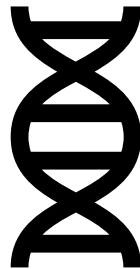
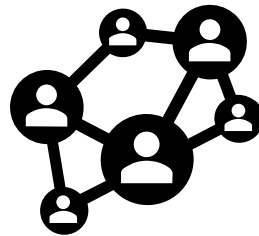


Alaska COVID Genomic Surveillance

Situation Report

9 June 2021



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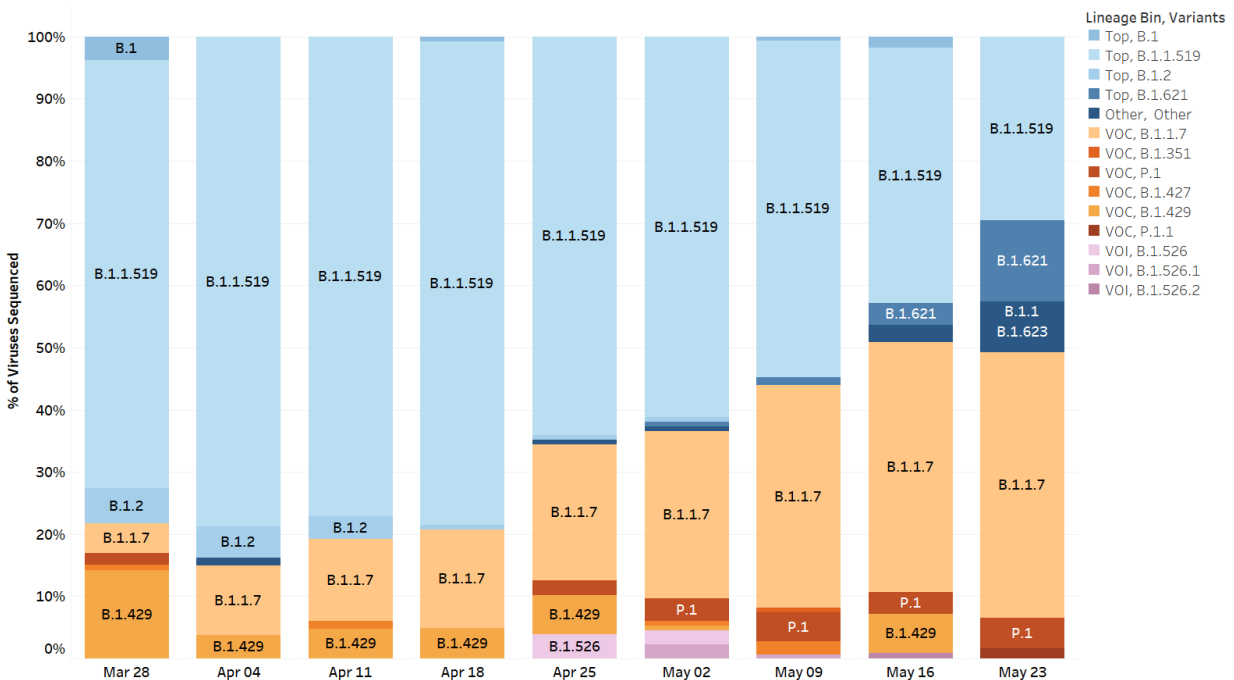
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Executive Summary: Sequence Analysis of COVID-19 in Alaska

- **First cases of VOC Delta (B.1.617.2/AY.1) detected in Alaska.** To date, we have detected 2 cases in Anchorage-Mat Su region on May 30, 2021.
- **The proportion of cases of Variant of Concern (VOC) Alpha (B.1.1.7) continues to increase.** To date, we have detected 287 cases across the state. During the week beginning May 23, B.1.1.7 represents 43% of sequenced cases in Alaska. According to data from the CDC, B.1.1.7 proportions are 69% nationwide (CDC website on genomic variants: [CDC Variant Link](#)).
- **The proportion of cases of the VOC B.1.429/427 remains low.** To date, we have detected 134 cases across the state. In recent weeks, B.1.429 represents <10% of sequenced cases in Alaska. Nationwide, these VOC have declined and account for <1% of cases.
- **Additional cases of the VOC Gamma (P.1/P.1.1) detected.** To date, we have detected 34 cases across the state. In recent weeks, P.1 represented <5% of sequenced cases in Alaska. According to data from the CDC, P.1 proportions are 8% nationwide
- **No additional case of VOC Beta (B.1.351) detected.** Nationwide, B.1.351 accounts for < 1% of cases.
- **Additional cases of Variant of Interest (VOI) Iota (B.1.526) detected.** To date, we have detected 19 cases across the state.
- **No additional cases of VOI Eta (B.1.525) 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

