RI sequences were increasingly available between 2/2020-5/2022 (**Figure 1**).
- **Table 1** lists cases identified as VOCs and VBMs in RI, according to the current CDC definitions.
- Almost all described VOC and VBM, and multiple non-VOC/non-VBM lineages have been circulating in RI, with the variant landscape changing over time (**Figure 2**).
- Dynamics of variants circulating in RI paralleled the five major COVID-19 global waves, predominated by the Wuhan-Hu-1, D614G, Alpha, Delta, and Omicron variants, respectively (**Figure 3**).
- Phylogenetic analysis demonstrated expected clustering of local variants **(Figure 4)**.
- Genomic analysis revealed that local Delta or Omicron-defining mutations are not exclusive to those specific variants (**Figure 5**).

Figure 1. SARS-CoV-2 Sequencing in RI

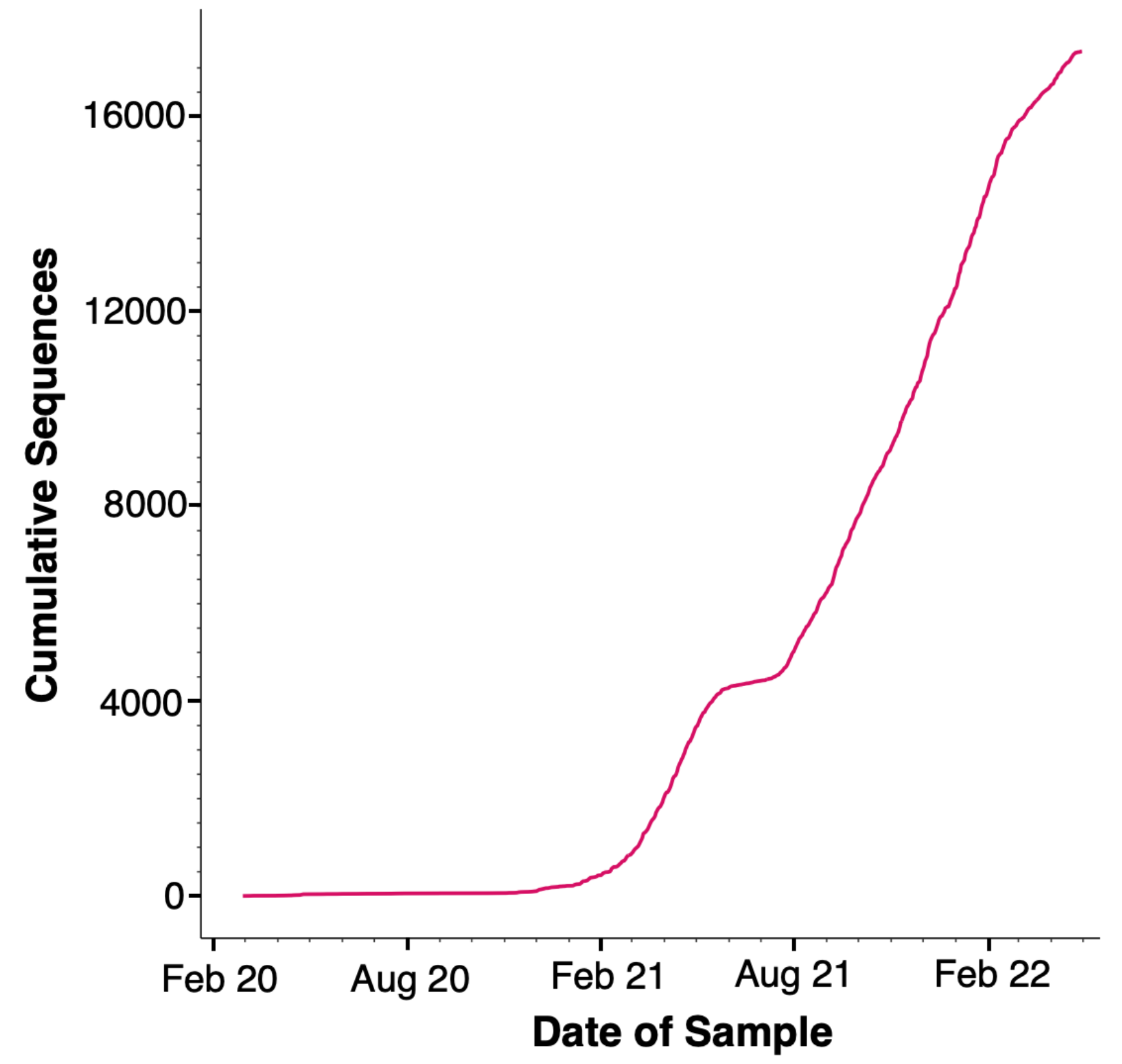


Table 1. SARS-CoV-2 VOC and VBM in RI

Variant of Concern	Country of Origin	Total Cases in RI	Range of Sampling Dates
Omicron (B.1.1.529 and BA lineages)	South Africa	5313	Nov 30, 2021 to Apr 30, 2022

