Subject **Fw: DOH Public Records Center :: D000656-012522**
From [redacted]
To christinem@fluoridefreepeel.ca <christinem@fluoridefreepeel.ca>
Date 2022-01-28 02:50 PM

roundcube

Hello Christine,

I live in Washington State. I submitted a public records request to the WA State Department of Health for the studies and/or reports purification of the SARS COV 2 virus as per your example.

"The Washington State Public Health Lab (PHL) provided the following statement in response to your request, "The WAPHL has not attempted to isolate SARS-CoV-2 from any specimen or matrix. Nor does the PHL have in its possession isolated viable SARS-CoV-2 virus. The WAPHL performs diagnostic testing that is PCR based and does not require virus isolation. Next generation sequencing is performed on SARS-CoV-2 positive patient samples using extracted genomic material, not virus isolates."

You will receive the next installment on or before July 25, 2022 and will continue to receive installments until your request has been fulfilled.

Should you no longer need this information, please contact our office by responding directly to this email.

Sincerely,

Washington State Department of Health
Disease Control and Health Statistics
Public Records

Please see their email below.

Thank you for all you are doing to bring truth to light!

Be Well,

[redacted]

----- Forwarded Message -----
**From:** WA State DOH Records Center <washingtondoh@govqa.us>
**To:** [redacted]
**Sent:** Thursday, January 27, 2022, 04:03:09 PM PST
**Subject:** DOH Public Records Center :: D000656-012522

--- Please respond above this line ---

Washington State Department of Health

Reference # D000656-012522

Dear [redacted]

The Department of Health received a public records request from you on January 25, 2022. You requested the following:

"This is a formal request for access to general records, made under the Freedom of Information Act.

Description of Requested Records:

All studies and/or reports in the possession, custody or control of the Washington Department of Health describing the purification of the alleged "COVID-19 virus" (aka "SARS-COV-2", including any alleged "variants") directly from a sample taken from a diseased human, where the patient sample was not first combined with any other source of genetic material (i.e. monkey kidney cells aka Vero cells; fetal bovine serum).

Clarification of Request:

Please note that I am not requesting studies/reports where researchers failed to purify the suspected "virus" and instead: cultured something, and/or performed an amplification test (i.e. PCR), and/or fabricated a genome from sequences (allegedly) detected in an impure substance, and/or produced electron microscopy images of unpurified things. I am already aware that according to virus theory a "virus" requires host cells in order to replicate, and am not requesting records that describe replication of a 'virus' without host cells. Nor am I requesting records that describe a strict fulfillment of Koch's Postulates, or records that describe a suspected "virus" floating in a vacuum, or private patient information.

I simply request records that describe purification (separation of the alleged virus from everything else in the patient sample, as per standard laboratory practices for the purification of other very small things).

Please note that my request includes any study/report matching the above description, authored by anyone, anywhere.

If any records match the above description of requested records and are currently available in the public domain, please provide enough information about each record so that I may identify and access each one with certainty (i.e. title, author(s), date, journal, where the public may access it). Please provide URLs where possible.

Format: Pdf documents sent to me via email; I do not wish for anything to be shipped to me."

The Department of Health (DOH) is currently experiencing a high volume of public records requests. Our estimate of time is based on the number of requests in the queue received prior to your request, the volume of records we have, the volume of records you have asked us to search for, and the availability of staff to search for, review, and produce responsive records. There is also a delay with turnaround times as DOH staff are helping support the COVID-19 pandemic response.

The Department of Health is in the process of identifying, gathering, and reviewing the records responsive to your request.

WAC 246-08-990 (RCW 42.56.120) authorizes the Department of Health to collect fees for providing copies either electronically or in paper format. After we have determined the number of records responsive to your request, we will give you a cost estimate for production of the records. Here is a link to the public records fee schedule.
Your request requires collecting, copying and reviewing a large number of records. Completed documents will be provided to you in installments.

We have located and assembled records responsive to your request for **installment #1**, copies of which are now available to you. These records have been uploaded to the DOH Public Records Center. You will need to log into your portal account to access your requested records.

**NOTE: Pop-up Blockers on your web browser will need to be disabled to download files from this site.**

The Washington State Public Health Lab (PHL) provided the following statement in response to your request, "The WAPHL has not attempted to isolate SARS-CoV-2 from any specimen or matrix. Nor does the PHL have in its

possession isolated viable SARS-CoV-2 virus. The WAPHL performs diagnostic testing that is PCR based and does not require virus isolation. Next generation sequencing is performed on SARS-CoV-2 positive patient samples using extracted genomic material, not virus isolates."

You will receive the next installment on or before July 25, 2022 and will continue to receive installments until your request has been fulfilled.

Should you no longer need this information, please contact our office by responding directly to this email.

Sincerely,

Washington State Department of Health
Disease Control and Health Statistics
Public Records

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# SARS-CoV-2 Sequencing and Variants in Washington State

## Washington State Department of Health

**August 04, 2021**

**To request this document in another format, call 1-800-525-0127. Deaf or hard of hearing customers, please call 711 (Washington Relay) or email civil.rights@doh.wa.gov.**

**Publication Number:** 420-316

**For more information or additional copies of this report:**

Disease Control and Health Statistics
Public Health Outbreak Coordination, Information, and Surveillance
1610 NE 150th Street, MS: K17-9
Shoreline, WA 98155

Phone: 206-418-5700 (24-hour contact for local health jurisdictions only)
Email: CommDisEpi@doh.wa.gov

# SARS-CoV-2 Sequencing and Variants in Washington State

# Washington State Department of Health

# August 04, 2021

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 August 03, 2021)

- During the month of June 2021, **23%** 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.

- **33685 (7.7%)** 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.

