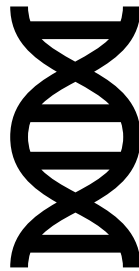




Alaska COVID-19 Genomic Surveillance

Situation Report

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Prepared by the Alaska Sequencing Consortium*, including
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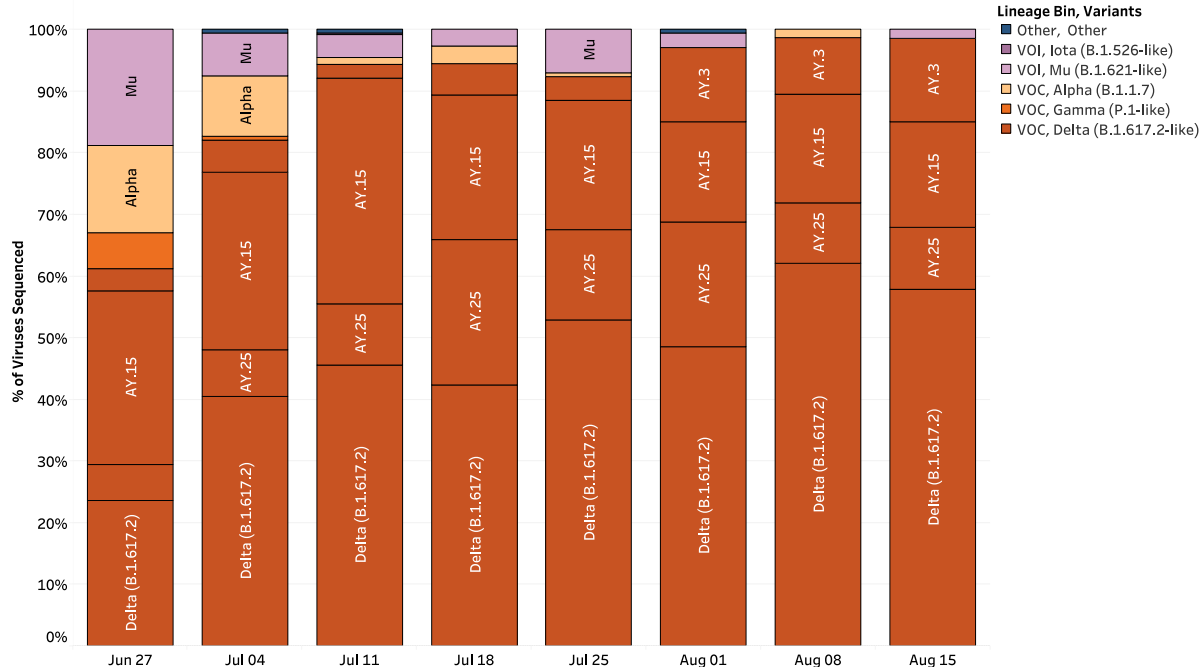
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Executive Summary: Sequence Analysis of COVID-19 in Alaska

- **Variant of Concern (VOC) Delta (B.1.617.2-like) accounts for almost all newly detected cases.** To date, we have detected 1,438 cases in multiple locations across the state. During the week beginning August 15, Delta represented 99% of sequenced cases in Alaska. According to data from the CDC, the proportion of cases attributed to Delta nationwide is estimated to be 99% for the week ending Aug 28. ([CDC Variant Proportions website](#)).
- **Continued detection of VOC Delta sub-lineages (B.1.617.2, AY.1-25):** Sub-lineages of VOC Delta continue to be detected. In Alaska, we have detected the original lineage as well as a significant proportion of AY.3 (14%), AY.15 (17%), and AY.25 (10%). Rare sub-lineages include AY.4, AY.5, AY.7.2, AY.10-14, and AY.19-24.
- **VOC Alpha (B.1.1.7) proportion has appreciably declined.** To date, we have detected 452 cases across the state. During the week beginning August 15, no Alpha was detected in sequenced cases in Alaska. Alpha proportions are nearly absent nationwide.
- **No recent cases of VOC Beta (B.1.351) or VOC Gamma (P.1) detected.**
- **The WHO recently designated B.1.621 as Variant of Interest (VOI) Mu.** To date, we have detected 147 cases in multiple locations across the state. During the week beginning August 15, only 2 recent cases were detected. This is a decline from a peak proportion in June (20%).
- **No recent cases of 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. Rare sub-lineages of Delta are aggregated with the parent lineage, B.1.617.2, proportion.

