

Hawaii sequencing and variants of SARS-Cov-2

Hawaii Department of Health

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Introduction

Next generation sequencing is a set of laboratory methods that are used to determine the full genome sequence of a virus, which in the case of the SARS-Cov-2 virus, the virus that causes COVID-19, is a sequence of approximately 30,000 letters, each letter being one of A,C,G or T.

A genome sequence of a virus can reveal mutations in a virus that make it unique. Mutations are changes in a genome sequence (usually one-letter changes) and occur naturally over time.

Collecting the genome sequence of virus specimens can also reveal information about the relatedness of viruses and the similarities shared among groups of viruses. Groups of same-species viruses that share a set of genome mutations are referred to as a lineage.

Scientists compare viral genomes to better understand virus transmission, how viruses can spread from person to person. Sequencing allows Public Health Officials to monitor viruses involved in outbreaks, characterize outbreaks, detect clusters of cases and monitor new lineages. Novel mutations can emerge with new lineages and scientists refer to these new lineages as emerging variants.

Some of these variants are classified by CDC as variants of concern and others as variants of interest, because of their attributes, which can be for example: increased transmissibility, decreased neutralization by antibodies generated during previous infection or vaccination, or increased severity of disease. The Centers for Disease Control and Prevention (CDC) has extensive information about the variant classification (<https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html>), which is updated as new evidence becomes available.

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.

The State of Hawaii has conducted sequencing on approximately 6% of positive specimens that were detected since the beginning of the testing, which ranks among the best in the nation according to the Centers for Disease Control and Prevention (CDC) (<https://covid.cdc.gov/covid-data-tracker/#published-covid-sequences>)

In February 2021, the State Laboratories Division of the Hawaii Department of Health has ramped up the sequencing done on positive samples to increase the ability to detect the new variants of concern and variants of interest early. Since then, between 15-20% of the samples that were detected positive on PCR Covid-19 tests were sequenced (see below for details).

Short summary

- Since Jan 1, 2021, the State Laboratories Division of the Department of Health has sequenced 1784 viral genomes (1044 in Honolulu County, 365 in Maui County, 220 in Hawaii County, 48 in Kauai County and 107 lacking county information).
- This report also integrates 261 viral genomes that have been generated by CDC and its commercial partners and submitted to GISAID (these viral genomes lack the county information, so they are only reported at the state level), also 2 genomes submitted by Tripler Army Medical Center to GISAID, therefore uses a total of 2047 genomes.
- Since the last version of this variant report was generated (6/23/2021), 53 additional samples belonging to the “Delta” variant of concern have been detected.
- All 4 counties have cases of “Delta” variants.
- There are 10 cases that belong to a specific version of the “Delta” variant - “Delta+K417N”, containing an additional mutation of interest - the spike K417N mutation (8 in Maui County and 2 in Honolulu County)
- Based on the genetic data of the sequenced specimens, we have identified 8-12 possible distinct introductions for the “Delta” variant.
- There is also evidence of local transmission of the introduced “Delta” variant - cases that are very close genetically and one case of inter-county transmission.

Significance of variants of concern and variants of interest

It is important to note that evidence to date shows that vaccination leads to milder cases, not requiring hospitalization, for all the variants of concern and variants of interest that are described here, even if the efficacy of antibodies is diminished against some of these variants compared to the original version of the virus.

Also, *none* of these variants are classified as a “*variant of high consequence*”, according to CDC variant categories (<https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html#Consequence>), which is a category that would imply a variant has the ability to evade diagnosis, significantly reduce the vaccines effectiveness and protection against severe disease, significantly reduce susceptibility to treatments or lead to more severe disease and increased hospitalizations.

Variants of concern

Variant B.1.1.7 (“Alpha”)

B.1.1.7 was first identified in the United Kingdom and it is also known as VOC202012/01 and 20I/501Y.V1. WHO labeled it “Alpha” on May 31, 2021. This variant contains the N501Y mutation and a short deletion in the Spike (S) protein. This variant is concerning because it has been 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.

Variant B.1.351 (“Beta”)

B.1.351 was first identified in South Africa and it is also known as 20H/501Y.V2. WHO labeled it “Beta” on May 31, 2021. This variant is highly infectious and can quickly spread from person to person. Preliminary studies suggest that antibodies from previous infection or from vaccination may be less effective at preventing infection against this variant.

Variant P.1 (“Gamma”)

P.1 was first identified in Brazil and it also known as variant 20J/501Y.V3. WHO labeled it “Gamma” on May 31, 2021. This variant also contains the N501Y mutation, like B.1.1.7 but not the deletion in the spike protein. Preliminary studies suggest that antibodies from previous infection or from vaccination may be less effective at preventing infection against this variant.

Variant B.1.617.2 (“Delta”)

B.1.617.2 was first identified in India and it is also known as variant 20A/S:478K. WHO labeled it “Delta” on May 31, 2021. This variant contains the L452R mutation in the spike protein that is present in Epsilon variants, plus a few additional spike mutations predicted to have functional consequences (e.g. T478K). Preliminary studies suggest that this variant is more transmissible and it might be responsible for more severe disease.

Variants of interest

Variants B.1.429 / B.1.427 (“Epsilon”)

These closely related variants, B.1.429 and B.1.427, were first identified in California and designated initially as CA VUI1. WHO labeled them “Epsilon” on May 31, 2021. They can quickly spread from person-to-person, with an estimated ~20% higher efficiency than the original virus. CDC has deescalated “Epsilon” from a “variant of concern” to “variant of interest” on June 29, 2021, due to the significant decrease in the proportion of B.1.429/B.1.427 lineage viruses circulating nationally and available data indicating that vaccines and treatments are effective against this variant.