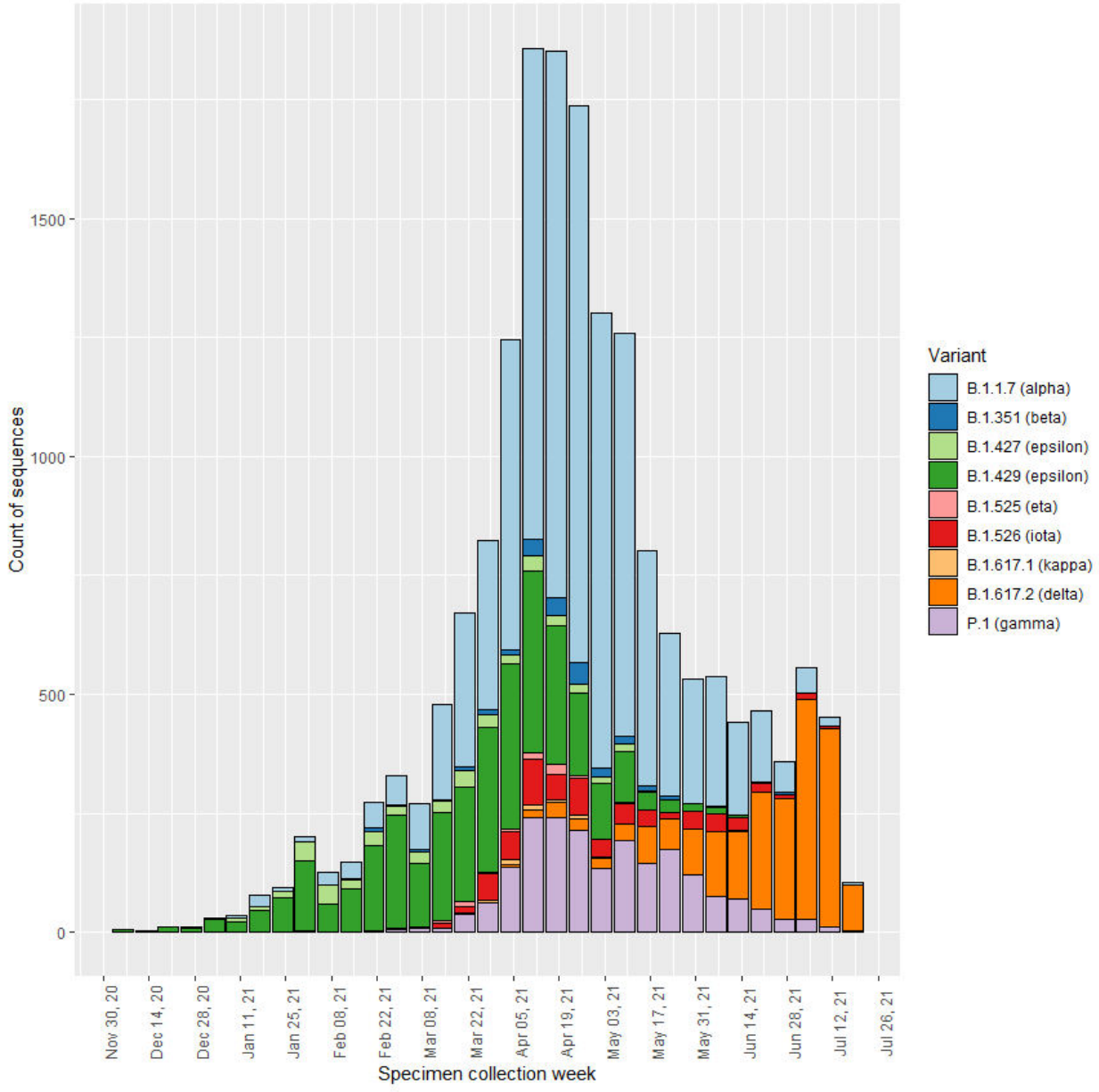
These include:

| 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 | 8,866 | 2021-01-07 | 2021-07-19 |
| B.1.351 (beta) | South Africa | Variant of concern | 233 | 2021-01-29 | 2021-06-29 |
| P.1 (gamma) | Brazil | Variant of concern | 1,988 | 2021-02-06 | 2021-07-19 |
| B.1.617.2 (delta) | India | Variant of concern | 2,123 | 2021-04-03 | 2021-07-21 |
| B.1.427 (epsilon) | California | Variant of interest | 410 | 2020-12-11 | 2021-06-21 |
| B.1.429 (epsilon) | California | Variant of interest | 3,330 | 2020-11-20 | 2021-06-24 |
| B.1.526 (iota) | New York | Variant of interest | 657 | 2021-01-21 | 2021-07-19 |
| B.1.525 (eta) | New York | Variant of interest | 73 | 2021-02-02 | 2021-06-08 |
| B.1.617.1 (kappa) | India | Variant of interest | 43 | 2021-03-22 | 2021-06-14 |
| 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.
- Sublineages of P.1 and B.1.351 (P.1.1, P.1.2, B.1.351.2, B.1.351.3) are aggregated with the parent lineage. AY.1, AY.2, and AY.3 are aggregated with B.1.617.2.
- P.2 (Zeta) was removed from the variants of interest list by CDC on 7/27/21 due to declining prevalence and very few detections in recent months. DOH will no longer be reporting on P.2.

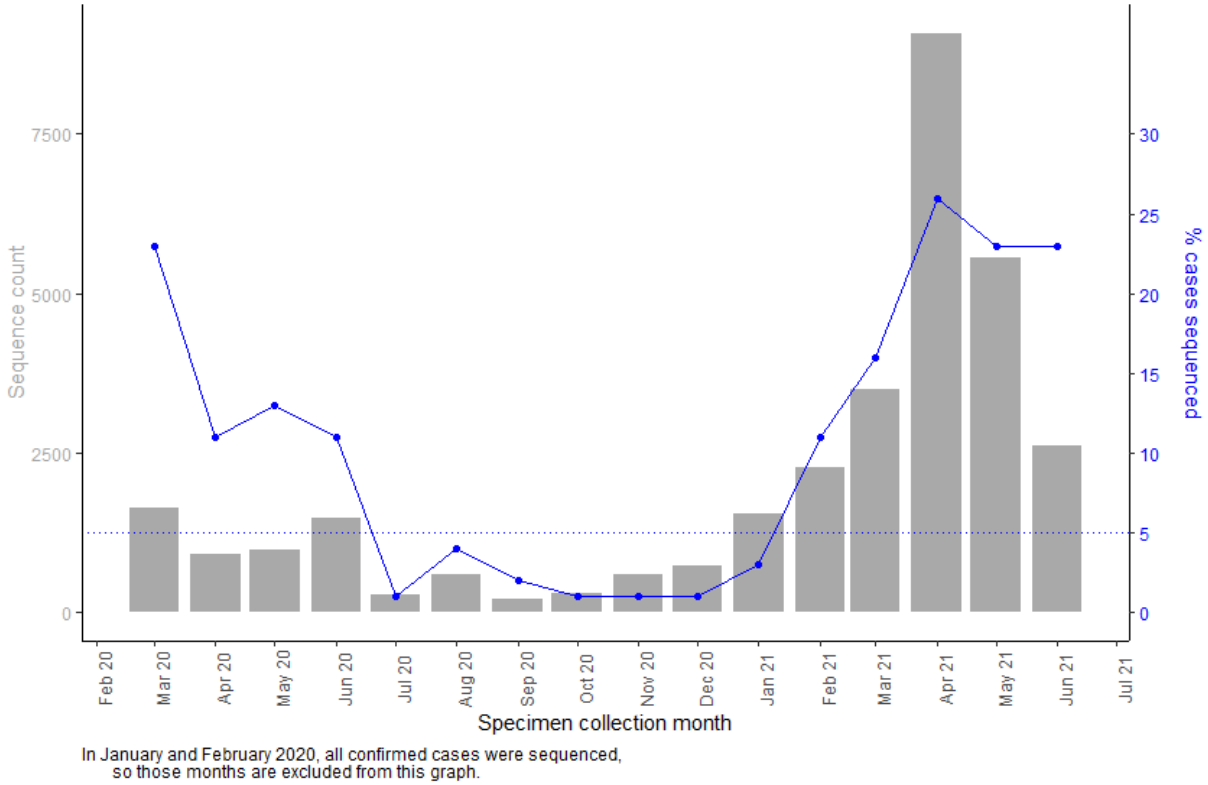
# Sequencing Trends Over Time

## Epidemiologic curve of variants of interest and concern by week of specimen collection date as of Aug 03, 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.
- Sublineages of P.1 and B.1.351 (P.1.1, P.1.2, B.1.351.2, B.1.351.3) are aggregated with the parent lineage. AY.1, AY.2, and AY.3 are aggregated with B.1.617.2.

