

SARS-CoV-2 Sequencing and Variants in Washington State

Washington State Department of Health

July 07, 2021



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Next generation sequencing is a set of laboratory methods that scientists use to scan a viral genome to determine the genome sequence of a virus. A genome sequence of a virus is referred to as its “genomic fingerprint,” and can reveal mutations in a virus that make it unique. Mutations are changes in a genome sequence and occur naturally over time.

Scientists compare viral genomes to better understand how viruses can spread from person to person. Sequencing allows public health officials to detect clusters of cases, and monitor new lineages. Groups of same-species viruses that share a set of genome mutations are referred to as a lineage. Some lineages may have characteristics such as the ability to spread more quickly, or cause more severe disease. These lineages are classified as variants of interest, or variants of concern.

Throughout this report, we refer to the scientific name of the virus SARS-CoV-2 that causes COVID-19. Sequencing can only be performed on samples that contain SARS-CoV-2 RNA, which means only samples used for molecular tests (such as PCR) can be included. For this reason, this report is limited to confirmed cases only. The genomes that are sequenced and compared are those of the virus, not humans.

Sequencing can be performed on stored specimens at any time. For this reason, the dataset used for this report is dynamic, and batches of stored specimens that are newly sequenced will be added to the dataset as sequencing occurs. Because of this, trends based on historical data can change over time.

Washington State has increased sequencing capacity, and is currently sequencing at least 10% of positive specimens, which [ranks among the best](#) in the nation according to the Centers for Disease Control and Prevention (CDC).

At a glance (data through July 06, 2021)

- During the month of May 2021, **23.2%** of all confirmed molecular COVID-19 cases were sequenced. This number is preliminary and will change over time as additional specimens are received from the previous month.
- **31024 (7.4%)** specimens from COVID-19 cases in Washington state have been sequenced since January 2020.

*This represents the total number of sequences available, a small number of individuals may have had multiple specimens sequenced

Washington State follows the [Center for Disease Control and Prevention's variants of concern](#).

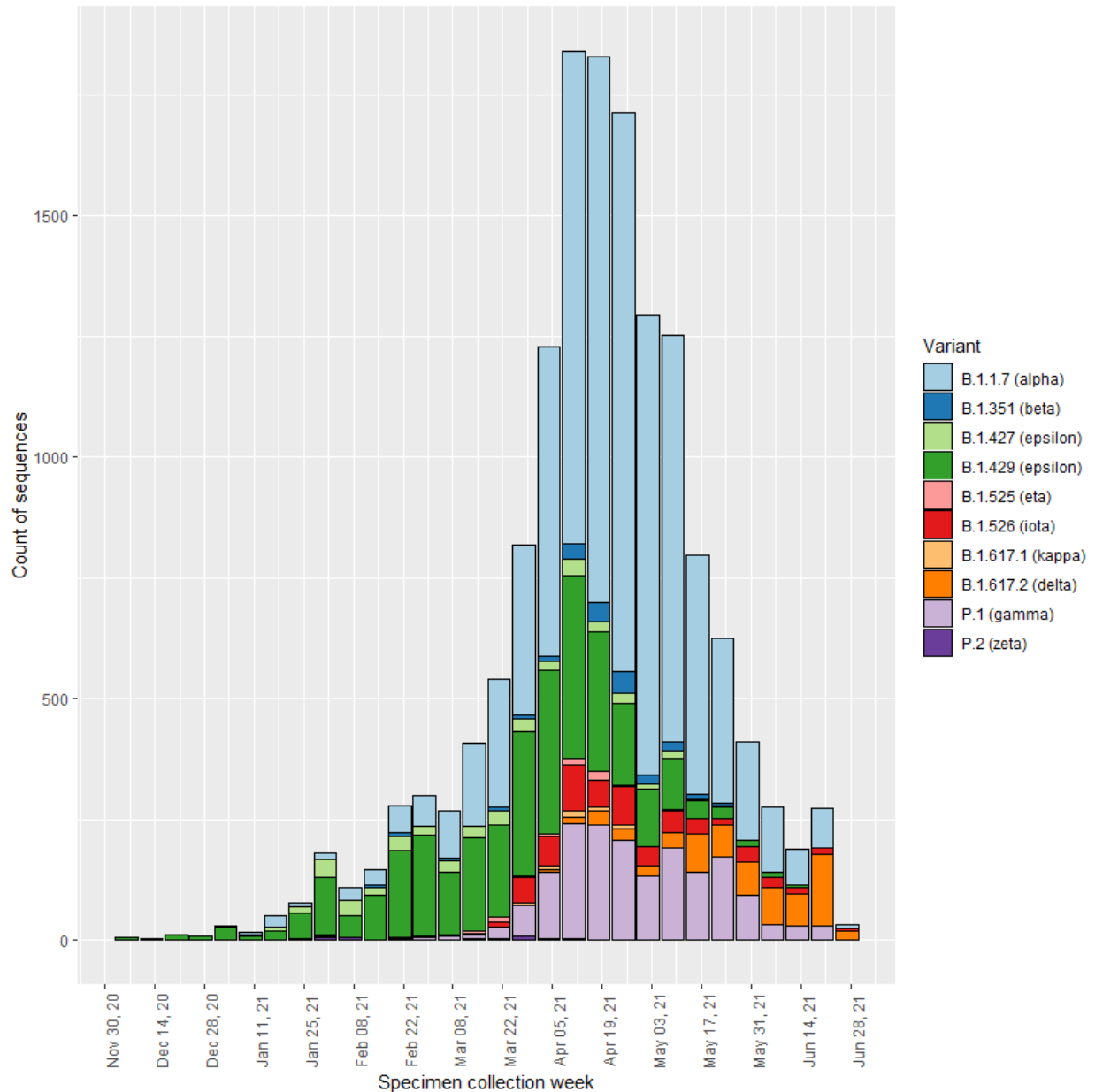
These include:

