

Alaska COVID Genomic Surveillance

Situation Report

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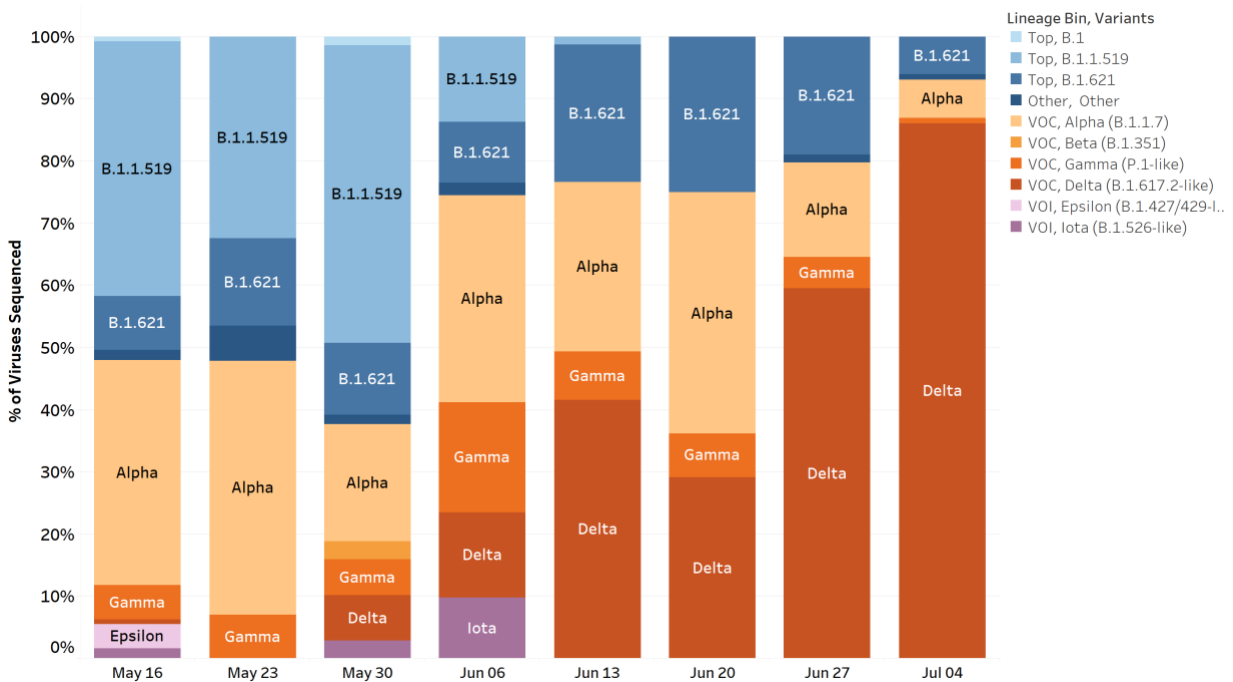
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Executive Summary: Sequence Analysis of COVID-19 in Alaska

- **Variant of Concern (VOC) infections make up 93% of recent cases.**
- **VOC Delta (B.1.617.2-like) accounts for most new detected cases.** To date, we have detected 251 cases in multiple locations across the state. During the week beginning July 4, VOC Delta represented 86% of sequenced cases in Alaska. According to data from the CDC, the proportion of cases attributed to VOC Delta nationwide is estimated to be 83% for the two-week period ending July 17.
- **VOC Alpha (B.1.1.7) proportion is appreciably declining.** To date, we have detected 416 cases across the state. During the week beginning July 4, VOC Alpha represented 6% of sequenced cases in Alaska down from 33% at the start of June. According to data from the CDC, Alpha proportions are decreasing and now represent 8% of cases nationwide ([CDC Variant Proportions website](#)).
- **Additional case of the VOC Gamma (P.1) detected.** To date, we have detected 71 cases across the state. During the week beginning July 4, VOC Gamma represented 1% of sequenced cases in Alaska. According to the CDC, Gamma proportions are 3% nationwide
- **No additional cases of VOC Beta (B.1.351) detected.**
- **No recent cases of Variant of Interest (VOI) Epsilon (B.1.429/427), Eta (B.1.525), Iota (B.1.526), or Zeta (P.2) detected.**

Recent Prevalence of Variants in Alaska



*Estimated prevalence per week period beginning on the date. This estimate is based on genome sequencing from a non-targeted convenience sample of cases. This estimate excludes cases sequenced from targeted contact tracing. As sequencing effort increases and the number of genome sequences increases, the estimate will better reflect the population.