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



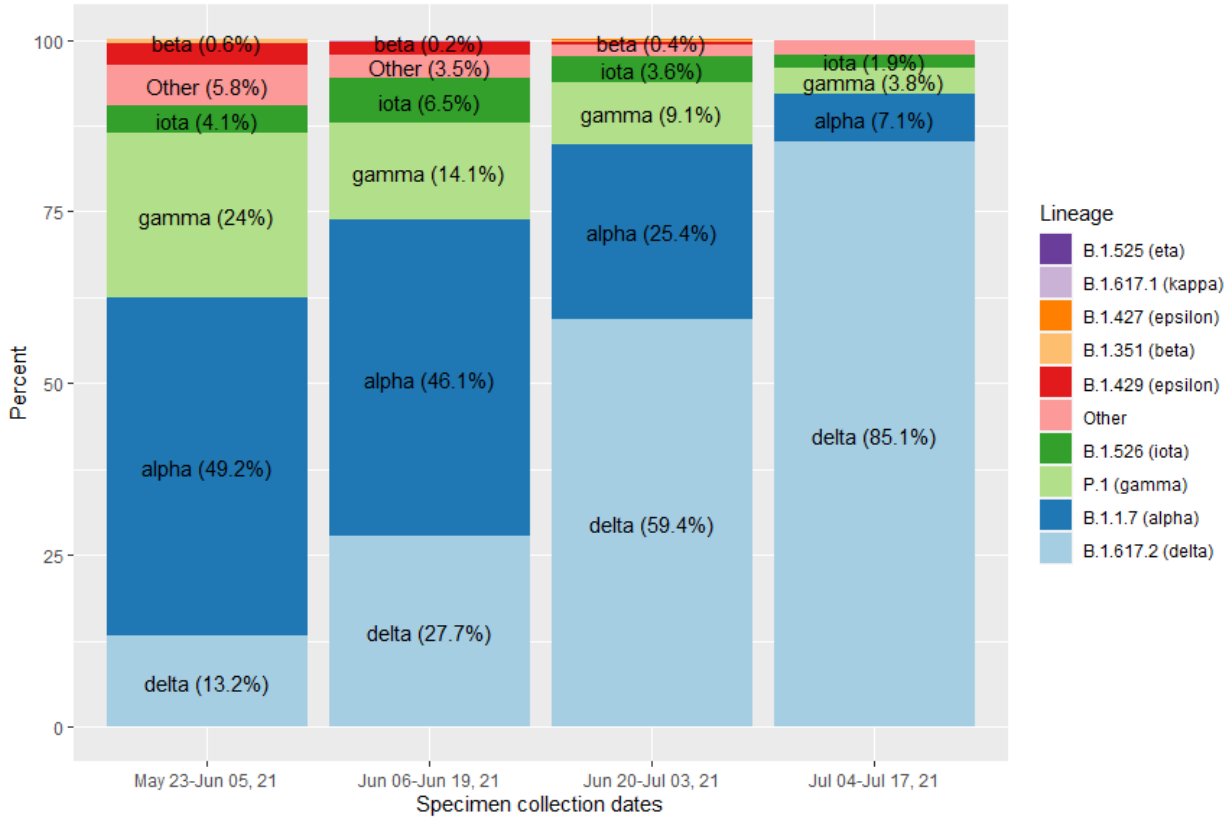

- We are not sequencing samples from every confirmed COVID-19 case at this time. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- 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.
- This includes all sequences available with a location of Washington in GISAID www.gisaid.org.

## 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), 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.
- Sublineages of P.1 and B.1.351 (P.1.1, P.1.2, B.1.351.2, B.1.351.3) are aggregated with the parent lineage and included in parent lineage's proportion. AY.1, AY.2, and AY.3 are aggregated with B.1.617.2.

To see the national trends, visit the CDC's variant proportions page.

**The table below shows the number of variants of concern detected by county of home address since the beginning of the pandemic**

| County | B.1.1.7 (alpha) count | B.1.351 (beta) count | P.1 (gamma) count | B.1.617.2 (delta) count |
|---|---|---|---|---|
| Adams | 22 | 0 | 3 | 4 |
| Asotin | 8 | 0 | 0 | 0 |
| Benton | 360 | 1 | 70 | 248 |
| Chelan | 16 | 0 | 1 | 1 |
| Clallam | 61 | 0 | 11 | 13 |
| Clark | 68 | 1 | 25 | 10 |
| Cowlitz | 29 | 0 | 27 | 1 |
| Douglas | 15 | 0 | 0 | 0 |
| Ferry | 2 | 0 | 0 | 0 |
| Franklin | 282 | 2 | 97 | 182 |
| Grant | 48 | 0 | 12 | 12 |
| Grays Harbor | 38 | 2 | 1 | 1 |
| Island | 28 | 0 | 6 | 13 |
| Jefferson | 23 | 0 | 0 | 1 |
| King | 4,586 | 163 | 902 | 994 |
| Kitsap | 54 | 2 | 6 | 6 |
| Kittitas | 26 | 0 | 15 | 7 |
| Klickitat | 7 | 0 | 0 | 4 |
| Lewis | 60 | 0 | 6 | 0 |
| Lincoln | 5 | 0 | 2 | 2 |
| Mason | 20 | 0 | 2 | 9 |
| Okanogan | 11 | 0 | 0 | 2 |
| Pacific | 19 | 0 | 7 | 1 |
| Pend Oreille | 2 | 0 | 1 | 0 |
| Pierce | 792 | 23 | 118 | 95 |

| County | B.1.1.7 (alpha) count | B.1.351 (beta) count | P.1 (gamma) count | B.1.617.2 (delta) count |
|---|---|---|---|---|
| San Juan | 6 | 0 | 0 | 0 |
| Skagit | 167 | 0 | 26 | 16 |
| Skamania | 2 | 0 | 0 | 0 |
| Snohomish | 1,067 | 20 | 193 | 157 |
| Spokane | 168 | 1 | 115 | 49 |
| Stevens | 10 | 0 | 1 | 0 |
| Thurston | 120 | 4 | 10 | 29 |
| Wahkiakum | 7 | 0 | 2 | 0 |
| Walla Walla | 8 | 0 | 5 | 23 |
| Whatcom | 435 | 3 | 218 | 36 |
| Whitman | 68 | 0 | 7 | 1 |
| Yakima | 224 | 11 | 98 | 205 |