Name	Area of emergence	CDC designation	Cumulative Washington cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.1.7 (alpha)	United Kingdom	Variant of concern	8,192	2021-01-07	2021-06-28
B.1.351 (beta)	South Africa	Variant of concern	224	2020-01-29	2021-06-28
P.1 (gamma)	Brazil	Variant of concern	1,749	2021-02-06	2021-06-26
B.1.617.2 (delta)	India	Variant of concern	656	2021-04-03	2021-06-28
B.1.427 (epsilon)	California	Variant of interest	386	2020-12-11	2021-05-28
B.1.429 (epsilon)	California	Variant of interest	3,089	2021-11-20	2021-06-24
B.1.526 (iota)	New York	Variant of interest	576	2021-01-21	2021-06-27
B.1.525 (eta)	New York	Variant of interest	71	2021-02-02	2021-05-13
P.2 (zeta)	Brazil	Variant of interest	37	2021-01-28	2021-04-20
B.1.617.1 (kappa)	India	Variant of interest	42	2021-03-22	2021-05-04
B.1.617.3	India	Variant of interest	0		

- Sequencing can be performed on stored specimens at any time, so the earliest collection date may change as additional specimens are sequenced.
- B.1.617 has been broken down to multiple sublineages: B.1.617.1, B.1.617.2, B.1.617.3. Although the original designation of B.1.617 is still listed on the CDC website as a variant of interest, it will not be tracked on this report because no sequences get assigned as this variant.

Sequencing Trends Over Time

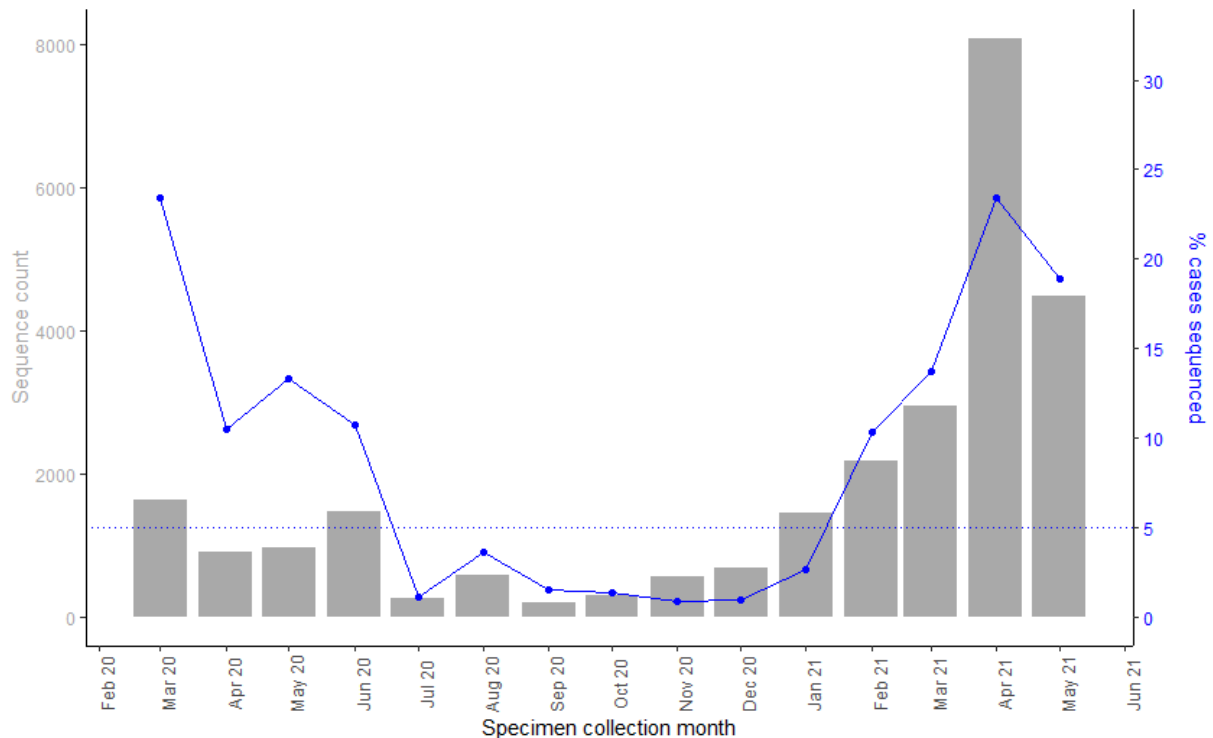
Epidemiologic curve of variants of interest and concern by week of specimen collection date as of Jul 06, 2021



* The above graph shows the total number of variants detected by the week the specimen was collected from a patient.

* Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.

Number of specimens sequenced and percent of Washington State confirmed COVID-19 cases that have been sequenced by specimen collection date



In January and February 2020, all confirmed cases were sequenced, so those months are excluded from this graph.