Variants of Concern/Interest

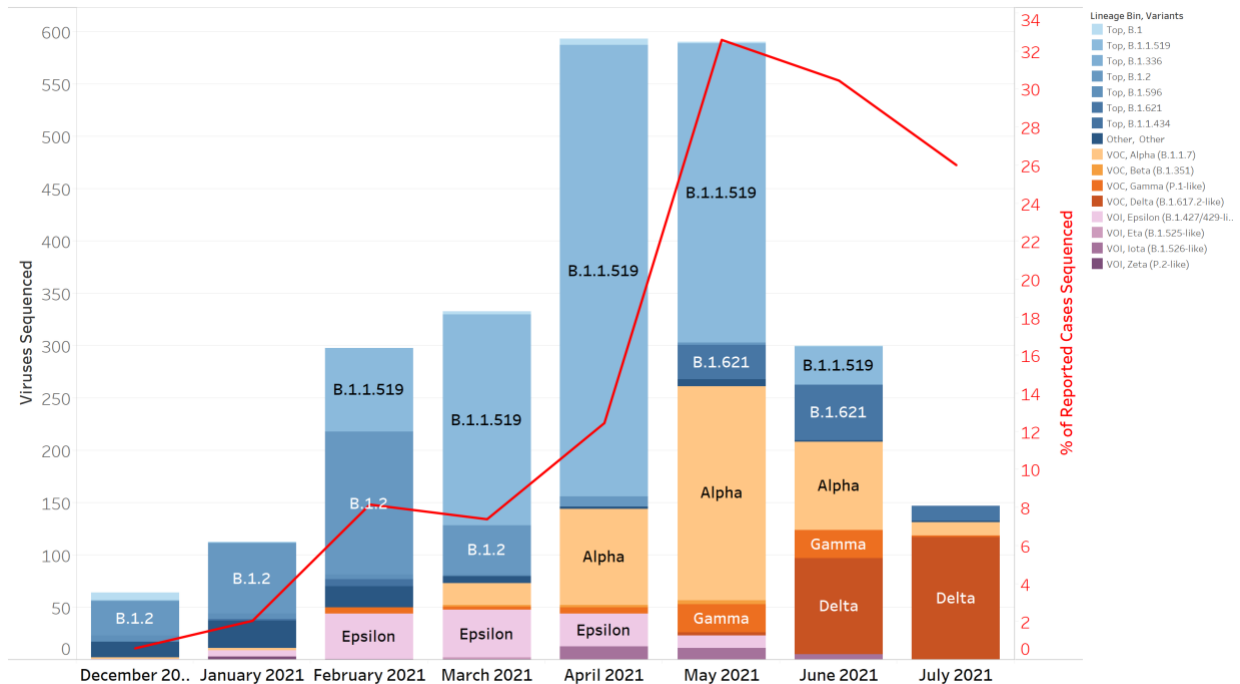
Name	Lineages	Cases Detected	Change from Previous Report*	First Identified in Alaska
VOC Alpha	B.1.1.7	416	+5	20 December 2020
VOC Beta	B.1.351	7	0	20 March 2021
VOC Gamma	P.1-like	71	+1	8 February 2021
VOC Delta	B.1.617.2-like	251	+137	30 May 2021
VOI Epsilon	B.1.427/429	139	0	24 December 2020
VOI Eta	B.1.525	1	0	16 March 2021
VOI Iota	B.1.526	30	0	4 February 2021
VOI Zeta	P.2	4	0	27 January 2021

*Detected variants are identified from sequencing a combination of retrospective and contemporary SARS-CoV-2 positive specimens. Therefore, changes to the previous report do not always reflect recent collections but add to the overall understanding of variant proportions

Table: Genomic Sequencing Effort in Alaska

	Samples
New Genomes released since last report	+152
Total Genomes released on GISAID	2753