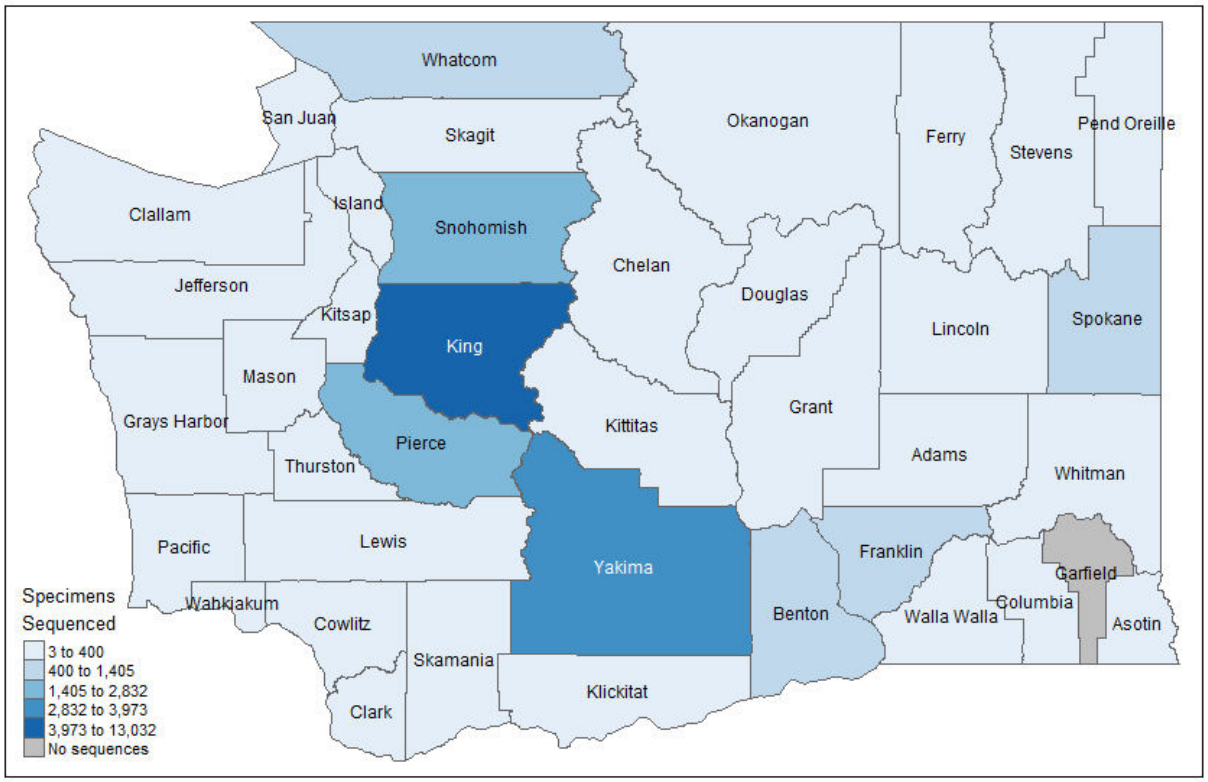
- Sublineages of P.1 and B.1.351 (P.1.1, P.1.2, B.1.351.2, B.1.351.3) are aggregated with the parent lineage. AY.1, AY.2, and AY.3 are aggregated with B.1.617.2.

**The table below shows the number of variants of interest detected by county of home address since the beginning of the pandemic.**

| County | B.1.427 (epsilon) count | B.1.429 (epsilon) count | B.1.526 (iota) count | B.1.525 (eta) count | B.1.617.1 (kappa) count | B.1.617.3 count |
|---|---|---|---|---|---|---|
| Adams | 12 | 6 | 1 | 0 | 0 | 0 |
| Asotin | 0 | 0 | 0 | 0 | 0 | 0 |
| Benton | 56 | 158 | 52 | 20 | 0 | 0 |
| Chelan | 0 | 7 | 0 | 0 | 0 | 0 |
| Clallam | 0 | 5 | 1 | 0 | 0 | 0 |
| Clark | 7 | 17 | 2 | 0 | 0 | 0 |
| Cowlitz | 9 | 14 | 0 | 0 | 0 | 0 |
| Douglas | 0 | 2 | 0 | 0 | 0 | 0 |
| Ferry | 0 | 1 | 0 | 0 | 0 | 0 |
| Franklin | 26 | 132 | 28 | 11 | 0 | 0 |
| Grant | 0 | 25 | 6 | 0 | 0 | 0 |
| Grays Harbor | 0 | 21 | 0 | 0 | 0 | 0 |
| Island | 0 | 2 | 0 | 0 | 0 | 0 |
| Jefferson | 0 | 6 | 2 | 0 | 0 | 0 |
| King | 108 | 1,633 | 356 | 28 | 37 | 0 |
| Kitsap | 1 | 27 | 4 | 0 | 0 | 0 |
| Kittitas | 1 | 6 | 0 | 0 | 0 | 0 |
| Klickitat | 0 | 0 | 1 | 0 | 0 | 0 |
| Lewis | 3 | 19 | 0 | 0 | 0 | 0 |
| Lincoln | 0 | 1 | 0 | 0 | 0 | 0 |
| Mason | 0 | 2 | 1 | 0 | 0 | 0 |
| Okanogan | 0 | 2 | 0 | 0 | 0 | 0 |
| Pacific | 10 | 10 | 0 | 0 | 0 | 0 |
| Pend Oreille | 0 | 0 | 3 | 0 | 0 | 0 |
| Pierce | 25 | 407 | 60 | 2 | 0 | 0 |