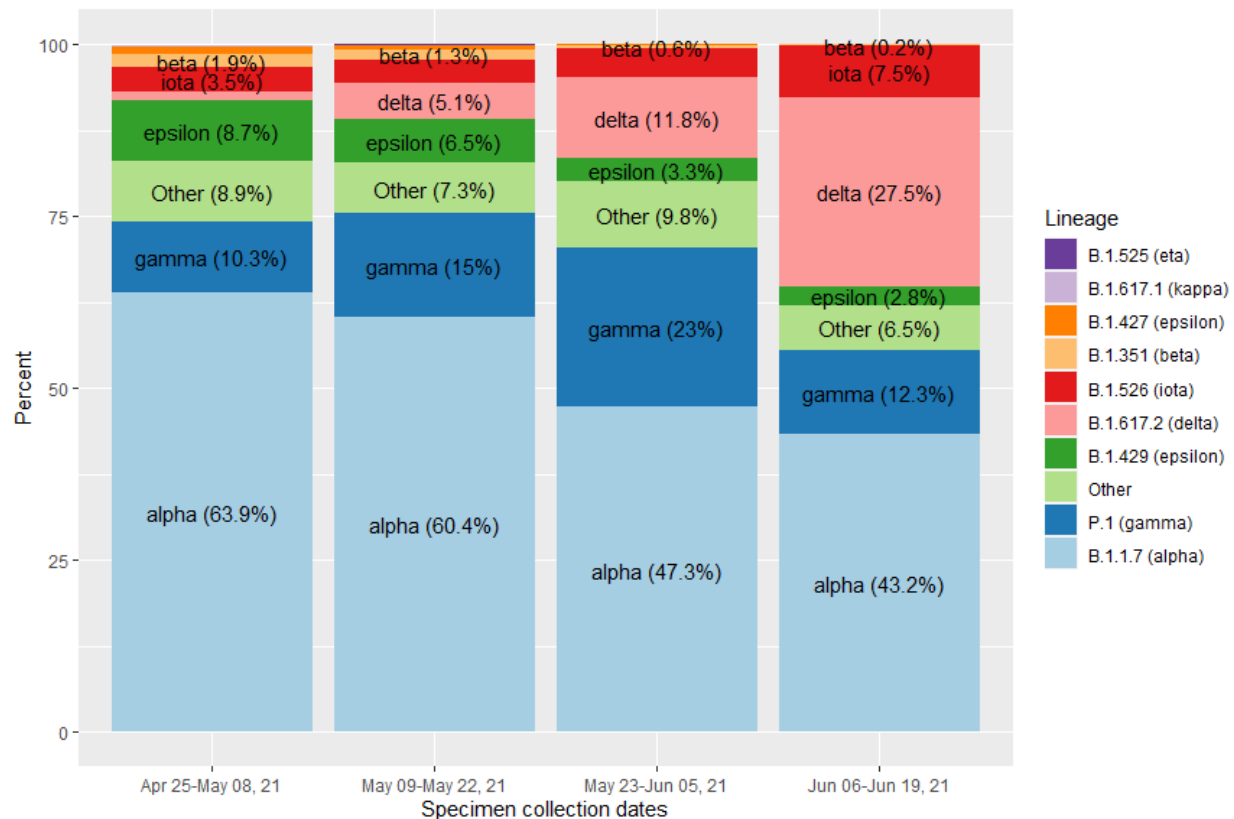
- We are not sequencing samples from every confirmed COVID-19 case at this time. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing can be performed on stored specimens at any time, so numbers from past months may change if stored specimens are sequenced.
- All sequencing performed through February 2021 occurred outside of Washington state Public Health Laboratories; sequence testing volume depended on funding and considerations of those laboratories performing testing. Since January 2021, DOH has been working on a plan to increase sequencing capacity in Washington. Part of this plan is a 5% representative sample of confirmed cases, which will give us an indicator of the variants in Washington state and an estimate of their prevalence.

SARS-CoV-2 Lineages Circulating in Washington State

The graph below shows the change in proportion of select SARS-CoV-2 lineages by time period. A viral lineage is a group of viruses with shared characteristics, allowing them to be grouped together.

NOTE: Not all positive SARS-CoV-2 specimens are sequenced, and sequenced specimens are not a random selection of all COVID-19 cases in Washington. Sequencing can be performed on stored specimens at any time. For this reason, the dataset used for this report is dynamic, and batches of stored specimens that are newly sequenced will be added to the dataset as sequencing occurs. Because of this, trends based on historical data can change over time.

Proportions are only available for sequenced specimens, and therefore do not necessarily represent true statewide proportions. There are many different lineages that are not variants of concern or interest. These are grouped together as 'Other' on this chart. As the proportions of variants of concern and variants of interest increase, the proportion of other lineages will decrease. Variants of concern and variants of interest include: B.1.1.7 (alpha) , B.1.351 (beta) , P.1 (gamma), B.1.617.2 (delta), B.1.427 (epsilon), B.1.429 (epsilon), B.1.526 (iota), B.1.525 (eta), P.2 (zeta), B.1.617.1 (kappa) and B.1.617.3.



The chart above shows the biweekly proportions of the most common SARS-CoV-2 lineages circulating in Washington grouped in two-week intervals. Proportions are calculated using data which are subject to change over time and will be updated as more data becomes available.

To see the national trends, visit the CDC's [variant proportions page](#).

Variants of concern by county of residence

County	B.1.1.7 (alpha) count	B.1.351 (beta) count	P.1 (gamma) count	B.1.617.2 (delta) count
Adams	6	0	3	0
Asotin	6	0	0	0
Benton	332	1	68	66
Chelan	14	0	0	0
Clallam	42	0	2	0
Clark	52	0	16	2
Cowlitz	18	0	20	0
Douglas	10	0	0	0
Ferry	2	0	0	0
Franklin	263	2	91	38
Grant	22	0	10	3
Grays Harbor	34	2	1	0
Island	28	0	4	0
Jefferson	12	0	0	0
King	4,403	158	835	413
Kitsap	52	2	4	0
Kittitas	10	0	10	1
Klickitat	4	0	0	0
Lewis	42	0	3	0
Lincoln	3	0	2	0
Mason	13	0	1	0
Okanogan	6	0	0	0
Pacific	14	0	5	0
Pend Oreille	2	0	1	0
Pierce	755	23	111	15
San Juan	6	0	0	0
Skagit	146	0	23	0