Variant B.1.526 (“Iota”)

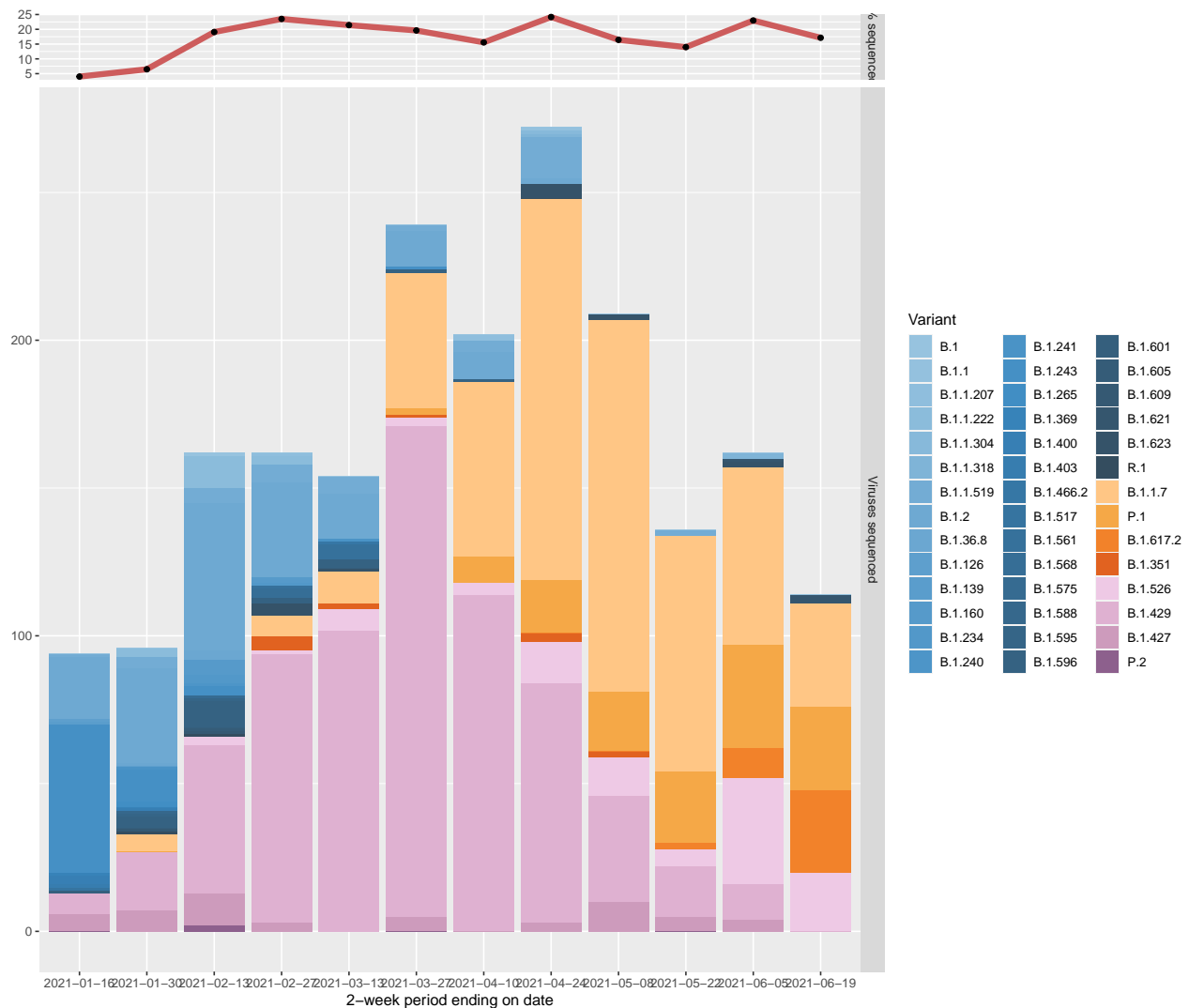
B.1.526 was first identified in New York and is classified by CDC as a variant of interest, because there are signs that it has increased transmissibility. WHO has labeled it “Iota” on May 31, 2021. Some of the samples (but not all) of this variant contain a mutation (E484K) that is also present in B.1.351 which can potentially make it less responsive to antibodies.

Variant P.2 (“Zeta”)

P.2 was first identified in Brazil and is classified by CDC as a variant of interest. It contains a mutation (E484K) that is also present in B.1.351 which can potentially make it less responsive to antibodies.