Variants of Concern/Interest

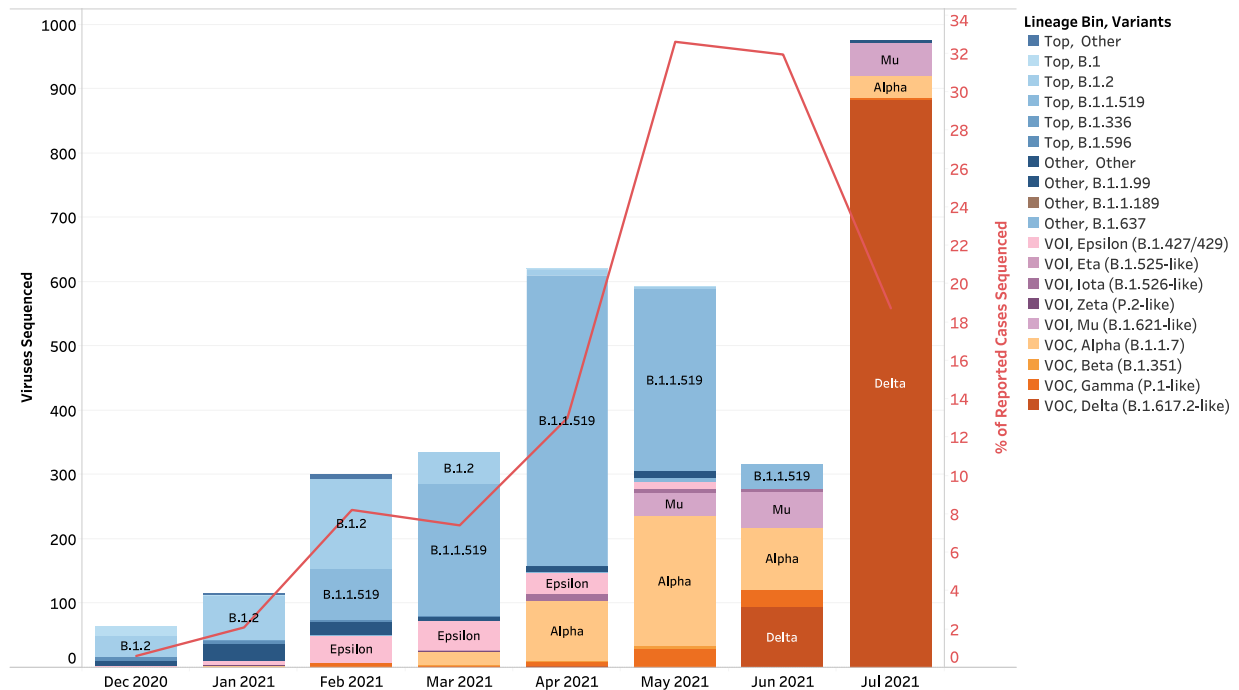
Name	Lineages	Cases Detected	Change from Previous Report*	First Identified in Alaska
VOC Alpha	B.1.1.7	452	+1	20 December 2020
VOC Beta	B.1.351	7	0	20 March 2021
VOC Gamma	P.1-like	74	0	8 February 2021
VOC Delta	B.1.617.2-like	1438	+242	30 May 2021
VOI Epsilon	B.1.427/429	139	0	24 December 2020
VOI Eta	B.1.525	1	0	16 March 2021
VOI Iota	B.1.526	24	0	4 February 2021
VOI Mu	B.1.621	147	+1	6 May 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	261
Total Genomes released on GISAID	4088