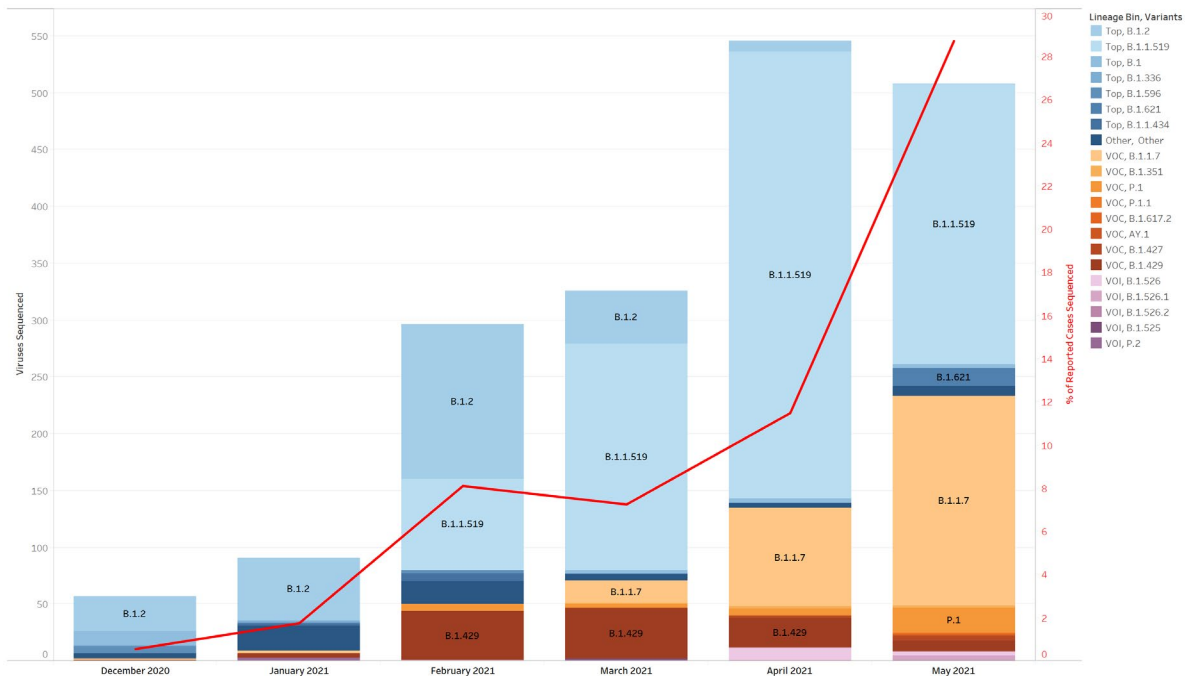
WHO Label	Lineage	Cases Detected	Change from Previous Report*	First Identified in Alaska
VOC Alpha	B.1.1.7	294	+64	20 December 2020
VOC Beta	B.1.351	5	0	20 March 2021
VOC Gamma	P.1/P.1.1	38	+10	8 February 2021
VOC Delta	B.1.617.2 / AY.1	2	+2	30 May 2021
VOC Epsilon	B.1.427	7	0	30 March 2021
VOC Epsilon	B.1.429	128	+4	24 December 2020
VOI Iota	B.1.526	21	+4	4 February 2021
VOI Eta	B.1.525	1	0	16 March 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	+188
Total Genomes released on GISAID	2096