State of Hawaii

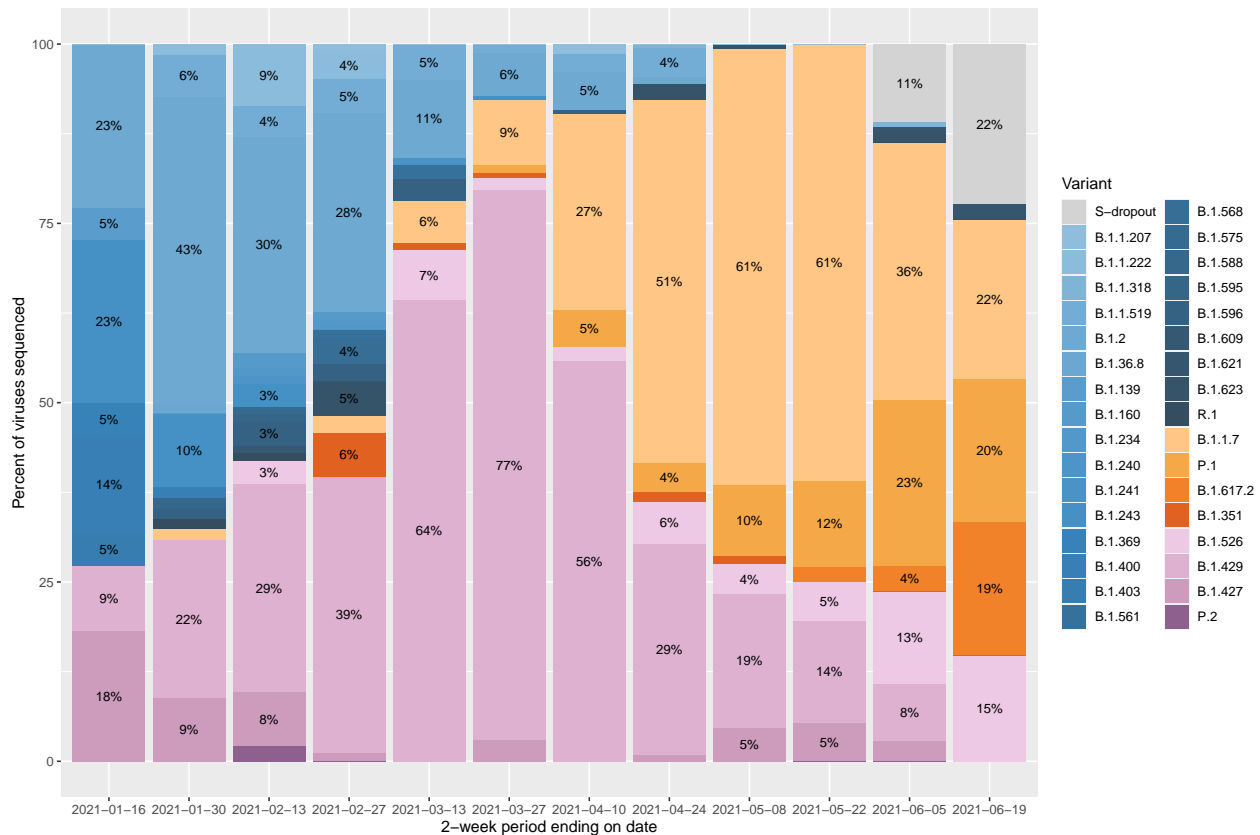
Total variants identified



Notes:

- The above bar graph shows the total number of variants detected in the State of Hawaii in each 2-week interval ending on the date shown (date represents when the specimen was collected from a patient)
- Variants of concern are shown in orange/brown colors (B.1.1.7, B.1.351, P.1 and B.1.617.2) and variants of interest are shown in pink (B.1.429, B.1.427, B.1.526 and P.2)
- The red line graph above it shows the percentage of the PCR-test positive samples from each 2-week time interval that were sequenced.
- SARS-CoV-2 genome sequencing may not be a random sample of all cases. This figure does not estimate the prevalence of the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced, especially for the last 2-week period, for which a number of samples are currently being processed.

Estimate of proportion of variants circulating in the State of Hawaii



Notes:

- The chart above shows the estimate of biweekly percentages of the SARS-CoV-2 lineages circulating in the State of Hawaii, grouped in two-week intervals (based on the date of collection of samples).
- Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases in Hawaii. This chart has been generated only counting samples that were selected randomly for the purpose of surveillance of community variants, to avoid over-representing the samples that were selected for investigations of clusters.
- The last 2-week interval numbers will most likely change, as a number of samples that are currently being processed will be added.
- Sequencing of certain specimens can be delayed for technical reasons. For this reason, the dataset used for this report is dynamic and 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.
- In June 2021, the sequencing of the specimens that were S-dropouts on the PCR test (which most likely belong to the B.1.1.7 variant - Alpha) were de-prioritized, in order to increase the probability of detection of the new Delta variant. These sequences are represented on this report as "S-dropout" samples. They will be added in future versions of the report as they are sequenced if they are confirmed as B.1.1.7 - Alpha variant.

Variants of concern in the State of Hawaii

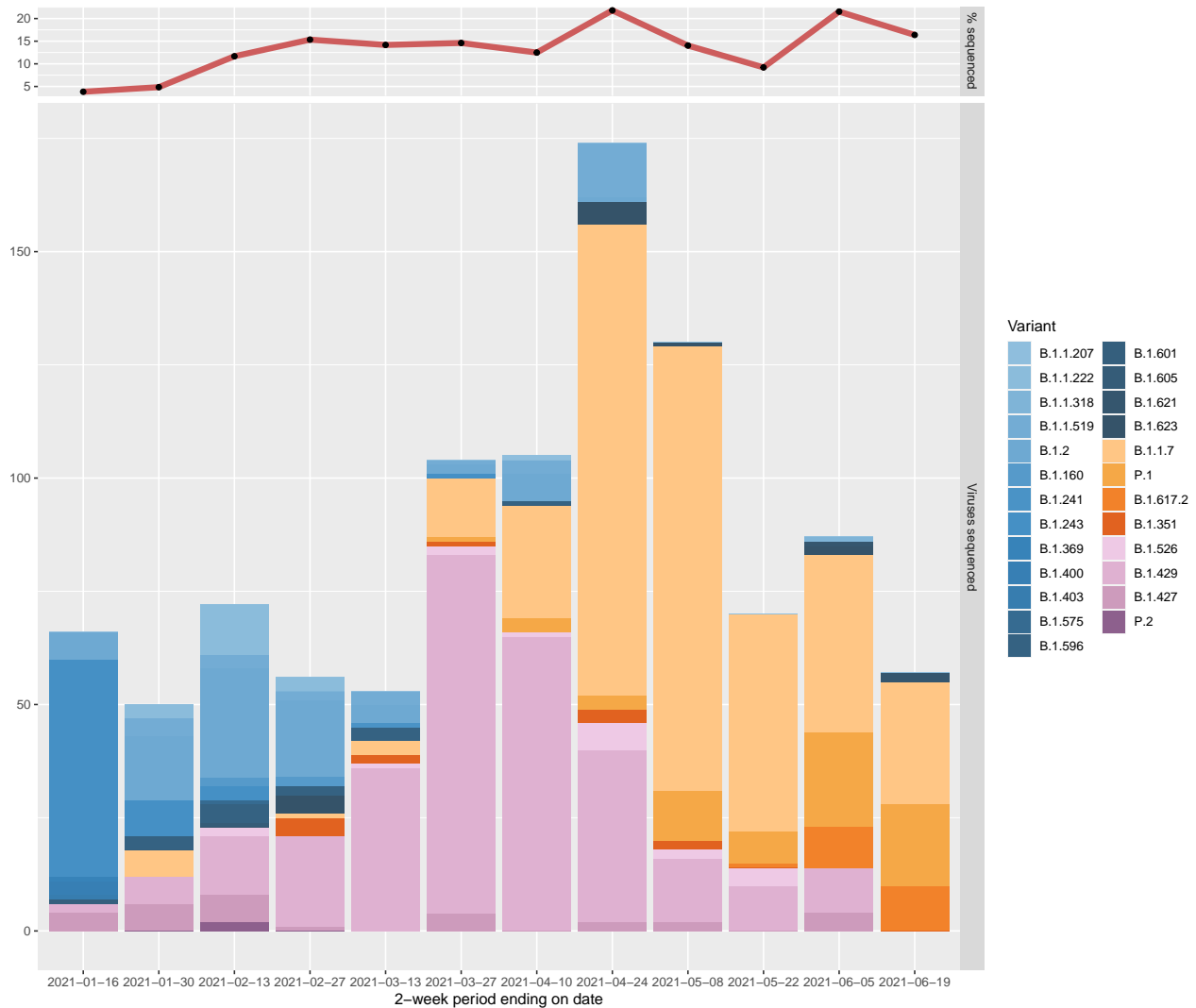
Name	Area of emergence	WHO label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.1.7	United Kingdom	Alpha	577	21 Jan 2021	24 Jun 2021
P.1	Brazil	Gamma	157	21 Mar 2021	28 Jun 2021
B.1.617.2	India	Delta	57	18 May 2021	29 Jun 2021
B.1.351	South Africa	Beta	13	16 Feb 2021	02 May 2021