Variants Identified in Alaska



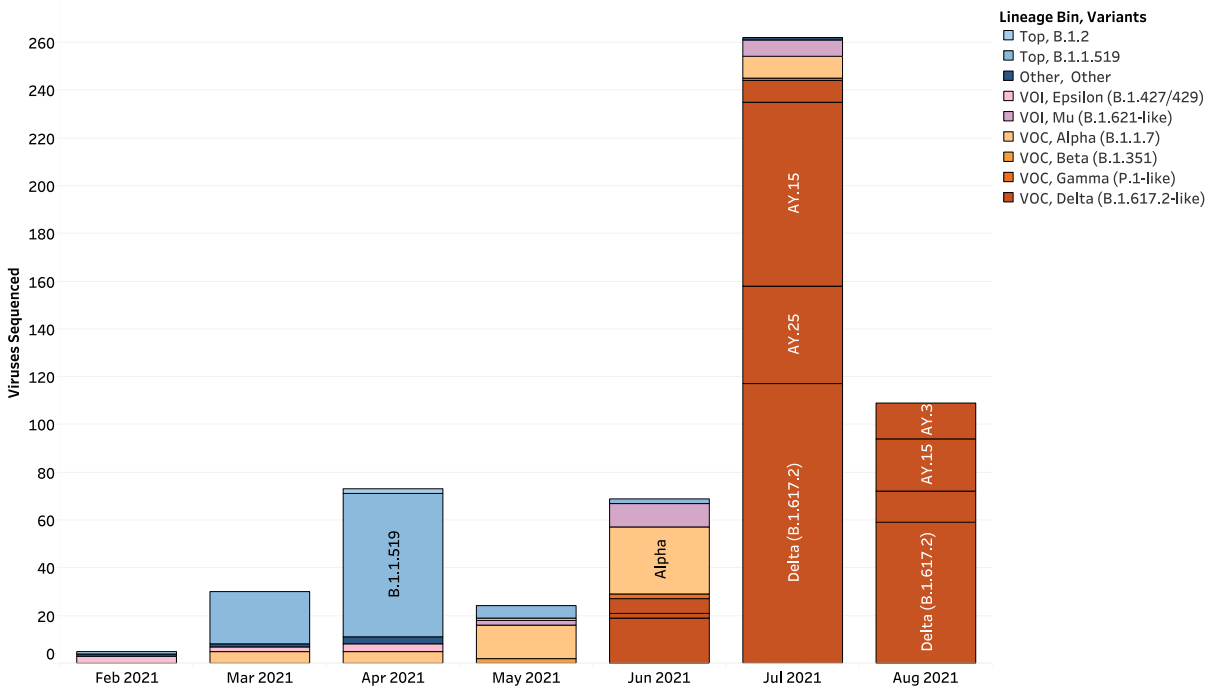
*Note that SARS-CoV-2 genome sequencing may not be a random sample of all cases. This figure does not estimate the prevalence of the population.

Table: Vaccine Breakthrough Investigation

Patients under investigation for Vaccine Breakthrough (VB)	4318
Specimens submitted to SPHL for VB investigation	926 (21.4%)
Specimens fitting criteria for sequencing	699
Sequencing effort to assess VB	690
Successful virus lineage identifications	584 (84.6%)

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

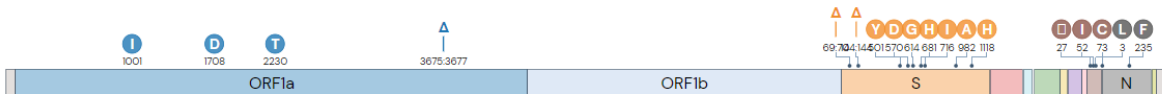


Variants of Concern, Individual Lineage Reports

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 lineage. Alpha does not appear to evade vaccine-induced neutralizing antibody responses. Alpha is still 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 Beta, like Gamma, may escape some vaccine-induced and naturally acquired antibody responses. However, as with all VOCs, the Pfizer, Moderna, and Johnson & Johnson/Janssen vaccines remain largely effective against this lineage.

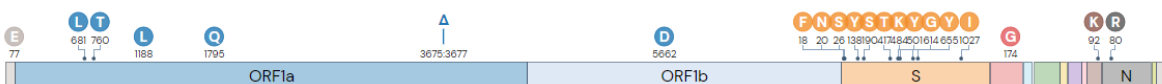
In Alaska: First identified in March 2021 in the Anchorage-Mat Su region. Cases were detected in the Anchorage/Mat-Su and Southeast regions in May.



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 Gamma, these vaccines remain largely effective against this lineage and demonstrate protection against serious illness, hospitalizations, and death. Recent analyses suggest that Gamma 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.

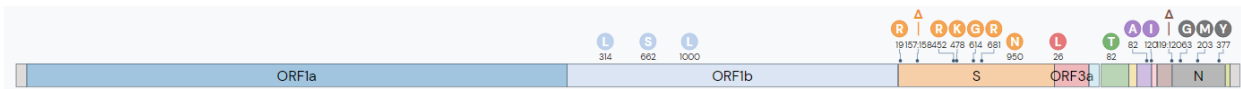


Delta - B.1.617.2-like

Delta was first identified in India in late 2020, also known as: Variant of Concern B.1.617.2, 20A/S:478K. The Delta variant has become widespread over the last few months and B.1.617.2 is the predominant lineage in many countries worldwide. In addition to B.1.617.2, Delta also contains lineages AY.1 – AY.25. The AY lineages break up B.1.617.2-like viruses into smaller related clusters that can be tracked separately. These lineages remain classified as the Delta variant and their designation as AY does not imply any functional biological difference from B.1.617.2.

Delta contains key mutations in the S gene: K417N, T478K, L452R, N501Y, P681R, and others of unknown significance. The spectrum of mutations in Delta is poorly understood but may contribute to higher virus titer, increased severity of infection in unvaccinated individuals, and significantly increased transmissibility. According to CDC data, Delta is currently driving case numbers and COVID-19 hospitalizations in the US, particularly among unvaccinated individuals and children.