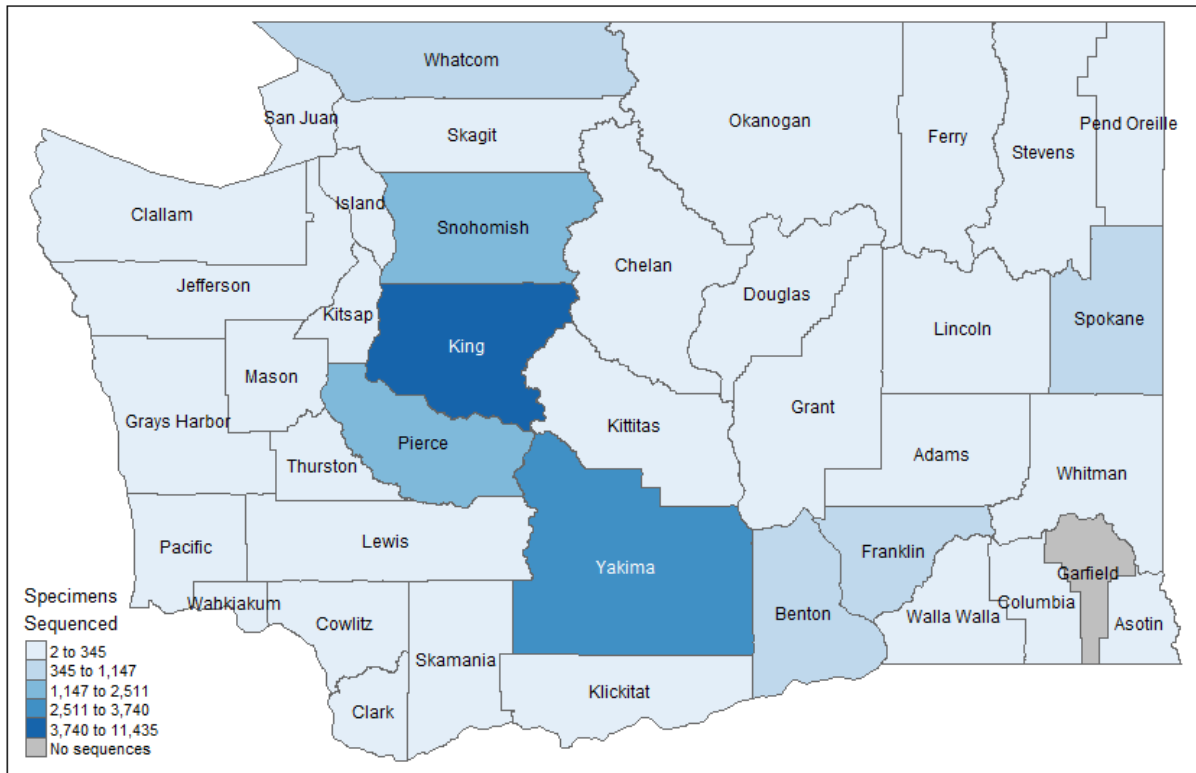
County	B.1.1.7 (alpha) count	B.1.351 (beta) count	P.1 (gamma) count	B.1.617.2 (delta) count
Skamania	2	0	0	0
Snohomish	994	17	164	52
Spokane	142	1	94	1
Stevens	8	0	1	0
Thurston	105	4	6	1
Wahkiakum	4	0	2	0
Walla Walla	7	0	4	1
Whatcom	379	3	176	1
Whitman	62	0	5	0
Yakima	190	11	87	62

Variants of interest by county of residence

County	B.1.427 (epsilon) count	B.1.429 (epsilon) count	B.1.526 (iota) count	B.1.525 (eta) count	P.2 (zeta) count	B.1.617.1 (kappa) count	B.1.617.3 count
Adams	12	6	1	0	0	0	0
Asotin	0	0	0	0	0	0	0
Benton	56	157	44	20	0	0	0
Chelan	0	7	0	0	0	0	0
Clallam	0	5	1	0	0	0	0
Clark	6	17	2	0	0	0	0
Cowlitz	9	13	0	0	0	0	0
Douglas	0	2	0	0	0	0	0
Ferry	0	1	0	0	0	0	0
Franklin	26	132	25	11	1	0	0
Grant	0	25	4	0	0	0	0
Grays Harbor	0	21	0	0	0	0	0
Island	0	2	0	0	0	0	0
Jefferson	0	6	2	0	0	0	0
King	91	1,466	330	27	24	37	0
Kitsap	1	25	4	0	0	0	0
Kittitas	1	6	0	0	0	0	0
Klickitat	0	0	0	0	0	0	0
Lewis	3	19	0	0	1	0	0
Lincoln	0	1	0	0	0	0	0
Mason	0	2	1	0	0	0	0
Okanogan	0	2	0	0	0	0	0
Pacific	10	10	0	0	0	0	0
Pend Oreille	0	0	1	0	0	0	0
Pierce	19	367	54	2	2	0	0

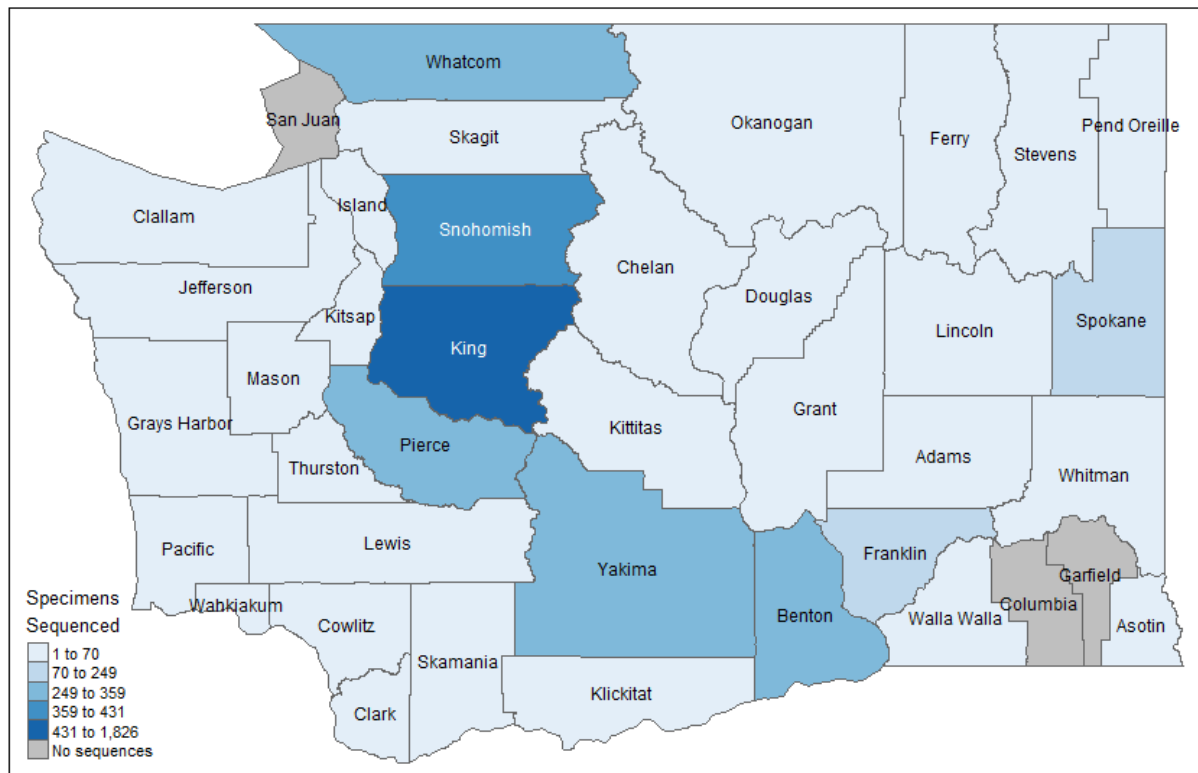
County	B.1.427 (epsilon) count	B.1.429 (epsilon) count	B.1.526 (iota) count	B.1.525 (eta) count	P.2 (zeta) count	B.1.617.1 (kappa) count	B.1.617.3 count
San Juan	0	0	0	0	0	0	0
Skagit	1	18	1	0	0	0	0
Skamania	0	0	0	0	0	0	0
Snohomis h	31	277	29	5	1	3	0
Spokane	4	47	28	3	0	1	0
Stevens	0	0	0	0	0	1	0
Thurston	5	27	2	0	0	0	0
Wahkiaku m	0	0	0	0	0	0	0
Walla Walla	7	4	1	0	0	0	0
Whatcom	6	31	16	2	0	0	0
Whitman	6	8	2	0	0	0	0
Yakima	92	385	28	1	8	0	0