Variants of interest in the State of Hawaii

Name	Area of emergence	WHO label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.429	California	Epsilon	703	31 Dec 2020	03 Jun 2021
B.1.526	New York	Iota	111	06 Feb 2021	21 Jun 2021
B.1.427	California	Epsilon	56	07 Dec 2020	05 Jun 2021
P.2	Brazil	Zeta	2	Feb 2021	Feb 2021

Honolulu County

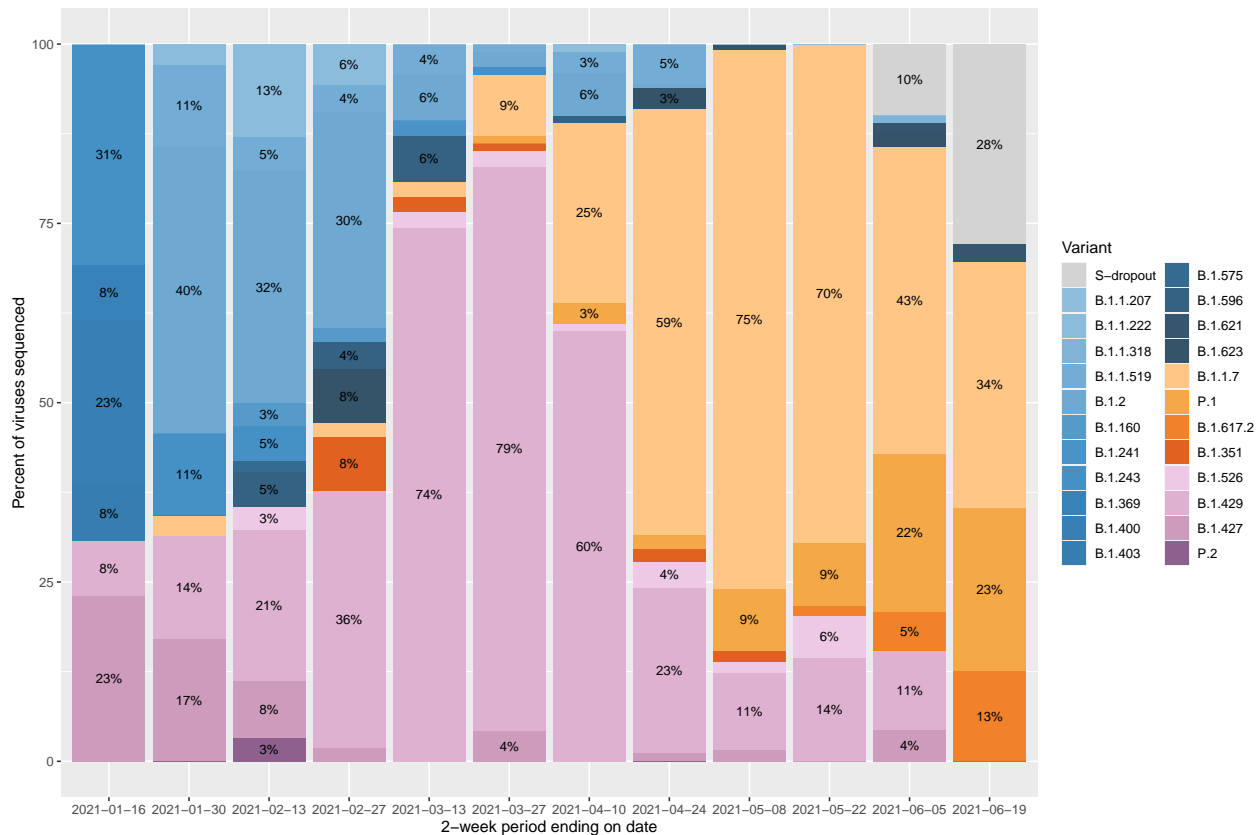
Total variants identified in Honolulu County



Notes:

- The above bar graph shows the total number of variants detected in Honolulu County in each 2-week interval ending on the date shown (date represents when the specimen was collected from a patient)
- Variants of concern are shown in orange/brown colors (B.1.1.7, B.1.351, P.1 and B.1.617.2) and variants of interest are shown in pink (B.1.429, B.1.427, B.1.526 and P.2)
- The red line graph above it shows the percentage of the PCR-test positive samples from each 2-week time interval that were sequenced.
- SARS-CoV-2 genome sequencing may not be a random sample of all cases. This figure does not estimate the prevalence of the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced, especially for the last 2-week period, for which a number of samples are being currently processed.

Estimate of proportion of variants circulating in Honolulu County



Notes:

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- In June 2021, the sequencing of the specimens that were S-dropouts on the PCR test (which most likely belong to the B.1.1.7 variant - Alpha) were de-prioritized, in order to increase the probability of detection of the new Delta variant. These sequences are represented on this report as "S-dropout" samples. They will be added in future versions of the report as they are sequenced if they are confirmed as B.1.1.7 - Alpha variant.