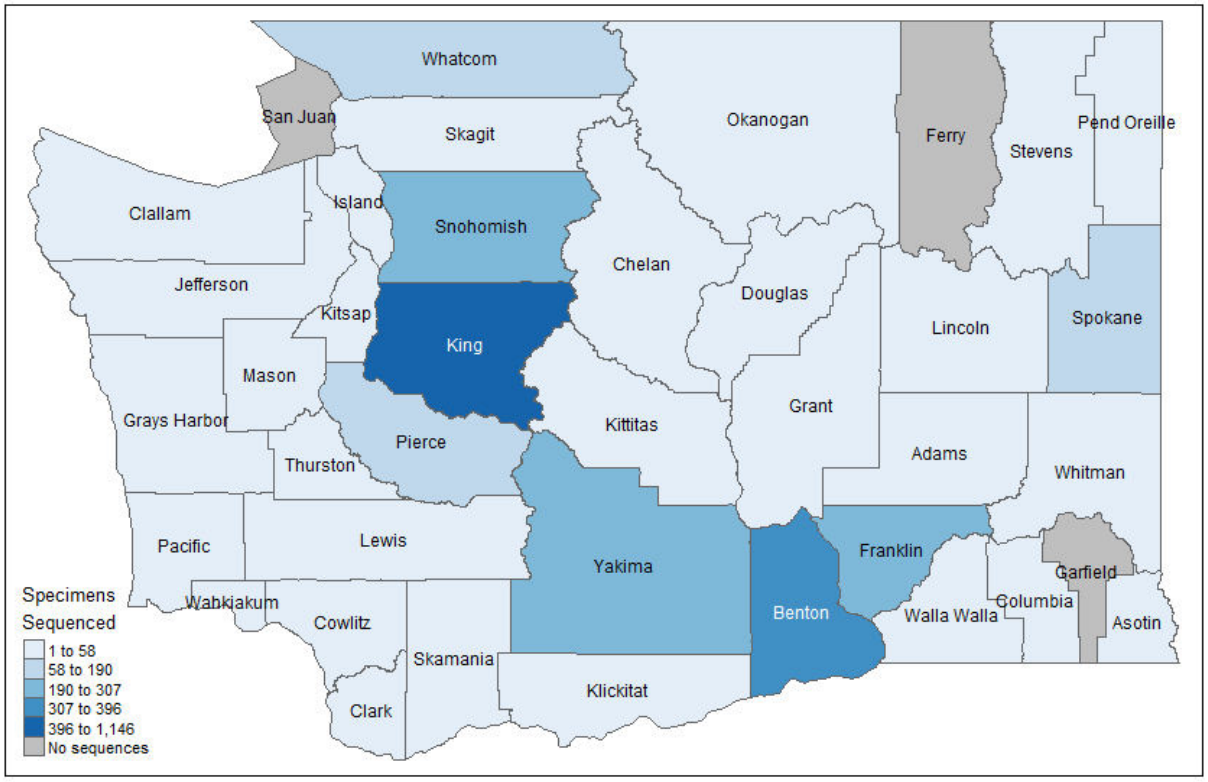
| County | B.1.427 (epsilon) count | B.1.429 (epsilon) count | B.1.526 (iota) count | B.1.525 (eta) count | B.1.617.1 (kappa) count | B.1.617.3 count |
|---|---|---|---|---|---|---|
| San Juan | 0 | 0 | 0 | 0 | 0 | 0 |
| Skagit | 1 | 18 | 1 | 0 | 0 | 0 |
| Skamania | 0 | 0 | 2 | 0 | 0 | 0 |
| Snohomish | 31 | 304 | 32 | 5 | 3 | 0 |
| Spokane | 4 | 49 | 40 | 4 | 1 | 0 |
| Stevens | 0 | 0 | 2 | 0 | 1 | 0 |
| Thurston | 5 | 28 | 2 | 0 | 0 | 0 |
| Wahkiakum | 0 | 0 | 0 | 0 | 0 | 0 |
| Walla Walla | 7 | 4 | 3 | 0 | 0 | 0 |
| Whatcom | 6 | 31 | 18 | 2 | 1 | 0 |
| Whitman | 6 | 8 | 4 | 0 | 0 | 0 |
| Yakima | 92 | 385 | 36 | 1 | 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 15% 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.1.617.2 (delta) | 405 | 35% | 10% |
| B.1.1.7 (alpha) | 343 | 30% | 41% |
| P.1 (gamma) | 175 | 15% | 9% |
| B.1.429 (epsilon) | 116 | 10% | 15% |
| B.1.526 (iota) | 27 | 2% | 3% |
| B.1.427 (epsilon) | 11 | 1% | 2% |
| B.1.351 (beta) | 10 | 1% | 1% |
| B.1.525 (eta) | 4 | 0% | 0% |
| B.1.617.1 (kappa) | 1 | 0% | 0% |
| Other | 50 | 4% | 19% |
| Total | 1,142 | 100% | 100% |

- Sublineages of P.1 and B.1.351 (P.1.1, P.1.2, B.1.351.2, B.1.351.3) are aggregated with the parent lineage and included in parent lineage's proportion. AY.1, AY.2, and AY.3 are aggregated with B.1.617.2.

## Variant of Concern: B.1.1.7 (alpha)

Total B.1.1.7 (alpha) Detections: 8866

## Why are we concerned about this variant?:

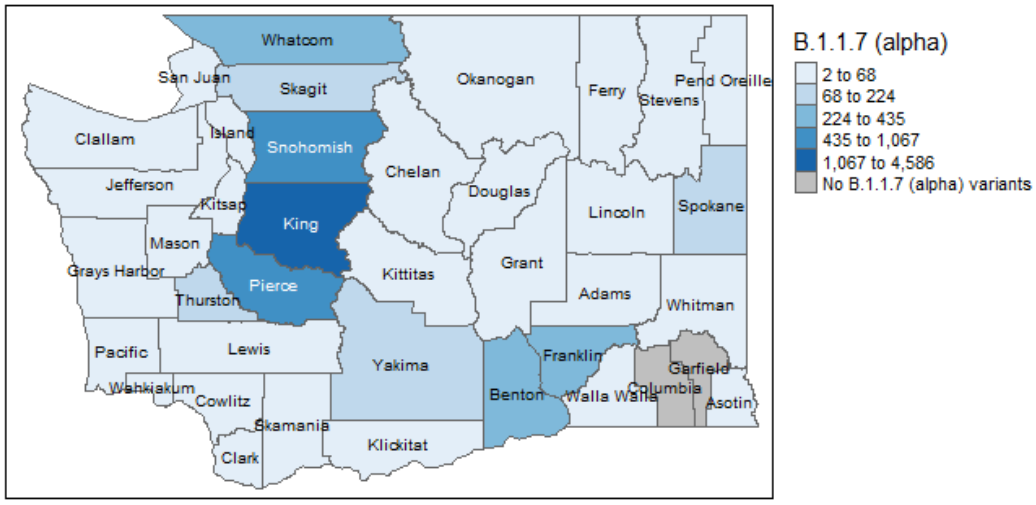
The B.1.1.7 (alpha) variant is highly infectious, transmissible and can quickly spread from person to person. Based on published studies, the B.1.1.7 (alpha) variant potentially causes more severe symptoms and increased risk of death in individuals who are infected.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 3.1% |
| Cases who died from COVID | 0.9% | 0.6% | 0.5% |
| Cases age 0-19 | 21.3% | 25.4% | 27% |
| Cases age 20-34 | 30.3% | 31.7% | 32.2% |
| Cases age 35-49 | 21.9% | 22.5% | 22.4% |
| Cases age 50-64 | 15.7% | 12.8% | 12% |
| Cases age 65-79 | 6.5% | 4.3% | 3.3% |
| Cases age 80+ | 2.1% | 1.3% | 1% |
| Cases Unknown age | 2.5% | 2% | 2% |