Variant Being Monitored	Country of Origin	Total Cases in RI	Range of Sampling Dates
Delta (B.1.617.2 and AY lineages)	India	7567	Apr 20, 2021 to Feb 04, 2022
Alpha (B.1.1.7 and Q lineages)	UK	1415	Jan 19, 2021 to Jul 27, 2021
Beta (B.1.351 and sub-lineages)	South Africa	7	Mar 16, 2021 to May 25, 2021
Gamma (P.1 and sub-lineages)	Brazil	286	Mar 03, 2021 to Sep 27, 2021
Epsilon (B.1.427 and B.1.429)	California, USA	156	Jan 06, 2021 to May 04, 2021
Eta (B.1.525)	New York, USA	57	Feb 03, 2021 to Apr 27, 2021
Iota (B.1.526)	New York, USA	1051	Jan 07, 2021 to Jun 28, 2021
Kappa (B.1.617.1)	India	0	-
B.1.617.3	India	0	-
Mu (B.1.621, B.1.621.1)	USA	26	May 22, 2021 to Aug 10, 2021
Zeta (P.2)	Brazil	0	-

Figure 2. Proportions of VOC, VBM, and non-VOC/non-VBM in RI

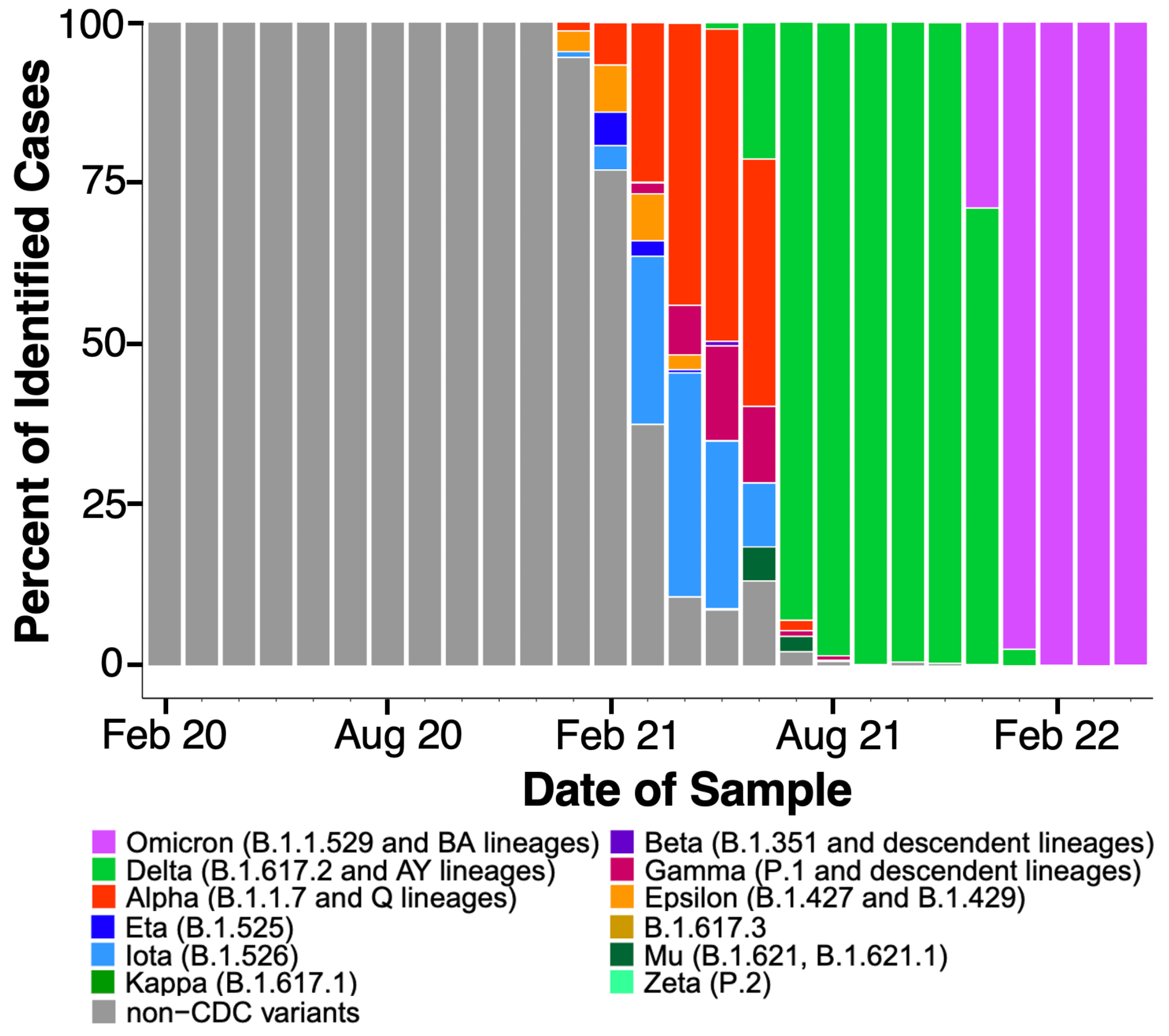


Figure 3. SARS-CoV-2 waves and cases in RI

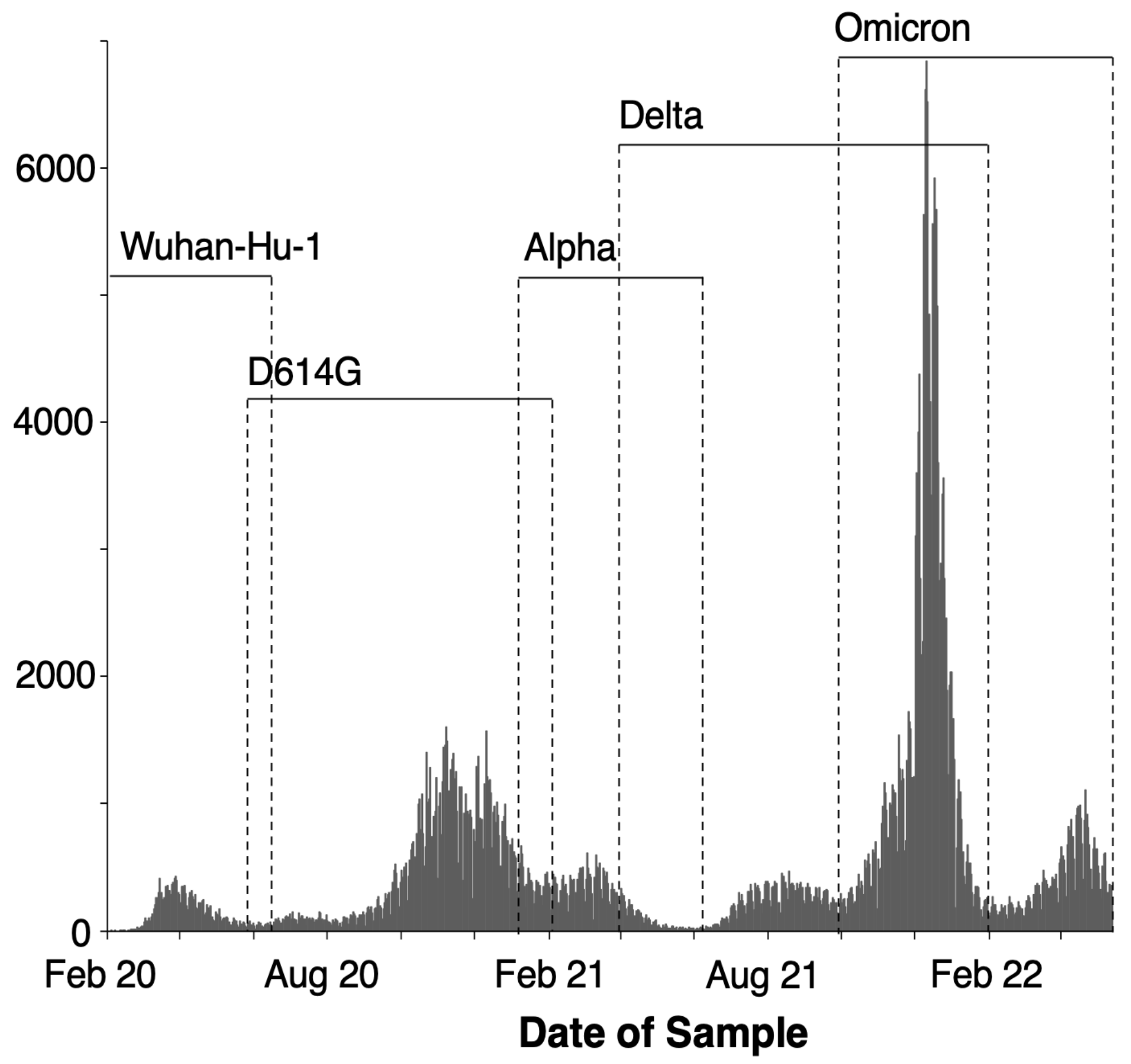


Figure 4. Phylogenetic tree of SARS-CoV-2 sequences in RI

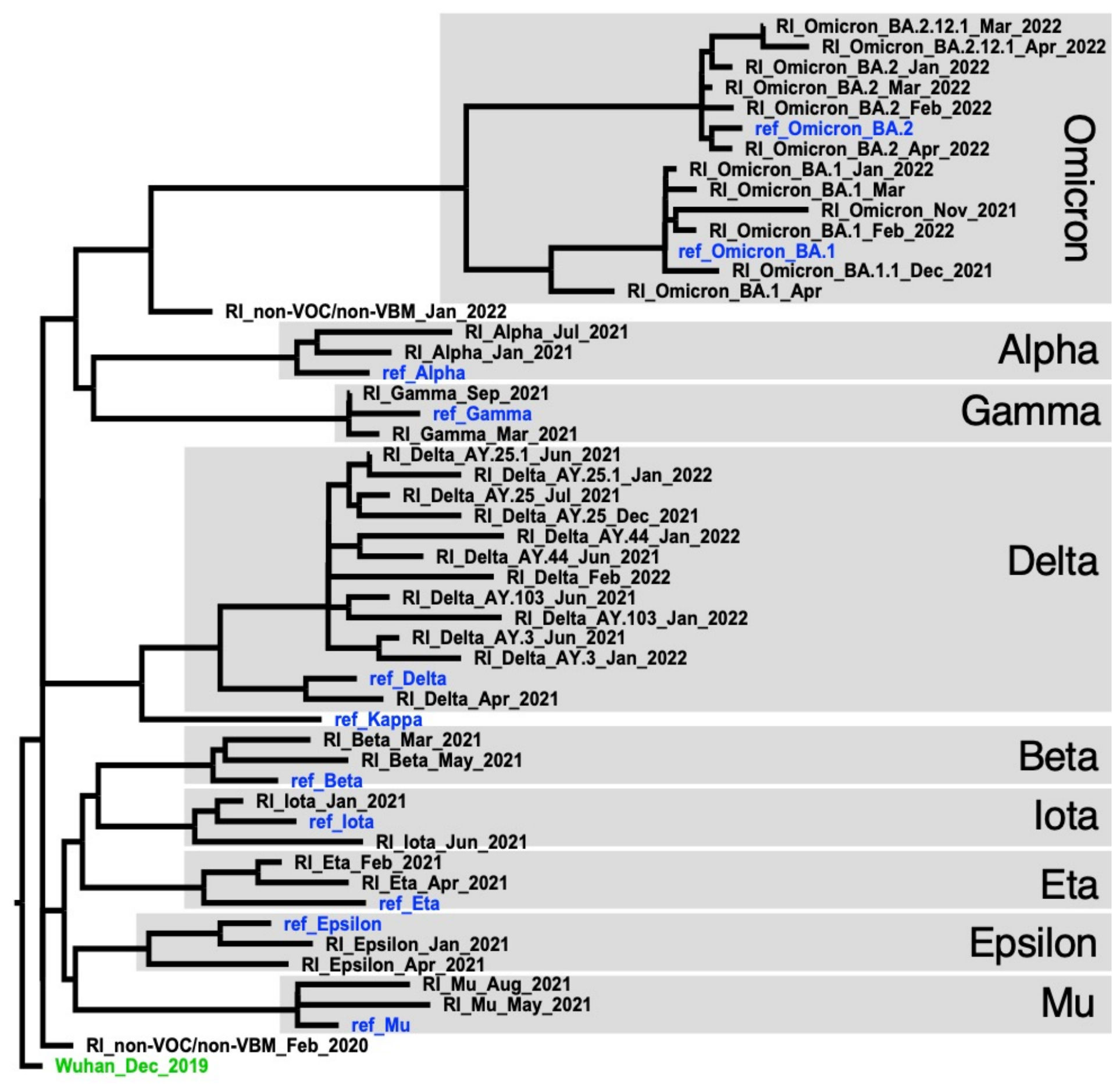