Variants Identified in Alaska

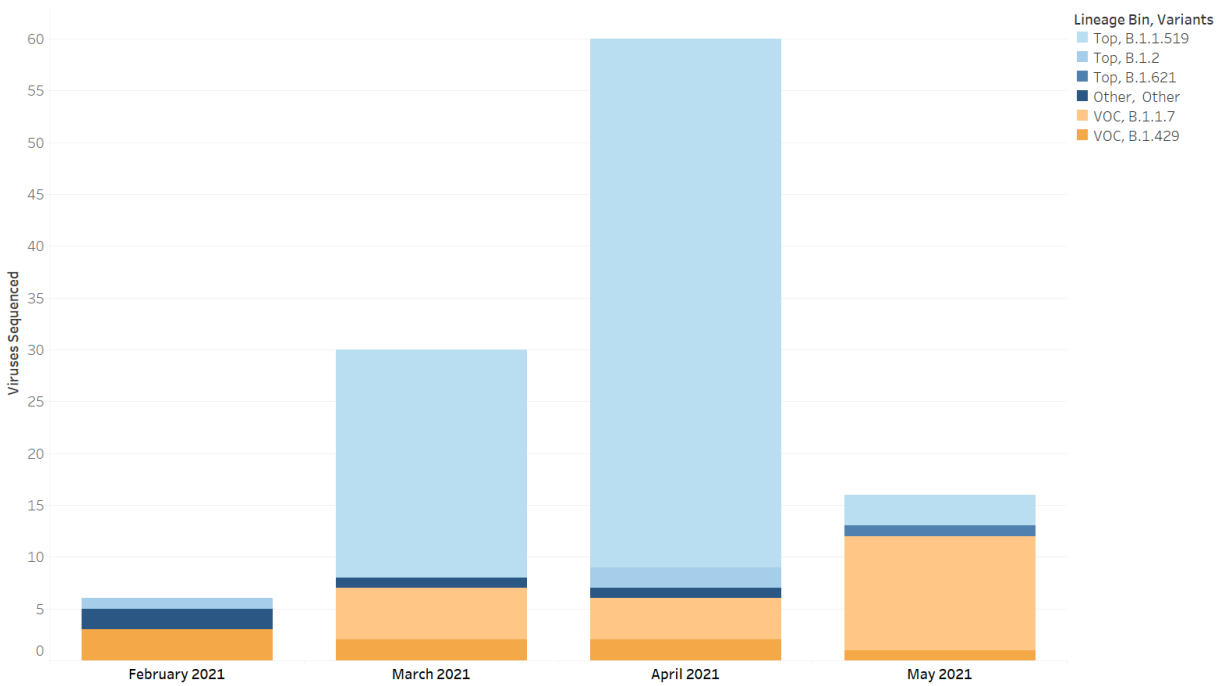


**Note that SARS-CoV-2 genome sequencing may not be a random sample of all cases. This figure does not estimate the prevalence of the population.

Table: Vaccine Breakthrough Investigation

Patients under investigation for Vaccine Breakthrough VB	328
Specimens submitted to SPHL for VB investigation	216 (65.8%)
Specimens fitting criteria for sequencing	200
Sequencing effort to assess VB	189
Successful virus lineage identifications	120 (63.5%)
Specimens in progress	11

Vaccine Breakthrough refers to patients 14 days out from being fully vaccinated who test positive for SARS-CoV-2. VBs may have a very low virus titer and are difficult to sequence. As of May 1, 2021, CDC will be tracking only patients with VB infections who are hospitalized or have died. A summary of Alaska VB cases is [available here](#):

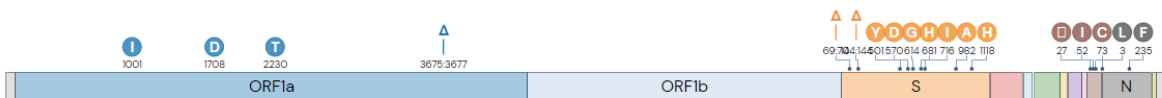


Variants of Concern, Individual Lineage Reports

Alpha - B.1.1.7

B.1.1.7 was first identified in the United Kingdom, also known as: Variant of Concern Alpha, 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: B.1.1.7 was detected in December 2020 in the Anchorage/Mat-Su region. Cases are now found throughout Alaska.



Beta - B.1.351

The B.1.351 variant (also known as: Beta, 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 Southeast region in May.



Gamma - P.1

P.1 was first identified in Brazil, also known as: Variant of Concern Gamma, 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.

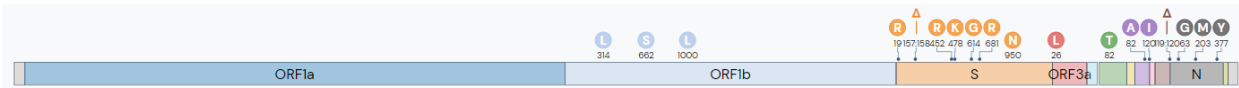
In Alaska: P.1 was identified in early February 2021 in the Anchorage/Mat-Su region. Cases have been found throughout Alaska.



Delta - B.1.617.2 / AY.1

B.1.617.2 was first identified in India, also known as: Variant of Concern Delta, 20A/S:478K. This variant was first detected in India in late 2020 and has expanded in India, the UK and recently the US. VOC Delta contains key mutations in the S gene: T478K, L452R, E484Q, N501Y, P681R, and others of unknown significance. Recently, B.1.617.2 variants containing an additional S gene mutation (K417N) have been reclassified as lineage AY.1. WHO nomenclature VOC Delta encompasses both the B.1.617.2 and AY.1 lineages. 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.

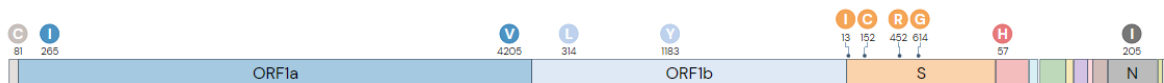
In Alaska: B.1.617.2. and AY.1 were identified in late May 2021 in the Anchorage/Mat-Su region.