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



## Variant of Concern: B.1.351 (beta) including sublineages B.1.351.2, B.1.351.3

Total B.1.351 (beta) Detections: 231

## Why are we concerned about this variant?:

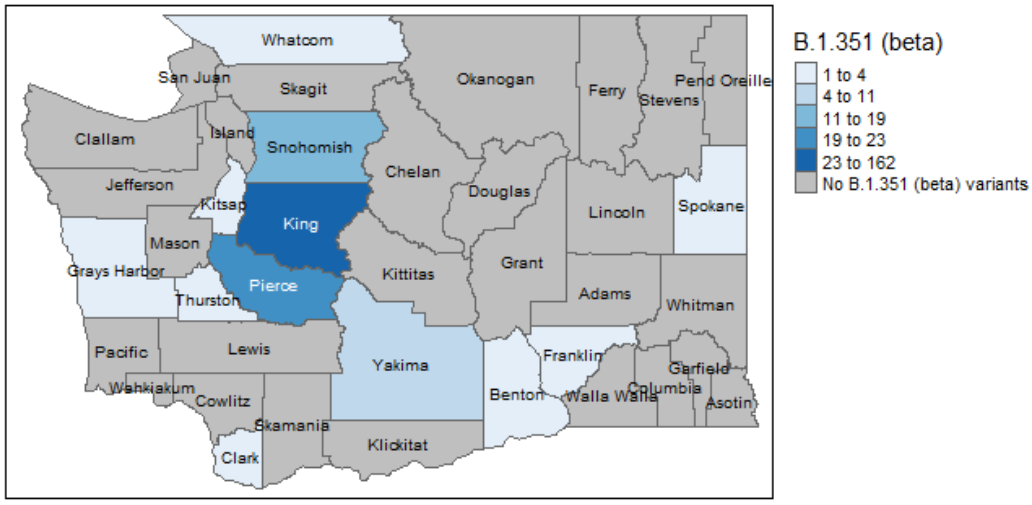
The B.1.351 (beta) variant is highly infectious, transmissible and can quickly spread from person to person. Results from experimental research studies show that the B.1.351 (beta) variant contains mutations that make it less likely to respond to antibody treatments.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 6.1% |
| Cases who died from COVID | 0.9% | 0.6% | 0.4% |
| Cases age 0-19 | 21.3% | 25.4% | 27.7% |
| Cases age 20-34 | 30.3% | 31.7% | 35.5% |
| Cases age 35-49 | 21.9% | 22.5% | 21.2% |
| Cases age 50-64 | 15.7% | 12.8% | 10.8% |
| Cases age 65-79 | 6.5% | 4.3% | 2.6% |
| Cases age 80+ | 2.1% | 1.3% | 0.4% |
| Cases Unknown age | 2.5% | 2% | 1.7% |

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



## Variant of Concern: P.1 (gamma) including sublineages P.1.1 and P.1.2.

Total P.1 (gamma) Detections: 1942

## Why are we concerned about this variant?:

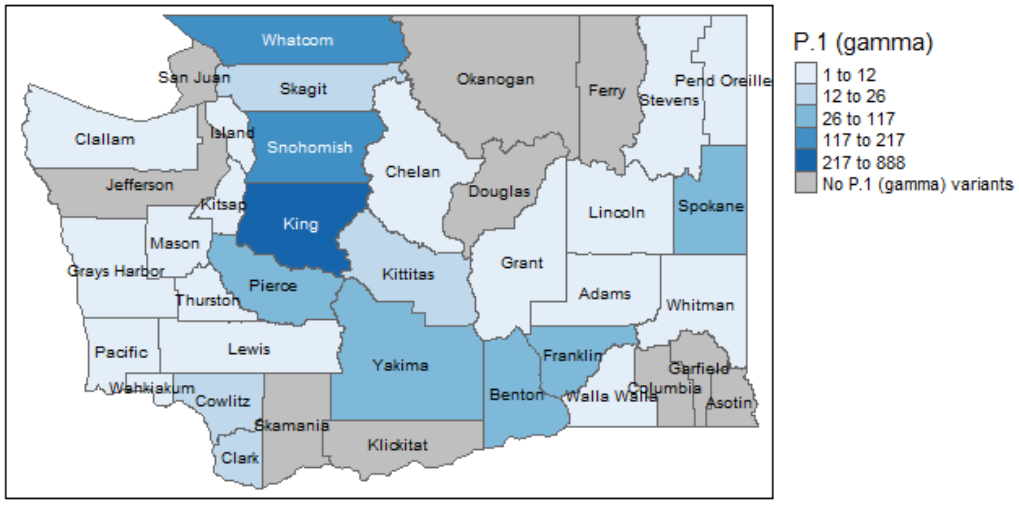
The P.1 (gamma) variant is highly infectious, transmissible and can quickly spread from person-to-person. Results from experimental research studies show that the P.1 (gamma) variant contains mutations that make it less likely to respond to antibody treatments.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 5.8% |
| Cases who died from COVID | 0.9% | 0.6% | 1.2% |
| Cases age 0-19 | 21.3% | 25.4% | 20% |
| Cases age 20-34 | 30.3% | 31.7% | 35.8% |
| Cases age 35-49 | 21.9% | 22.5% | 23.9% |
| Cases age 50-64 | 15.7% | 12.8% | 11.4% |
| Cases age 65-79 | 6.5% | 4.3% | 4.1% |
| Cases age 80+ | 2.1% | 1.3% | 2.7% |
| Cases 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) including sublineages AY.1, AY.2, and AY.3

Total B.1.617.2 (delta) Detections: 2123

## Why are we concerned about this variant?:

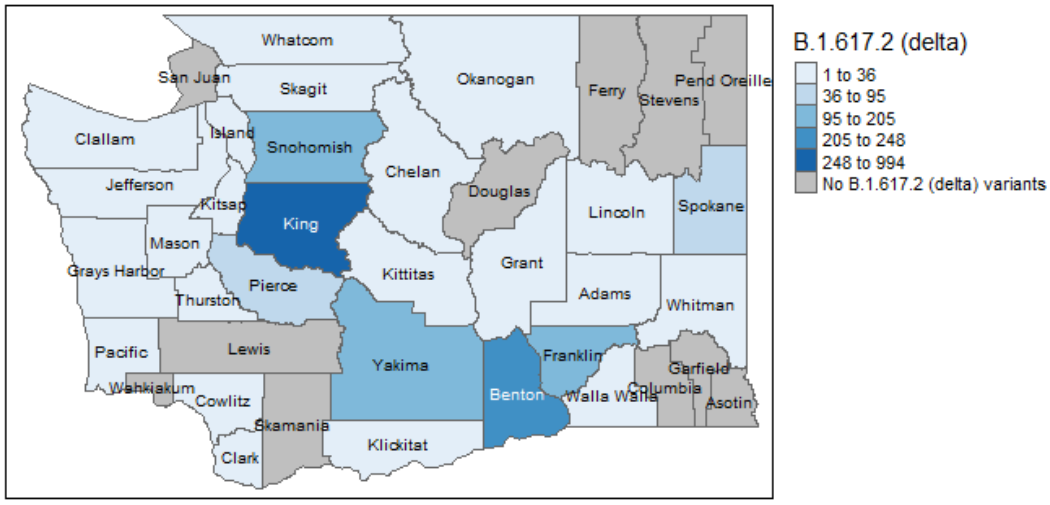
Based on preliminary evidence, some antibody treatments may be less effective against the B.1.617.2 (delta) variant, and vaccine effectiveness may be lower. Studies are ongoing to determine whether this variant is more transmissible.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 3.5% |
| Cases who died from COVID | 0.9% | 0.6% | 0.3% |
| Cases age 0-19 | 21.3% | 25.4% | 25.9% |
| Cases age 20-34 | 30.3% | 31.7% | 32.5% |
| Cases age 35-49 | 21.9% | 22.5% | 21.6% |
| Cases age 50-64 | 15.7% | 12.8% | 11.4% |
| Cases age 65-79 | 6.5% | 4.3% | 5.3% |
| Cases age 80+ | 2.1% | 1.3% | 1% |
| Cases 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: 410