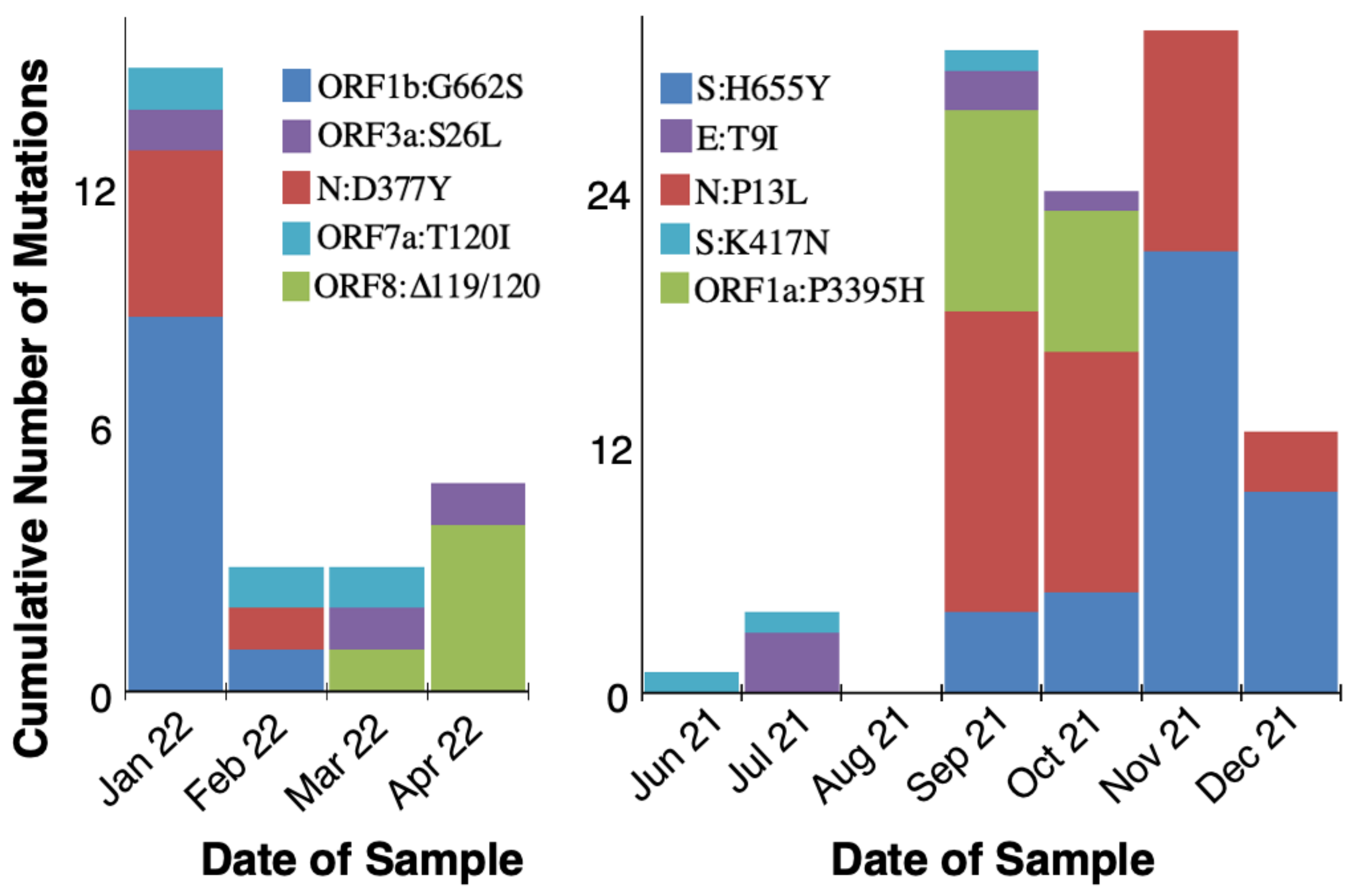


Figure 5. Left: Most common mutations unique to Delta occurring in Omicron sequences over time in RI. Right: Most common mutations unique to Omicron occurring in Delta sequences over time in RI.



CONCLUSIONS

- Enhanced statewide genomic surveillance allowed characterization of the RI variant landscape, capturing the clinical and public health impacts of COVID-19.
- SARS-CoV-2 has continued to evolve since its emergence, with or without epidemiologic impact, despite substantial scientific advances and mitigation efforts.
- Most recently, the VOC Omicron has become the predominant lineage in RI, the United States, and globally, attributed to its increased transmissibility compared to previous SARS-CoV-2 variants.
- The impact of continued SARS-CoV-2 genomic and mutational evolution beyond Omicron on public health remains to be determined.

Prior Report
Current Report

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