Variants of concern in Honolulu County

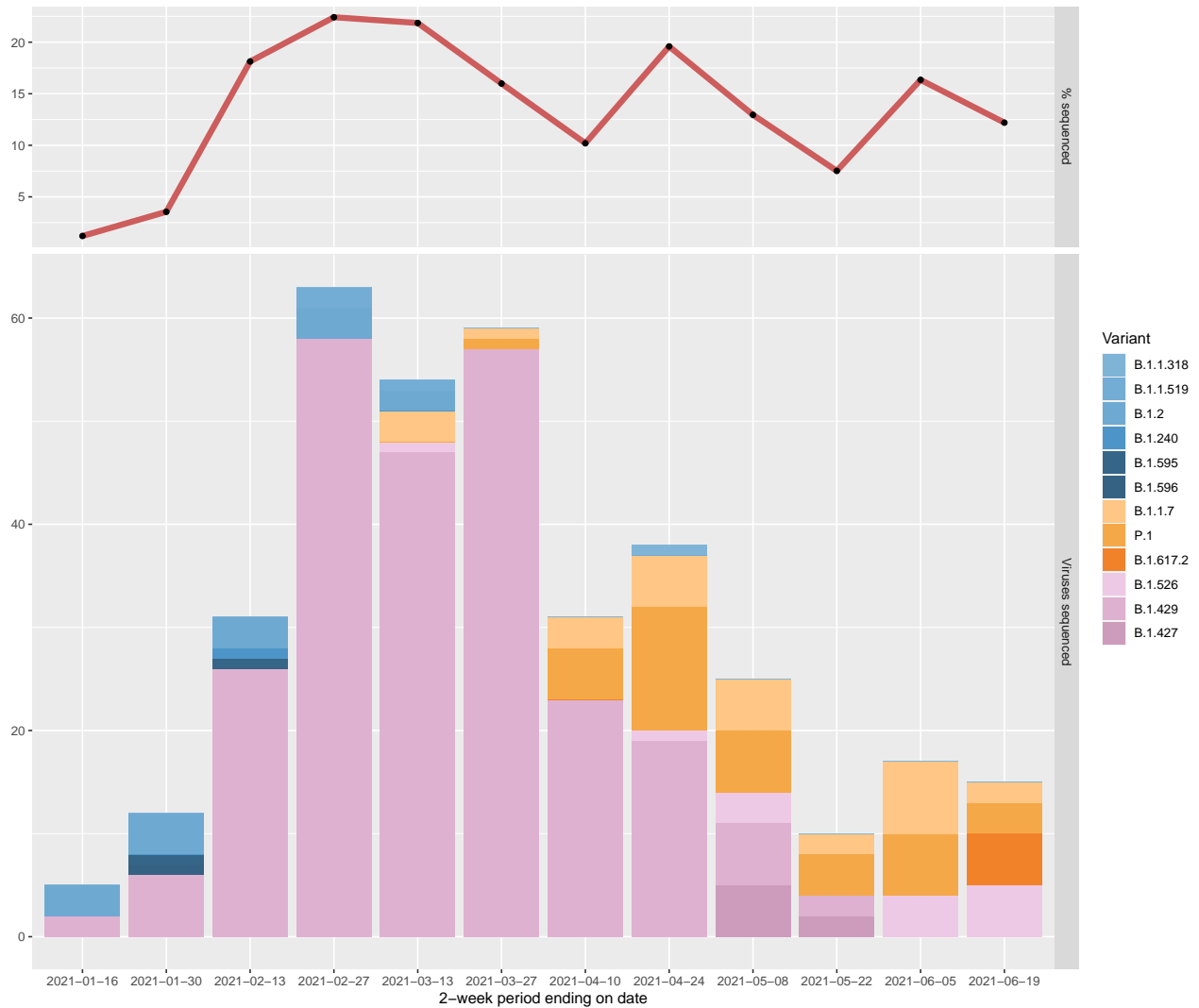
Name	Area of emergence	WHO label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.1.7	United Kingdom	Alpha	371	21 Jan 2021	24 Jun 2021
P.1	Brazil	Gamma	74	24 Mar 2021	28 Jun 2021
B.1.617.2	India	Delta	27	18 May 2021	24 Jun 2021
B.1.351	South Africa	Beta	12	16 Feb 2021	02 May 2021

Variants of interest in Honolulu County

Name	Area of emergence	WHO label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.429	California	Epsilon	293	05 Jan 2021	29 May 2021
B.1.427	California	Epsilon	29	07 Jan 2021	05 Jun 2021
B.1.526	New York	Iota	18	08 Feb 2021	19 May 2021
P.2	Brazil	Zeta	2	Feb 2021	Feb 2021

Maui County

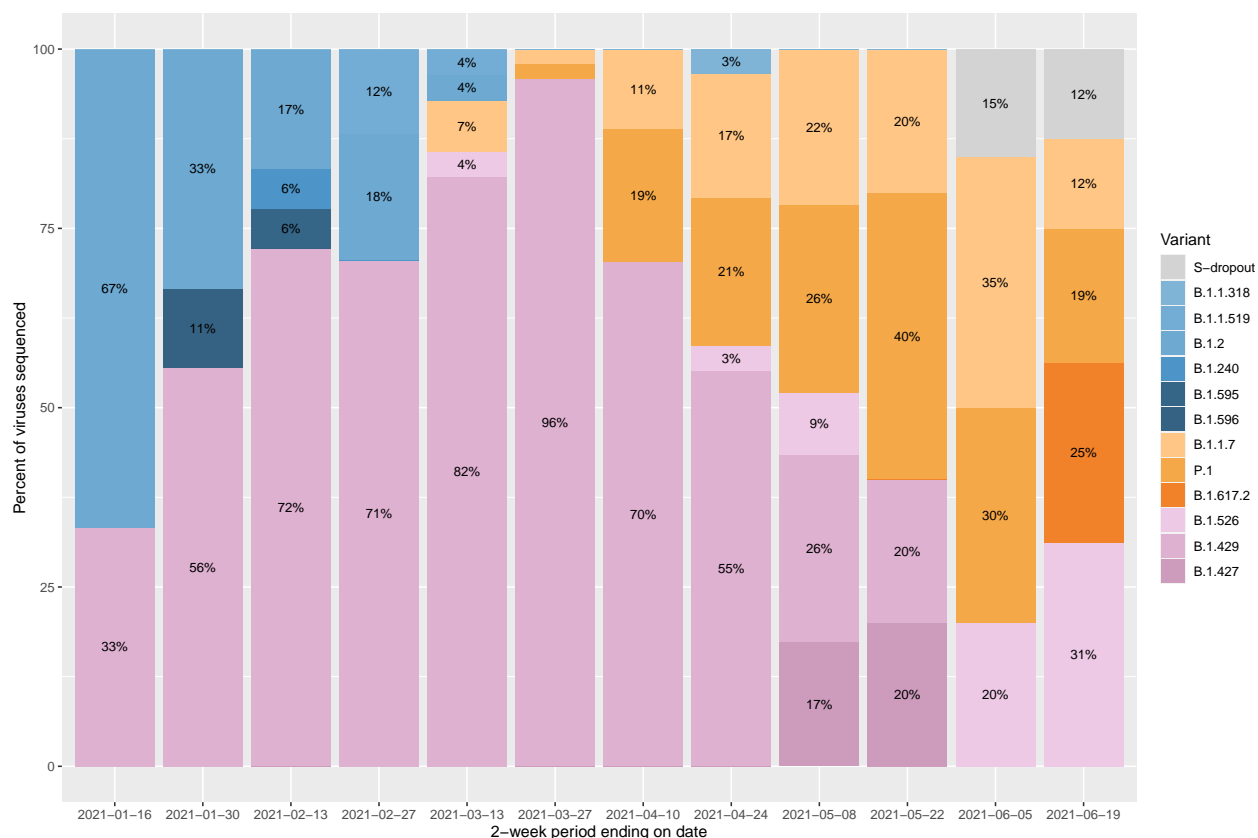
Total variants identified in Maui County