Variants Identified in Alaska



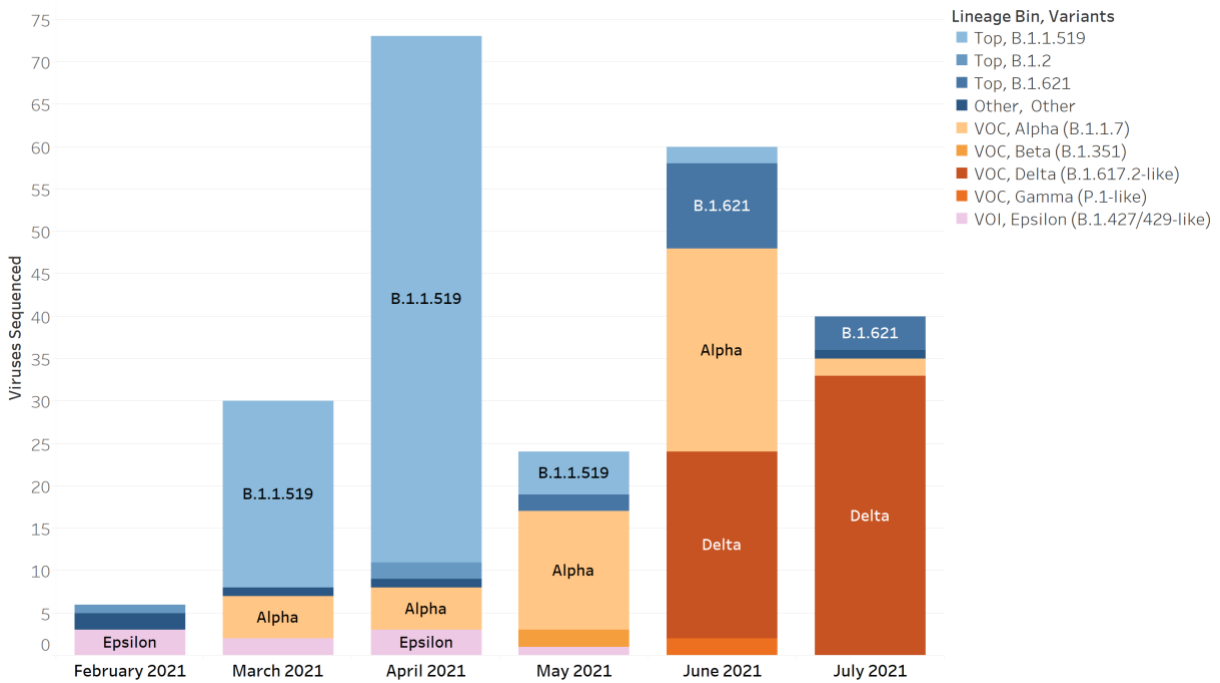
*Note that SARS-CoV-2 genome sequencing may not be a random sample of all cases. This figure does not estimate the prevalence of the population.

Table: Vaccine Breakthrough Investigation

Patients under investigation for Vaccine Breakthrough VB	869
Specimens submitted to SPHL for VB investigation	447 (51.4%)
Specimens fitting criteria for sequencing	339
Sequencing effort to assess VB	325
Successful virus lineage identifications	235 (72.3%)
Specimens in progress	14

Vaccine breakthrough refers to cases of COVID-19 which occur 14 or more days after receiving the second dose in a two-dose COVID-19 vaccine series or a single dose of a one-dose COVID-19 vaccine series. VBs may have a very low virus titer and are difficult to sequence.

Identified Vaccine Breakthrough Lineages

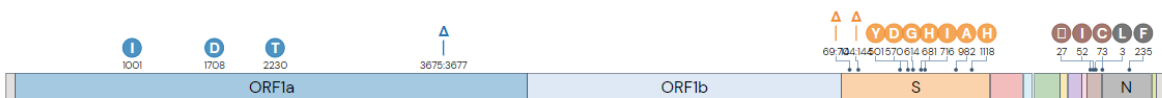


Variants of Concern, Individual Lineage Reports

Alpha - B.1.1.7

Alpha was first identified in the United Kingdom, also known as: Variant of Concern B.1.1.7, 202012/01, VOC-202012/01, 20B/501Y.V1, 20I/501Y.V1. This variant contains the N501Y mutation and a short deletion in the Spike (S) protein. This variant is concerning because it has shown to be significantly more transmissible (~50%) than the original SARS-CoV-2 lineages, and recent analyses from the United Kingdom suggest that B.1.1.7 cases are more likely to require hospitalization. B.1.1.7 does not appear to evade vaccine-induced neutralizing antibody responses. B.1.1.7 is widely circulating in the US.