The map below shows the number of specimens sequenced by county of home address for all sequences since the beginning of the pandemic.



- Geographic information is currently lacking for 18% of sequences which may result in apparent low coverage in some areas.
- Only sequences matched to confirmed case data are included.

The map below shows the number of specimens sequenced by county of home address for specimens collected in the past 60 days.



Vaccine Breakthrough

A complete report on vaccine breakthrough cases can be found in the reports section of the [DOH data dashboard](#).

A vaccine breakthrough case is defined as someone who tests positive for SARS-CoV-2 at least 14 days after their final dose of SARS-CoV-2 vaccine. DOH is prioritizing sequencing of specimens obtained from vaccine breakthrough cases. This can help scientists determine whether any specific variants of the virus are causing more breakthrough cases than expected.

Variants are assigned to lineages, groups of SARS-CoV-2 sequences that share a set of mutations. Some lineages are classified as variants of interest (VOI) or variants of concern (VOC). The table below shows the counts and percentages of Vaccine Breakthroughs based on lineages belonging to either VOI or VOC. Lineages not designated to either VOI or VOC are marked as 'other'.

It is important to remember when reviewing these data:

- If a variant is common among the general population, it will also be commonly found among breakthrough cases.
- The proportion of variants found in Washington changes rapidly over time, see page 7 for more information. Specimens are not randomly selected for sequencing, so the proportions are not representative.
- A detailed study is necessary to see if any variants are found in higher than expected proportions among vaccine breakthrough cases.
- These data are limited to sequences from specimens collected after 1/19/2021, the first date when a vaccine breakthrough case could have been identified according to the above definition.

Variants identified among vaccine breakthrough (VB) cases with sequencing results compared to variants identified among all COVID-19 cases during the same timeframe

Variant	Number of VB cases with variant	Percent of VB cases with variant	Percent of sequences from all COVID-19 cases with variant
B.1.1.7 (alpha)	297	41%	44%
P.1 (gamma)	139	19%	9%
B.1.429 (epsilon)	113	16%	16%
B.1.617.2 (delta)	70	10%	4%
B.1.526 (iota)	21	3%	3%
B.1.351 (beta)	11	2%	1%
B.1.427 (epsilon)	11	2%	2%
B.1.525 (eta)	4	1%	0%
B.1.617.1 (kappa)	1	0%	0%
P.2 (zeta)	0	0%	0%
Other	49	7%	20%
Total	716	100%	100%

Variant of Concern: B.1.1.7 (alpha)

Total B.1.1.7 (alpha) Detections: 8192

Why are we concerned about this variant?:

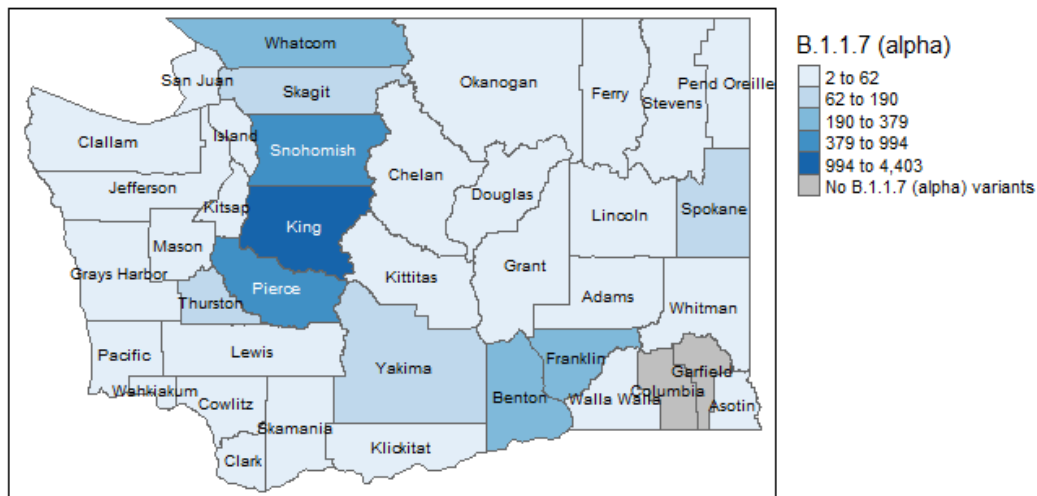
The B.1.1.7 (alpha) variant is highly infectious, transmissible and can quickly spread from person to person. Based on published studies, the B.1.1.7 (alpha) variant potentially causes more severe symptoms and increased risk of death in individuals who are infected.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of B.1.1.7 (alpha) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent B.1.1.7 (alpha)
Hospitalized	5.8%	2.9%	2.7%
Died from COVID	0.9%	0.6%	0.4%
Age 0-19	21.5%	25.7%	27.2%
Age 20-34	30%	31.9%	32.7%
Age 35-49	21.9%	22.6%	22.4%
Age 50-64	15.9%	12.6%	11.8%
Age 65-79	6.4%	3.9%	3%
Age 80+	2.2%	1.3%	0.9%
Unknown age	2.5%	2%	1.9%

Number of B.1.1.7 (alpha) cases sequenced by county of home address



Variant of Concern: B.1.351 (beta)

Total B.1.351 (beta) Detections: 224

Why are we concerned about this variant?:

The B.1.351 (beta) variant is highly infectious, transmissible and can quickly spread from person to person. Results from experimental research studies show that the B.1.351 (beta) variant contains mutations that make it less likely to respond to antibody treatments.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of B.1.351 (beta) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent B.1.351 (beta)
Hospitalized	5.8%	2.9%	5.4%
Died from COVID	0.9%	0.6%	0.4%
Age 0-19	21.5%	25.7%	28.1%
Age 20-34	30%	31.9%	36.6%
Age 35-49	21.9%	22.6%	20.1%
Age 50-64	15.9%	12.6%	10.7%
Age 65-79	6.4%	3.9%	2.7%
Age 80+	2.2%	1.3%	0.4%
Unknown age	2.5%	2%	1.3%

Number of B.1.351 (beta) cases sequenced by county of home address



Variant of Concern: P.1 (gamma)

Total P.1 (gamma) Detections: 1749

Why are we concerned about this variant?:

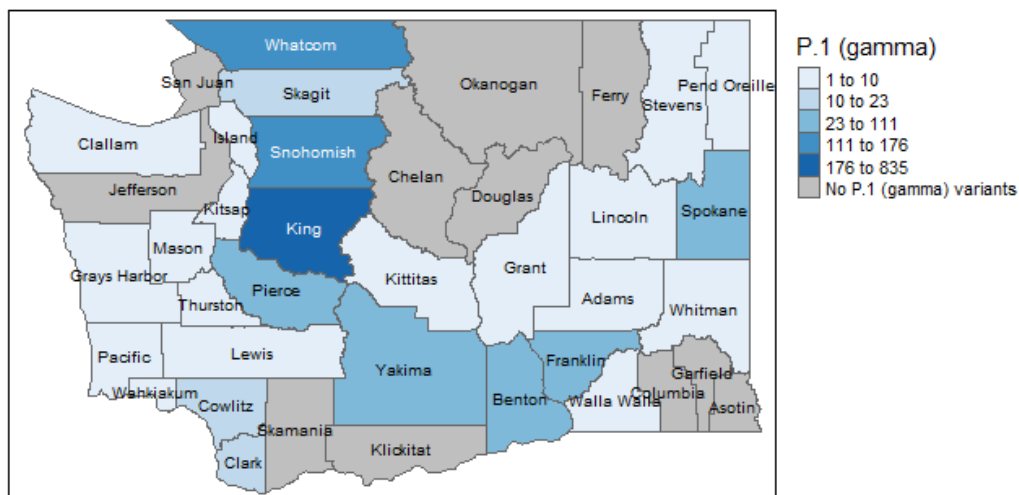
The P.1 (gamma) variant is highly infectious, transmissible and can quickly spread from person-to-person. Results from experimental research studies show that the P.1 (gamma) variant contains mutations that make it less likely to respond to antibody treatments.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of P.1 (gamma) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent P.1 (gamma)
Hospitalized	5.8%	2.9%	5.7%
Died from COVID	0.9%	0.6%	1.2%
Age 0-19	21.5%	25.7%	20.2%
Age 20-34	30%	31.9%	36%
Age 35-49	21.9%	22.6%	24.1%
Age 50-64	15.9%	12.6%	11.2%
Age 65-79	6.4%	3.9%	3.8%
Age 80+	2.2%	1.3%	2.7%
Unknown age	2.5%	2%	2%

Number of P.1 (gamma) cases sequenced by county of home address



Variant of Concern: B.1.617.2 (delta)

Total B.1.617.2 (delta) Detections: 656

Why are we concerned about this variant?:

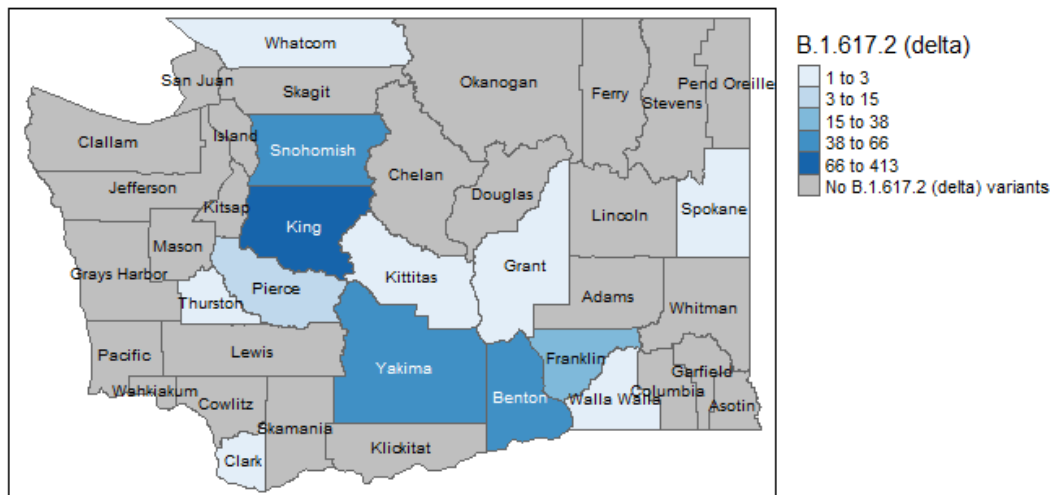
Based on preliminary evidence, some antibody treatments may be less effective against the B.1.617.2 (delta) variant, and vaccine effectiveness may be lower. Studies are ongoing to determine whether this variant is more transmissible.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of B.1.617.2 (delta) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent B.1.617.2 (delta)
Hospitalized	5.8%	2.9%	3.7%
Died from COVID	0.9%	0.6%	0.2%
Age 0-19	21.5%	25.7%	29.9%
Age 20-34	30%	31.9%	31.4%
Age 35-49	21.9%	22.6%	23.2%
Age 50-64	15.9%	12.6%	8.5%
Age 65-79	6.4%	3.9%	4.3%
Age 80+	2.2%	1.3%	0.5%
Unknown age	2.5%	2%	2.3%

Number of B.1.617.2 (delta) cases sequenced by county of home address



Variant of Interest: B.1.427 (epsilon)

Total B.1.427 (epsilon) Detections: 386

Why are we concerned about this variant?:

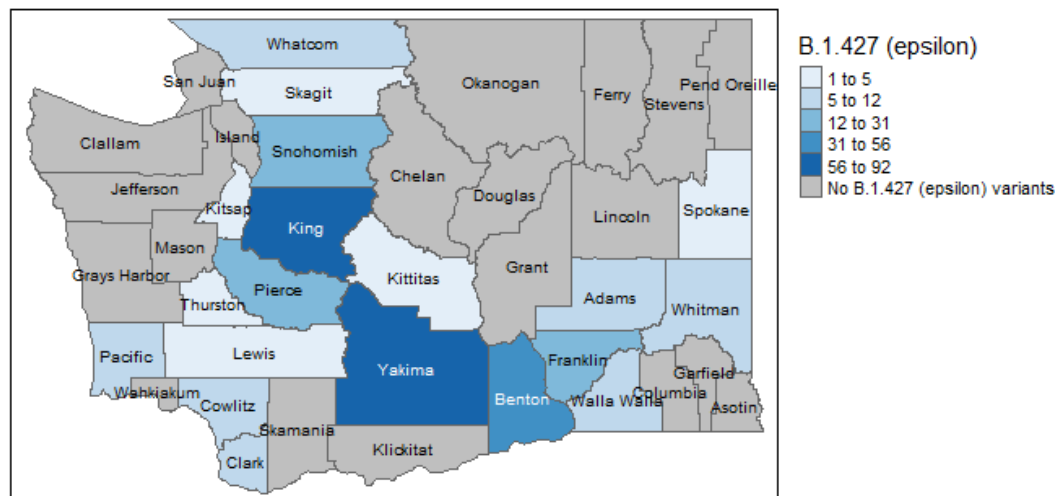
The B.1.427 (epsilon) variant can quickly spread from person-to-person. Results from experimental research studies show that this variant contains mutations that make it less likely to respond to antibody treatments.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of B.1.427 (epsilon) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent B.1.427 (epsilon)
Hospitalized	5.8%	2.9%	0.8%
Died from COVID	0.9%	0.6%	0.8%
Age 0-19	21.5%	25.7%	27.5%
Age 20-34	30%	31.9%	30.6%
Age 35-49	21.9%	22.6%	22.8%
Age 50-64	15.9%	12.6%	12.2%
Age 65-79	6.4%	3.9%	3.6%
Age 80+	2.2%	1.3%	2.1%
Unknown age	2.5%	2%	1.3%

Number of B.1.427 (epsilon) cases sequenced by county of home address



Variant of Interest: B.1.429 (epsilon)

Total B.1.429 (epsilon) Detections: 3089

Why are we concerned about this variant?:

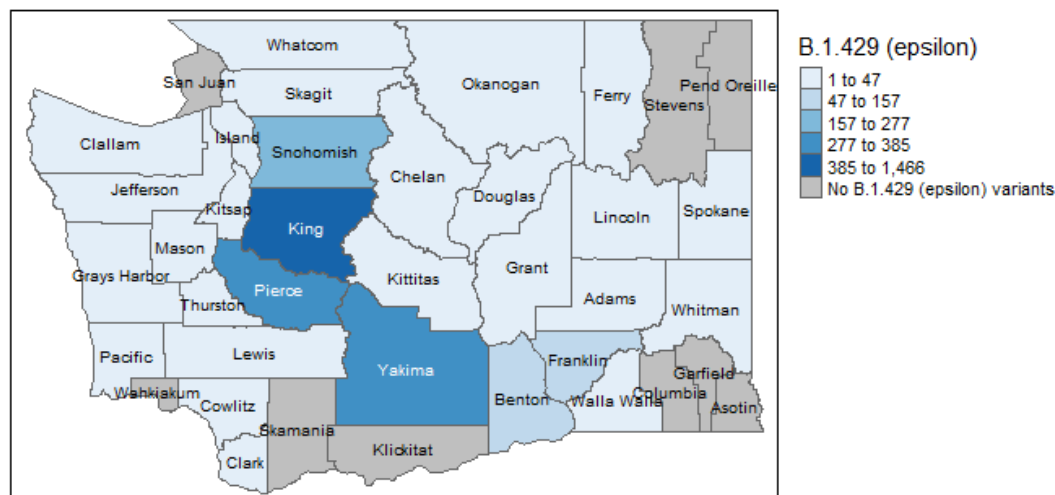
The B.1.429 (epsilon) variant can quickly spread from person-to-person. Results from experimental research studies show that the B.1.429 (epsilon) variant contains mutations that make it less likely to respond to antibody treatments.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of B.1.429 (epsilon) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent B.1.429 (epsilon)
Hospitalized	5.8%	2.9%	2.3%
Died from COVID	0.9%	0.6%	0.6%
Age 0-19	21.5%	25.7%	24.3%
Age 20-34	30%	31.9%	31.7%
Age 35-49	21.9%	22.6%	22%
Age 50-64	15.9%	12.6%	14%
Age 65-79	6.4%	3.9%	4.5%
Age 80+	2.2%	1.3%	1.1%
Unknown age	2.5%	2%	2.4%

Number of B.1.429 (epsilon) cases sequenced by county of home address



Variant of Interest: B.1.526 (iota)

Total B.1.526 (iota) Detections: 576

Why are we concerned about this variant?:

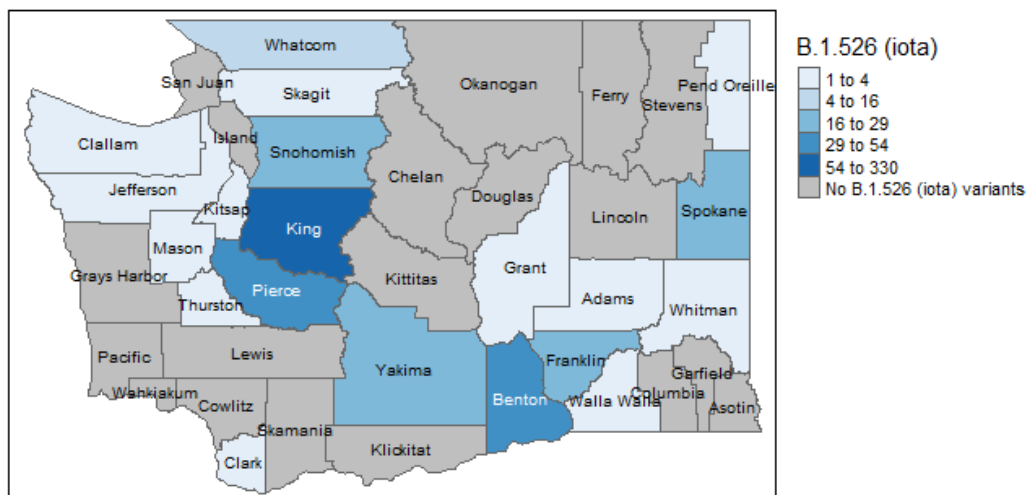
The B.1.526 (iota) variants contain mutations that can make it less responsive to antibody treatments.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of B.1.526 (iota) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent B.1.526 (iota)
Hospitalized	5.8%	2.9%	1.7%
Died from COVID	0.9%	0.6%	0.5%
Age 0-19	21.5%	25.7%	27.1%
Age 20-34	30%	31.9%	33.3%
Age 35-49	21.9%	22.6%	25.2%
Age 50-64	15.9%	12.6%	10.2%
Age 65-79	6.4%	3.9%	2.8%
Age 80+	2.2%	1.3%	0.7%
Unknown age	2.5%	2%	0.7%

Number of B.1.526 (iota) cases sequenced by county of home address



Variant of Interest: B.1.525 (eta)

Total B.1.525 (eta) Detections: 71

Why are we concerned about this variant?:

The B.1.525 (eta) variant contains mutations that can make it less responsive to antibody treatments.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of B.1.525 (eta) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent B.1.525 (eta)
Hospitalized	5.8%	2.9%	1.4%
Died from COVID	0.9%	0.6%	1.4%
Age 0-19	21.5%	25.7%	31%
Age 20-34	30%	31.9%	26.8%
Age 35-49	21.9%	22.6%	25.4%
Age 50-64	15.9%	12.6%	8.5%
Age 65-79	6.4%	3.9%	5.6%
Age 80+	2.2%	1.3%	0%
Unknown age	2.5%	2%	2.8%

Number of B.1.525 (eta) cases sequenced by county of home address



Variant of Interest: P.2 (zeta)

Total P.2 (zeta) Detections: 37

Why are we concerned about this variant?:

The P.2 (zeta) variant contains mutations that can make it less responsive to antibody treatments.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of P.2 (zeta) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent P.2 (zeta)
Hospitalized	5.8%	2.9%	0%
Died from COVID	0.9%	0.6%	0%
Age 0-19	21.5%	25.7%	29.7%
Age 20-34	30%	31.9%	24.3%
Age 35-49	21.9%	22.6%	24.3%
Age 50-64	15.9%	12.6%	18.9%
Age 65-79	6.4%	3.9%	0%
Age 80+	2.2%	1.3%	0%
Unknown age	2.5%	2%	2.7%

Number of P.2 (zeta) cases sequenced by county of home address



Variant of Interest: B.1.617.1 (kappa)

Total B.1.617.1 (kappa) Detections: 42

Why are we concerned about this variant?:

Based on preliminary evidence, some antibody treatments may be less effective against the B.1.617.1 (kappa) variant. Studies are ongoing to determine whether this variant is more transmissible.

For further information, see the [CDC's variant information website](#).

Demographics and clinical characteristics of B.1.617.1 (kappa) cases in Washington:

Characteristic	Percent 2021 positive cases	Percent 2021 sequenced cases	Percent B.1.617.1 (kappa)
Hospitalized	5.8%	2.9%	2.4%
Died from COVID	0.9%	0.6%	0%
Age 0-19	21.5%	25.7%	16.7%
Age 20-34	30%	31.9%	42.9%
Age 35-49	21.9%	22.6%	26.2%
Age 50-64	15.9%	12.6%	9.5%
Age 65-79	6.4%	3.9%	4.8%
Age 80+	2.2%	1.3%	0%
Unknown age	2.5%	2%	0%

Number of B.1.617.1 (kappa) cases sequenced by county of home address



We gratefully acknowledge the GISAID initiative, original laboratories responsible for obtaining the specimens, as well as the submitting laboratories where the genome data were generated and shared via GISAID.

The following labs have contributed sequencing data:

UW Virology Lab

Seattle Flu Study

Centers for Disease Control and Prevention

Altius Institute for Biomedical Research

Washington State Department of Health Public Health Laboratories

Curative Labs

Oregon Health Sciences University

Providence St. Joseph Health Molecular Genomics Laboratory

Quest

Institute for Systems Biology

Atlas Genomics

Ginkgo Bioworks

Virology, University of Washington

University of Washington Medical Center, Seattle Flu Study

Center for Genome Sciences, USAMRIID

NIH

Oregon State Public Health Laboratory

Andersen lab at Scripps Research

Gravity Diagnostics, LLC

Lauring Lab, University of Michigan, Department of Microbiology and Immunology

United States Air Force School of Aerospace Medicine

Grubaugh Lab - Yale School of Public Health

Kashi Clinical Laboratory

Arizona State University

Clinical Division, Fred Hutchinson Cancer Research Center

Hyde Lab
IDEH and ID Genomics
Molecular Infectious Disease
OHSU-MM Lab
The Jackson Laboratory
TwinStrand Biosciences, Inc.
VGTI/ONPRC, Oregon Health & Science University

The following clinical laboratories have contributed specimens for sequencing:

Laboratory Medicine, University of Washington
WA State Department of Health
Seattle Flu Study
Altius Institute for Biomedical Sciences
LabCorp
Northwest Laboratory
Atlas Genomics
OHSU Lab Services Molecular Microbiology Lab
Centers for Disease Control and Prevention
Providence Laboratories
Quest Diagnostics
Swedish Medical Center
Helix/Illumina
Evergreen Healthcare
The Vancouver Clinic
Benaroya Research Institute
Harborview Medical Center
Kashi Clinical Laboratory
United States Air Force School of Aerospace Medicine
Fidalab

IEH Laboratories and Consulting Group

Kaiser Permanente

Madigan Army Medical Center

Mayo Clinic Laboratories

Seattle VA Medical Center

TwinStrand Biosciences, Inc.

Valley Medical Center