## Why are we concerned about this variant?:

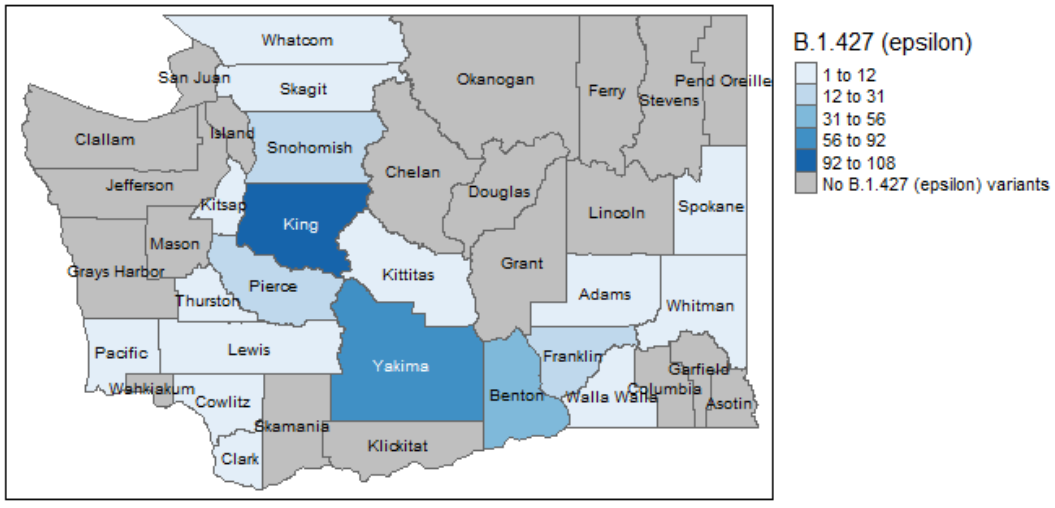
The B.1.427 (epsilon) variant can quickly spread from person-to-person. Results from experimental research studies show that this variant contains mutations that make it less likely to respond to antibody treatments.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 0.7% |
| Cases who died from COVID | 0.9% | 0.6% | 0.7% |
| Cases age 0-19 | 21.3% | 25.4% | 26.8% |
| Cases age 20-34 | 30.3% | 31.7% | 30.2% |
| Cases age 35-49 | 21.9% | 22.5% | 23.2% |
| Cases age 50-64 | 15.7% | 12.8% | 12.2% |
| Cases age 65-79 | 6.5% | 4.3% | 4.1% |
| Cases age 80+ | 2.1% | 1.3% | 2% |
| Cases Unknown age | 2.5% | 2% | 1.5% |

**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: 3330

## Why are we concerned about this variant?:

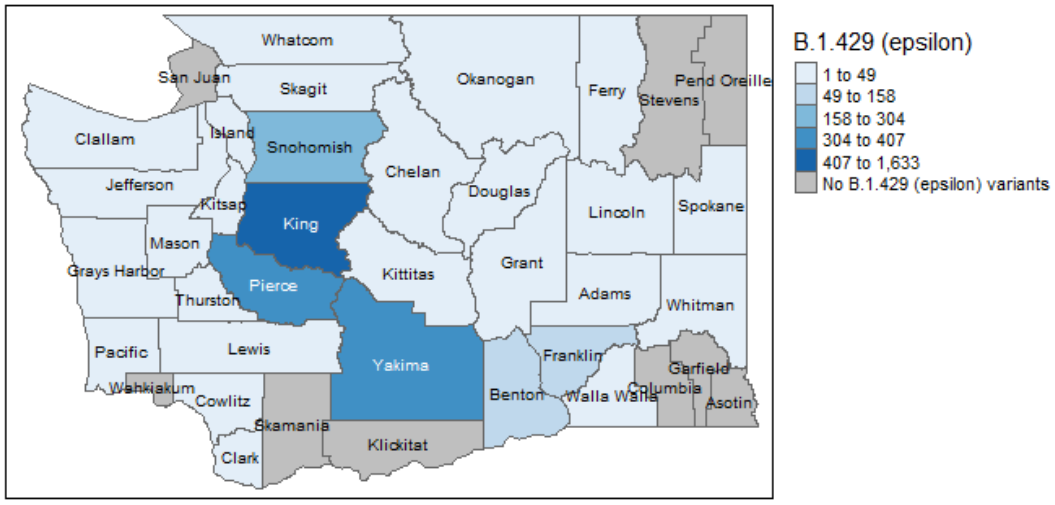
The B.1.429 (epsilon) variant can quickly spread from person-to-person. Results from experimental research studies show that the B.1.429 (epsilon) variant contains mutations that make it less likely to respond to antibody treatments.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 2.8% |
| Cases who died from COVID | 0.9% | 0.6% | 0.7% |
| Cases age 0-19 | 21.3% | 25.4% | 24.3% |
| Cases age 20-34 | 30.3% | 31.7% | 31.5% |
| Cases age 35-49 | 21.9% | 22.5% | 22.1% |
| Cases age 50-64 | 15.7% | 12.8% | 14% |
| Cases age 65-79 | 6.5% | 4.3% | 4.6% |
| Cases age 80+ | 2.1% | 1.3% | 1.1% |
| Cases 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: 657

## Why are we concerned about this variant?:

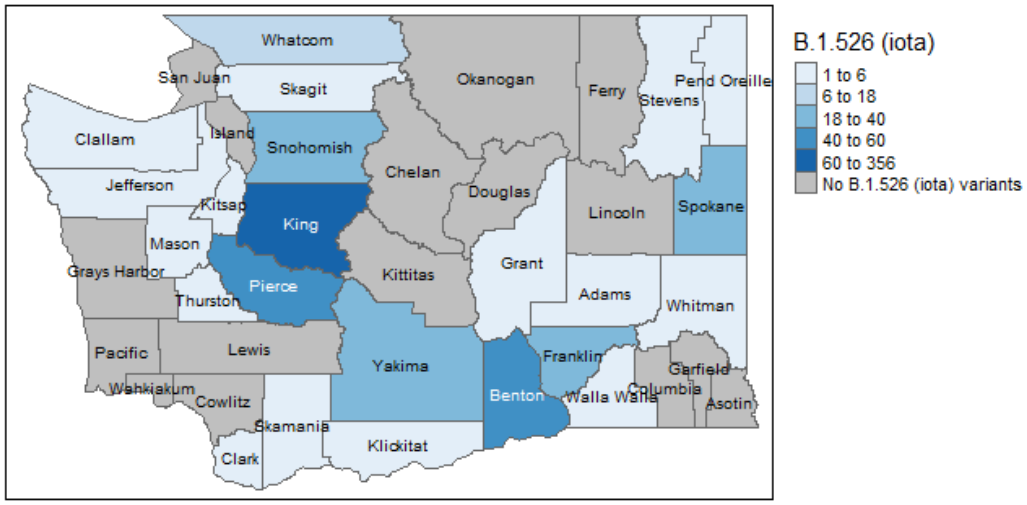
The B.1.526 (iota) variants contain mutations that can make it less responsive to antibody treatments.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 2.6% |
| Cases who died from COVID | 0.9% | 0.6% | 0.8% |
| Cases age 0-19 | 21.3% | 25.4% | 25.3% |
| Cases age 20-34 | 30.3% | 31.7% | 32.4% |
| Cases age 35-49 | 21.9% | 22.5% | 25.7% |
| Cases age 50-64 | 15.7% | 12.8% | 11.1% |
| Cases age 65-79 | 6.5% | 4.3% | 4.1% |
| Cases age 80+ | 2.1% | 1.3% | 0.6% |
| Cases Unknown age | 2.5% | 2% | 0.8% |