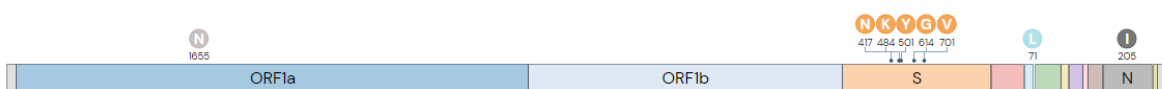
In Alaska: Alpha was detected in December 2020 in the Anchorage/Mat-Su region. Cases have been detected throughout Alaska.



Beta - B.1.351

Beta (also known as: B.1.351, 20H/501Y.V2) was first identified in South Africa and is circulating in the US. The B.1.351 has both N501Y and E484K mutations in the Spike protein. This variant is concerning because it is significantly more transmissible (~50%) than the original SARS-CoV-2 lineages. Preliminary studies suggest the B.1.351, like the P.1, may escape some vaccine-induced and naturally acquired antibody responses. However, as with P.1, the Pfizer, Moderna, and Johnson & Johnson/Janssen vaccines remain largely effective against this lineage.

In Alaska: First identified in March 2021 in the Anchorage/Mat-Su region. Cases were detected in the Anchorage/Mat-Su and Southeast regions in May.



Gamma - P.1

Gamma was first identified in Brazil, also known as: Variant of Concern P.1, B.1.1.28.1, 20J/501Y.V3. This variant contains three key mutations in the S gene: E484K, N501Y, and K417T. While preliminary studies suggest the Pfizer, Moderna, and Johnson & Johnson/Janssen vaccines currently deployed in Alaska may have reduced efficacy against P.1, these vaccines remain largely effective against this lineage and demonstrate protection against serious illness, hospitalizations, and death. Recent analyses suggest that P.1. may be more transmissible with higher risk of severe disease, to some degree.

In Alaska: Gamma was identified in early February 2021 in the Anchorage/Mat-Su region. Cases have been detected throughout Alaska.



Delta - B.1.617.2-like

Delta was first identified in India in late 2020, also known as: Variant of Concern B.1.617.2, 20A/S:478K. This variant has expanded in India, the UK and recently the US. VOC Delta contains key mutations in the S gene: K417N, T478K, L452R, E484Q, N501Y, P681R, and others of unknown significance. The spectrum of mutations in VOC Delta evades binding of antibodies induced by natural infection or vaccines to a marginal extent but may significantly increase transmissibility and severity of infection in those not vaccinated.

In Alaska: Delta was identified in late May, 2021 in the Anchorage/Mat-Su region. Cases have now been detected in many additional locations in Alaska.



Variants of Interest, Individual Lineage Reports

Epsilon - B.1.429 & B.1.427

Epsilon, includes B.1.429 and a related B.1.427 lineages, were first identified in California and known as: CA VUI1. The prevalence of these VOI grew in California from initial observations in summer 2020 and has spread to many other states. Research suggests an increased transmission (~20%). Deescalated from a VOC on June 29, 2021 due to the significant decrease in the proportion of B.1.429 lineage viruses circulating nationally and available data indicating that vaccines and treatments are effective against this variant. This variant is characterized by the L452R mutation in the S gene and is genetically like B.1.351 but lacks several key mutations.

In Alaska: These variants have been detected across Alaska beginning in December 2020. This VOI has not been detected in Alaska since May 2021.

Iota - B.1.526

Iota (also known as B.1.526) was first identified in New York and has begun circulating in other parts of the US. Little is known about this variant, but some genomes contain the E484K mutation in the Spike protein.

In Alaska: The B.1.526 variant was identified in February 2021, in the Anchorage-Mat Su region. Cases have been detected throughout Alaska.

Eta - B.1.525

Eta (also known as B.1.525) is circulating in New York and has begun circulating in other parts of the US. Little is known about this variant. The genomes contain the E484K, Q677H, and F888L mutations in the Spike protein.

In Alaska: The B.1.525 variant was identified in March 2021, in the Gulf Coast region. This VOI has not been detected recently in Alaska.