Notes:

- The above bar graph shows the total number of variants detected in Maui County in each 2-week interval ending on the date shown (date represents when the specimen was collected from a patient)
- The red line graph above it shows the percentage of the PCR-test positive samples from each 2-week time interval that were sequenced.
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Estimate of proportion of variants circulating in Maui County



Notes:

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Variants of concern in Maui County

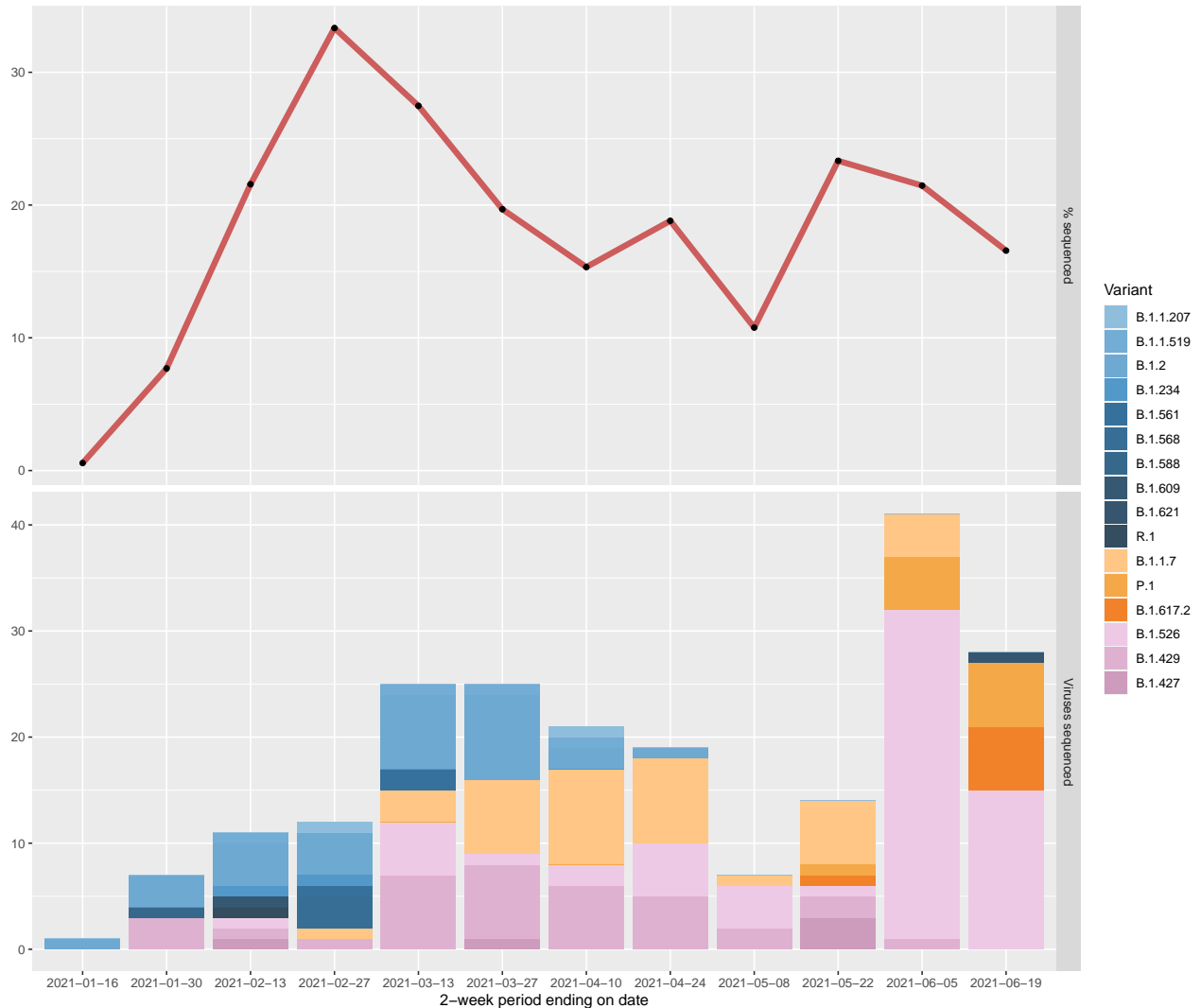
Name	Area of emergence	WHO label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
P.1	Brazil	Gamma	41	21 Mar 2021	20 Jun 2021
B.1.1.7	United Kingdom	Alpha	33	01 Mar 2021	21 Jun 2021
B.1.617.2	India	Delta	7	07 Jun 2021	22 Jun 2021