**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: 73

## Why are we concerned about this variant?:

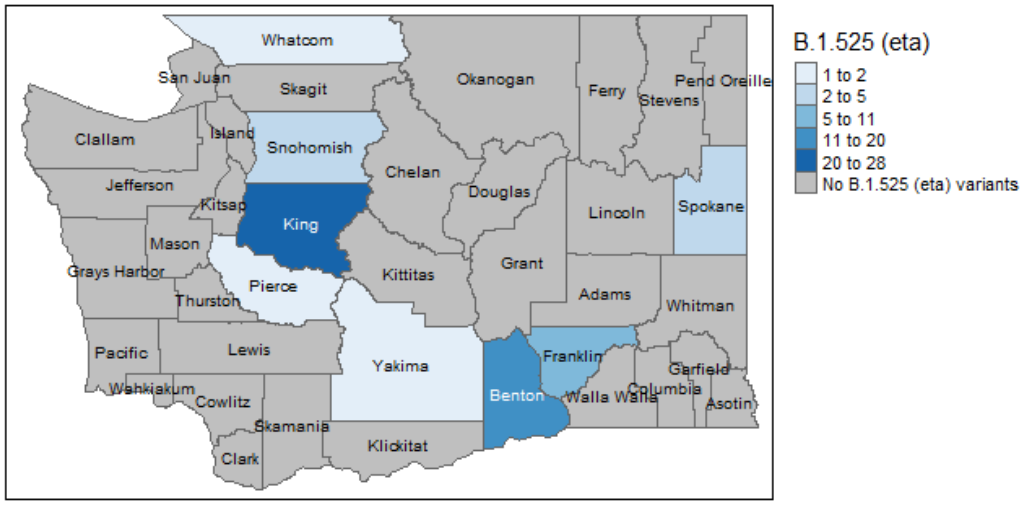
The B.1.525 (eta) variant contains mutations that can make it less responsive to antibody treatments.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 1.4% |
| Cases who died from COVID | 0.9% | 0.6% | 1.4% |
| Cases age 0-19 | 21.3% | 25.4% | 30.1% |
| Cases age 20-34 | 30.3% | 31.7% | 27.4% |
| Cases age 35-49 | 21.9% | 22.5% | 26% |
| Cases age 50-64 | 15.7% | 12.8% | 8.2% |
| Cases age 65-79 | 6.5% | 4.3% | 5.5% |
| Cases age 80+ | 2.1% | 1.3% | 0% |
| Cases Unknown age | 2.5% | 2% | 2.7% |

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



## Variant of Interest: B.1.617.1 (kappa)

Total B.1.617.1 (kappa) Detections: 43

## Why are we concerned about this variant?:

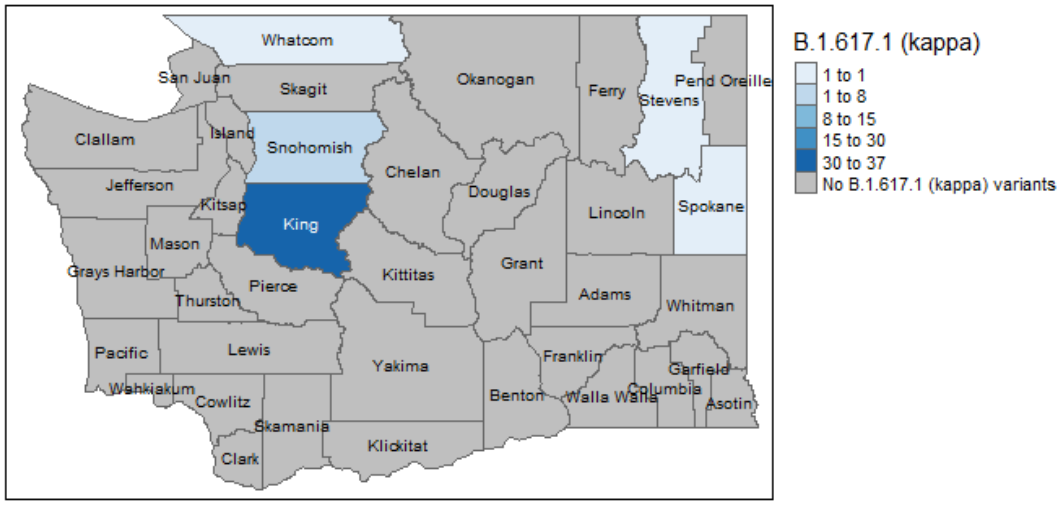
Based on preliminary evidence, some antibody treatments may be less effective against the B.1.617.1 (kappa) variant. Studies are ongoing to determine whether this variant is more transmissible.

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) |
|---|---|---|---|
| Cases who were hospitalized | 5.8% | 3.2% | 2.3% |
| Cases who died from COVID | 0.9% | 0.6% | 0% |
| Cases age 0-19 | 21.3% | 25.4% | 18.6% |
| Cases age 20-34 | 30.3% | 31.7% | 41.9% |
| Cases age 35-49 | 21.9% | 22.5% | 25.6% |
| Cases age 50-64 | 15.7% | 12.8% | 9.3% |
| Cases age 65-79 | 6.5% | 4.3% | 4.7% |
| Cases age 80+ | 2.1% | 1.3% | 0% |
| Cases 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

Altius Institute for Biomedical Research

Centers for Disease Control and Prevention

Washington State Department of Health Public Health Laboratories

Curative Labs

Oregon Health Sciences University

Providence St. Joseph Health Molecular Genomics Laboratory

Ginkgo Bioworks

Quest

Institute for Systems Biology

University of Washington Medical Center, Seattle Flu Study

Atlas Genomics

OHSU-MM Lab

Virology, University of Washington

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

Center for Genome Sciences, USAMRIID

NIH

Oregon State Public Health Laboratory

Andersen lab at Scripps Research

Gravity Diagnostics, LLC

United States Air Force School of Aerospace Medicine

Arizona State University

Grubaugh Lab - Yale School of Public Health

Kashi Clinical Laboratory

Boise VA Medical Center, PALMS

Clinical Division, Fred Hutchinson Cancer Research Center

Hyde Lab

IDEH and ID Genomics

Molecular Infectious Disease

Nevada State Public Health Laboratory

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

Northwest Laboratory

LabCorp

Atlas Genomics

OHSU Lab Services Molecular Microbiology Lab

Centers for Disease Control and Prevention

Quest Diagnostics

Providence Laboratories

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