Epsilon - B.1.429 & B.1.427

B.1.429 and a related B.1.427 lineages were first identified in California and known as: Epsilon, CA VUI1. The prevalence of these VOC grew in California from initial observations in summer 2020 and has spread to many other states. Research suggests an increased transmission (~20%) and potential escape from neutralizing antibodies. 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.



Variants of Interest, Individual Lineage Reports

Iota - B.1.526

The B.1.526 variant (also known as Iota) 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 found throughout Alaska.

Eta - B.1.525

The B.1.525 variant (also known as Eta) 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.

Zeta - P.2

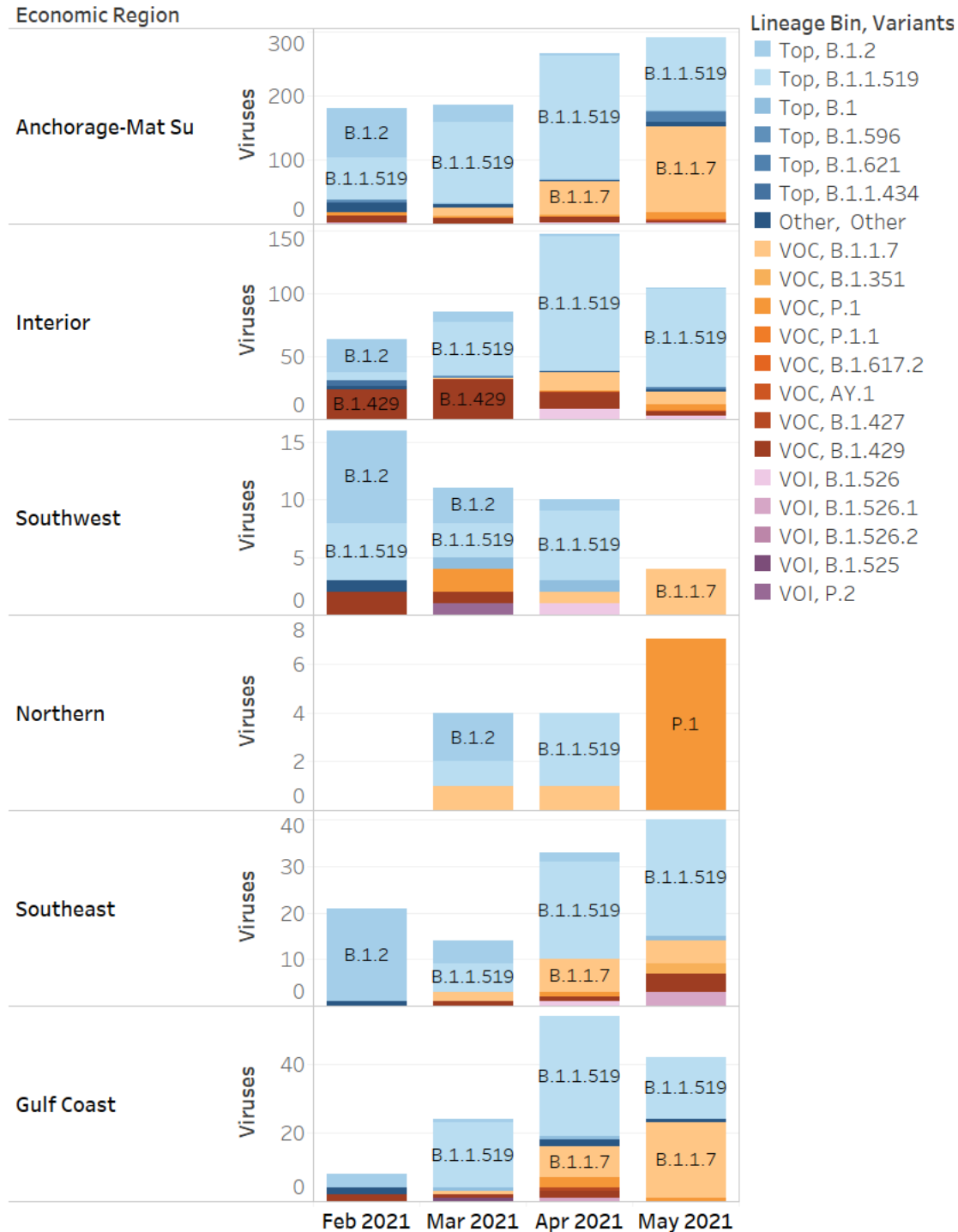
P.2 was first identified in Brazil and is also known as: Zeta or B.1.1.28.2. Little is known about this variant beyond that its prevalence grew in Brazil. This variant contains the E484K mutation in the Spike protein but lacks many key mutations in other variants of concern.

In Alaska: The P.2 variant was identified in January 2021, in the Southwest Alaska region.

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.