Zeta - P.2

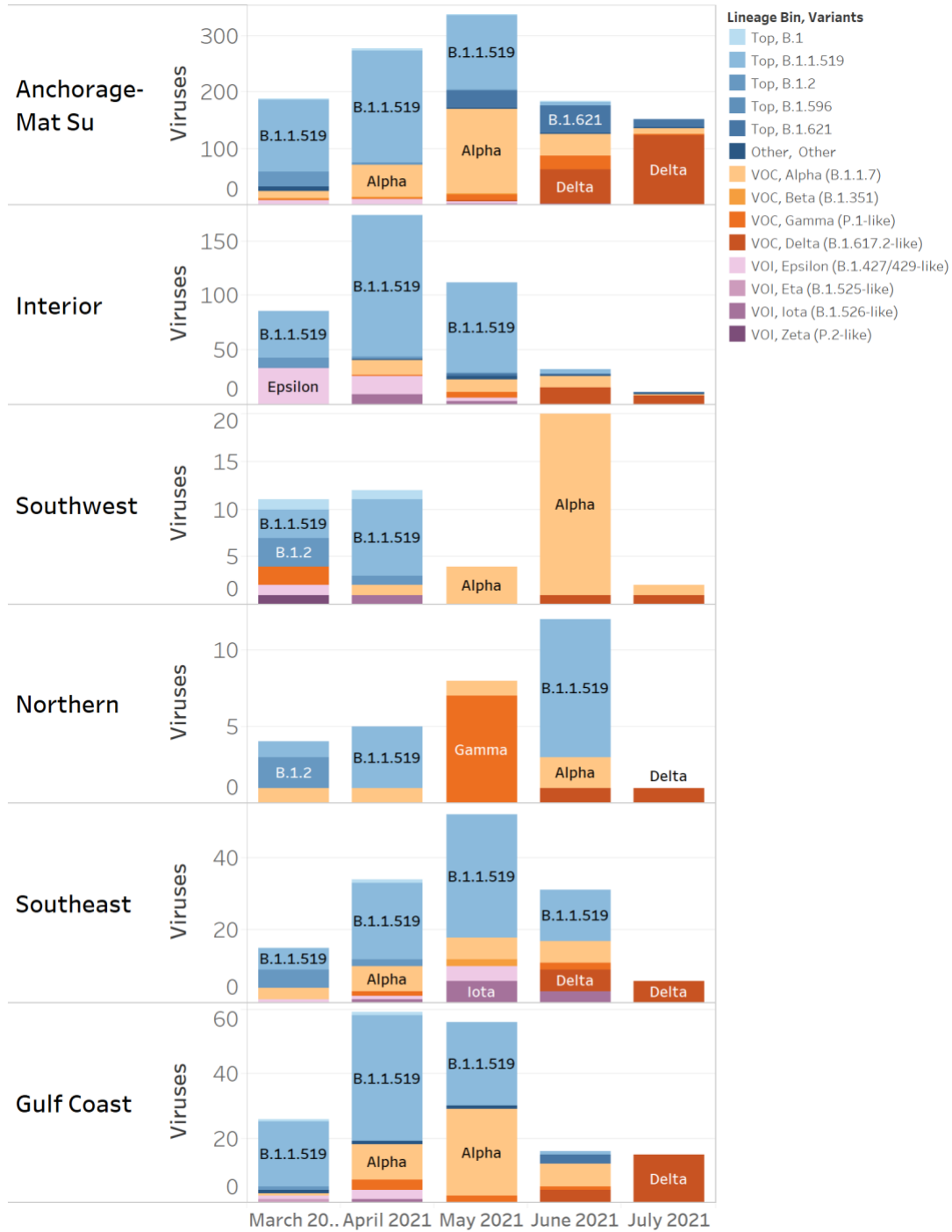
Zeta was first identified in Brazil and is also known as: P.2 or B.1.1.28.2. Little is known about this variant beyond that its prevalence grew in Brazil. This variant contains the E484K mutation in the Spike protein but lacks many key mutations in other variants of concern.

In Alaska: The P.2 variant was identified in January 2021, in the Southwest Alaska region. This VOI has not been detected recently in Alaska.

Lineages in Alaska

Lineages by Alaska Location

The graphs below indicate the number of genomes sequenced from Alaska cases per month within economic regions (map below). Colors and labels indicate PANGO lineages label the sections. Note that vertical axis ranges are independent across regions.



Additional Resources

CDC COVID-19 National Genomic Surveillance Dashboard - <https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/genomic-surveillance-dashboard.html>

SARS-CoV-2 (hCoV-19) Mutation Situation Reports - <https://outbreak.info/situation-reports>

Nextstrain SARS-CoV-2 resources - <https://nextstrain.org/sars-cov-2/>

CoVariants - <https://covariants.org/>

PANGO Lineage Reports - https://cov-lineages.org/global_report.html

Locations within Alaska are grouped by Economic Region as seen below.