Variants of interest in Maui County

Name	Area of emergence	WHO label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.429	California	Epsilon	246	08 Jan 2021	18 May 2021
B.1.526	New York	Iota	14	12 Mar 2021	19 Jun 2021
B.1.427	California	Epsilon	7	27 Apr 2021	10 May 2021

Hawaii County

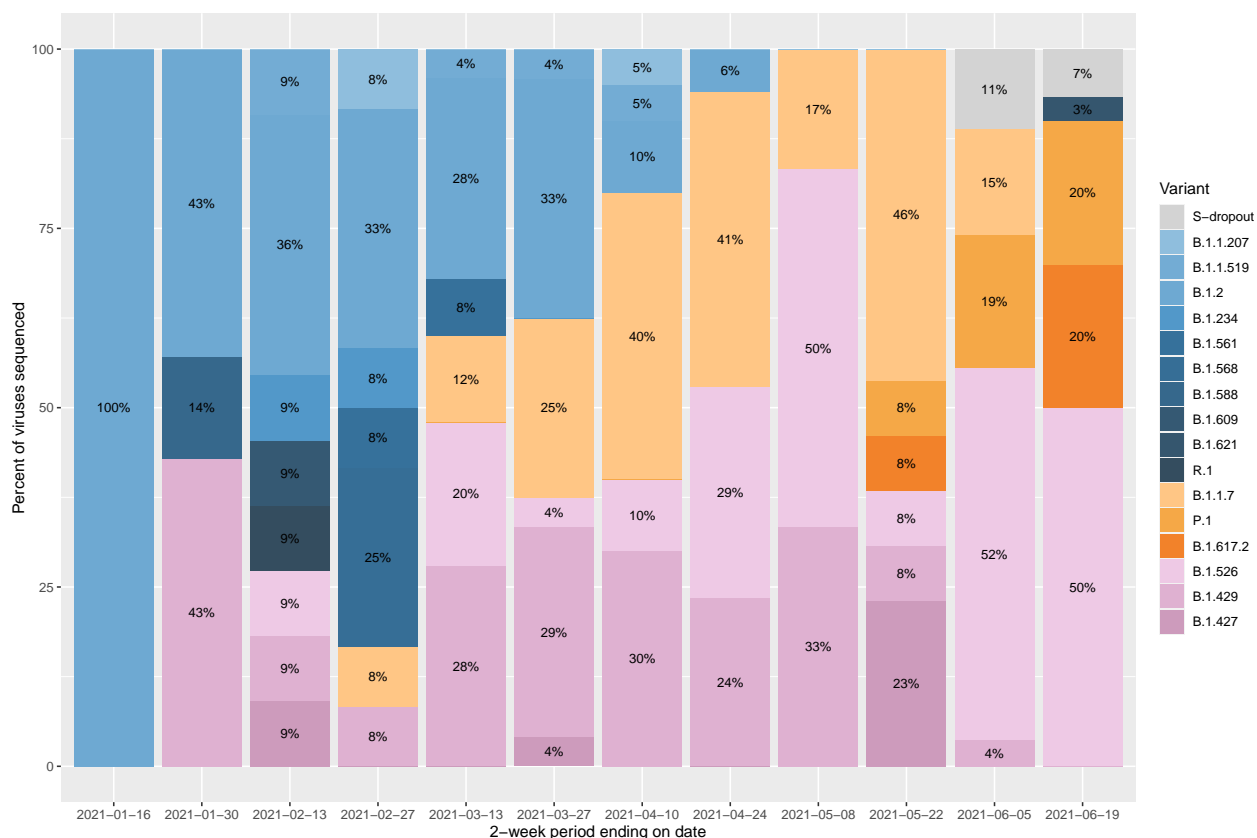
Total variants identified in Hawaii County



Notes:

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Estimate of proportion of variants circulating in Hawaii County



Notes:

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Variants of concern in Hawaii County

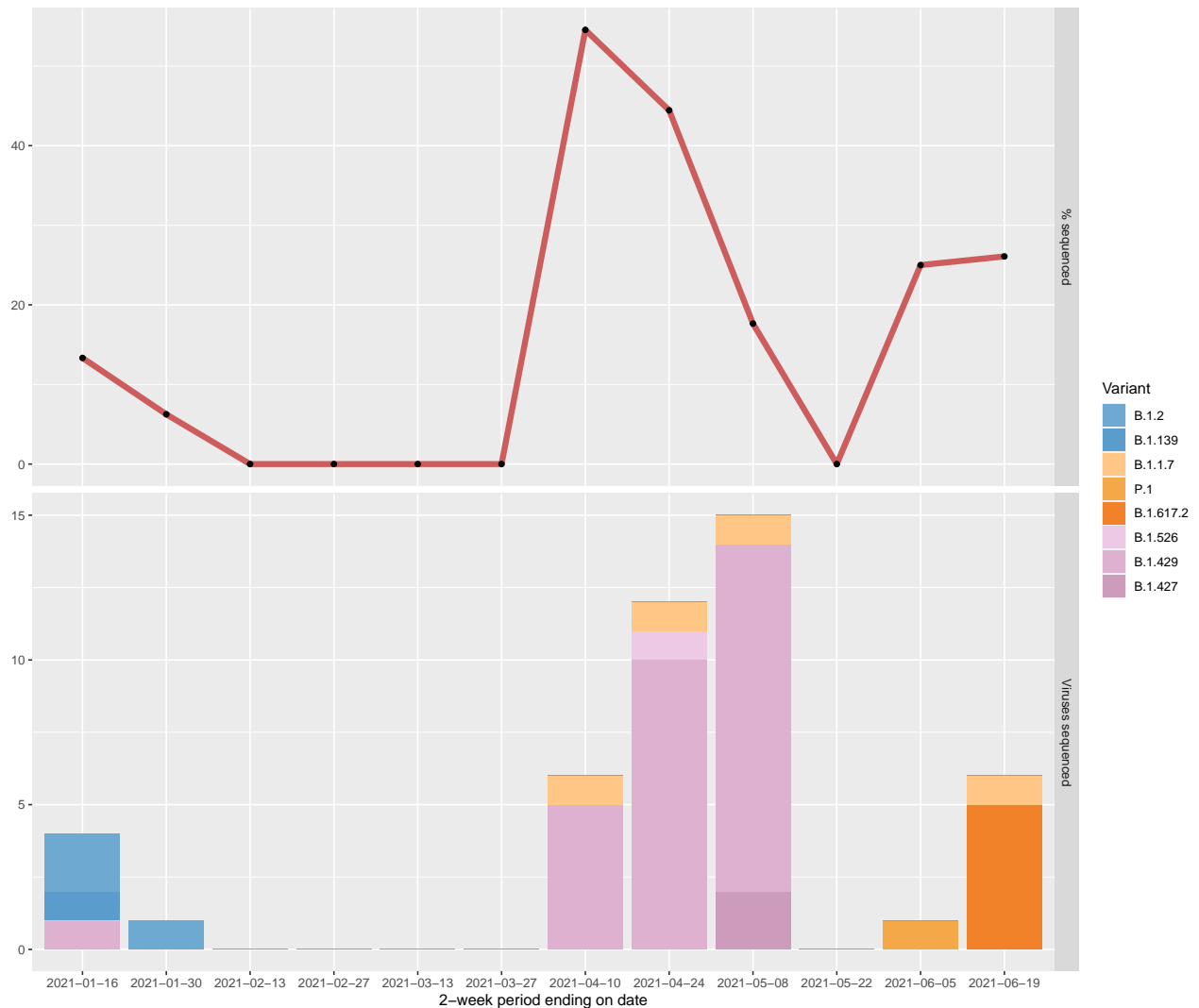
Name	Area of emergence	WHO label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.1.7	United Kingdom	Alpha	40	22 Feb 2021	21 Jun 2021
P.1	Brazil	Gamma	16	10 May 2021	14 Jun 2021
B.1.617.2	India	Delta	14	21 May 2021	23 Jun 2021