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. Delta VOC has predominated the surge of cases in July-August 2021 in Alaska, with multiple sub-lineages circulating across the state. In Alaska, the original B.1.617.2 as well as a significant proportion of AY.3, AY.15 and AY.25 make up the majority of cases, while AY.4, AY.5, AY.7.2, AY.10-14, and AY.19-24 make up a minority of cases.



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.

Mu – B.1.621

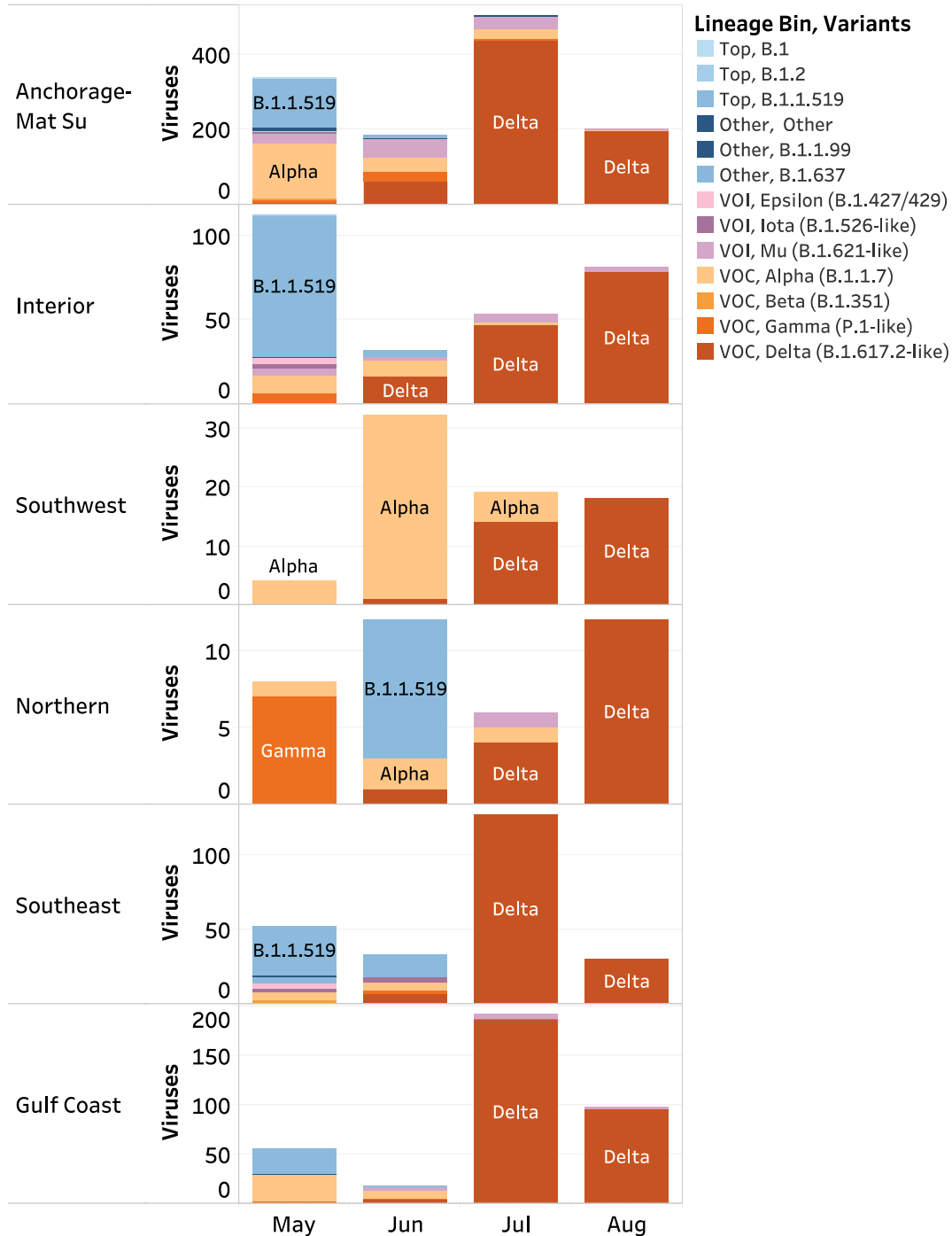
Mu was first identified in Columbia in January 2021 and is also known as: B.1.621. This variant has been detected in North and South America, Europe, and Asia. There are several mutations in this lineage that affect the Spike protein including I95I, Y144T, Y145S, R346K, E484K and N501Y in the Receptor Binding Domain and P681H in the S1/S2 cleavage site. Little is known about the potential biological and epidemiological roles of these mutations.

In Alaska: The B.1.621 variant was identified in May 2021, in the Anchorage-Mat Su Alaska region.

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.