Variants of interest in Hawaii County

Name	Area of emergence	WHO label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.526	New York	Iota	69	06 Feb 2021	21 Jun 2021
B.1.429	California	Epsilon	35	25 Jan 2021	26 May 2021
B.1.427	California	Epsilon	5	04 Feb 2021	17 May 2021

Kauai County

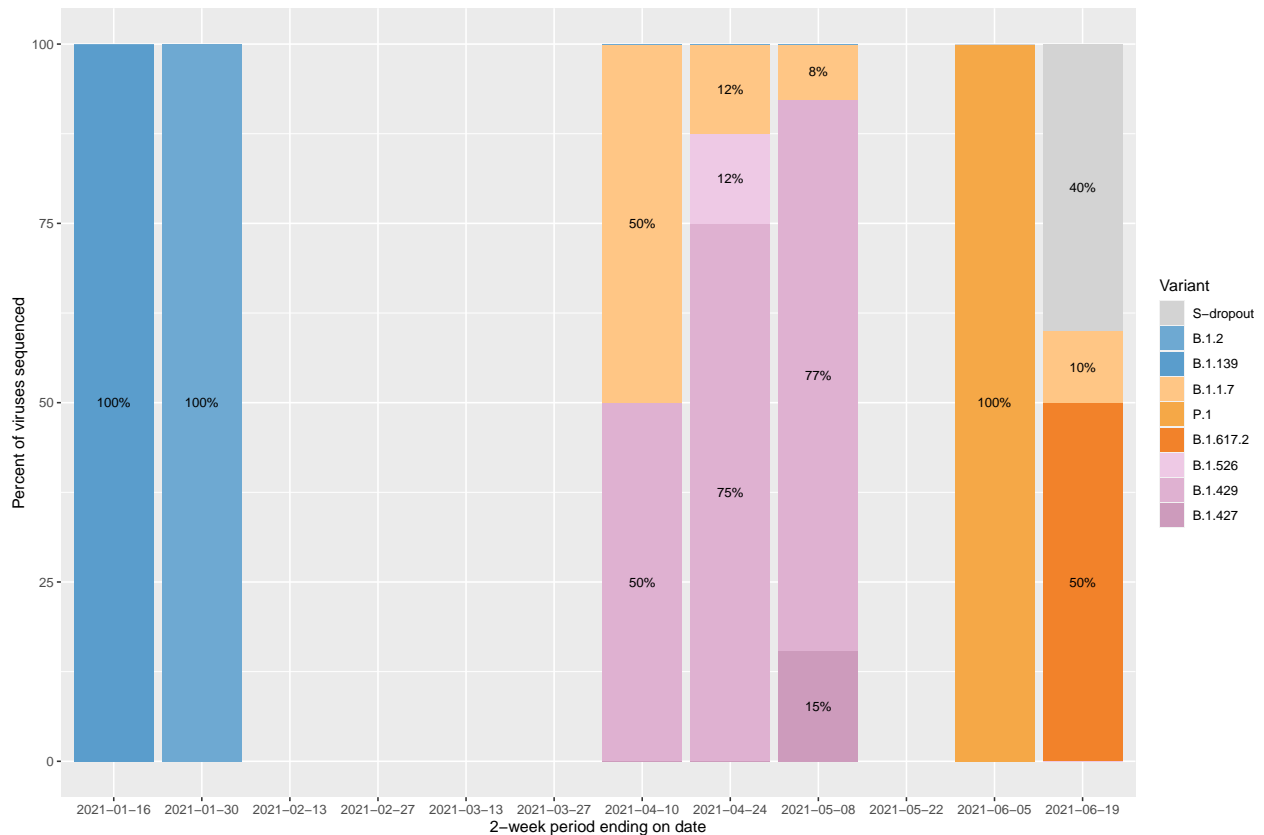
Total variants identified in Kauai County



Notes:

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Estimate of proportion of variants circulating in Kauai County



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Variants of concern in Kauai County

Name	Area of emergence	WHO_label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.1.7	United Kingdom	Alpha	7	05 Apr 2021	23 Jun 2021
B.1.617.2	India	Delta	5	06 Jun 2021	15 Jun 2021
P.1	Brazil	Gamma	1	May 2021	May 2021

Variants of interest in Kauai County

Name	Area of emergence	WHO_label	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
B.1.429	California	Epsilon	28	07 Jan 2021	08 May 2021
B.1.427	California	Epsilon	2	Apr 2021	Apr 2021
B.1.526	New York	Iota	1	Apr 2021	Apr 2021