

# 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 2393 viral genomes (1429 in Honolulu County, 408 in Maui County, 334 in Hawaii County, 82 in Kauai County and 140 lacking county information).
- This report also integrates 403 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 28 genomes submitted by Tripler Army Medical Center to GISAID, therefore uses a total of 2824 genomes.
- Since the last version of this variant report was generated on 8/4/2021 reporting 270 Delta samples detected, 312 additional samples belonging to the Delta variant of concern have been detected and the estimated proportion of the Delta variant (the cumulative total of B.1.617.2, AY.1, AY.2 and AY.3) has reached 93%.
- Since Delta variant now accounts for the vast majority of cases in US, researchers responsible for the variants nomenclature have decided to define sub-lineages of the “main” Delta lineage B.1.617.2, which show significant geographic clustering, to help researchers track the virus on a finer scale. These lineages are named AY.\* (e.g. AY.1, AY.2, AY.3, AY.4 - up to AY.22 so far). These sub-lineages have the same significance as the “main” Delta lineage, sharing its high transmissibility and so far having no additional characteristics described. In Hawaii, we have detected AY.1, AY.2 and AY.3 so far. AY.3 has reached ~12% in the last couple of weeks in US and we also estimate its prevalence in Hawaii to 12% (see below).
- In the same way, researchers have defined sub-lineages for the other variants of concern (these sub-lineages have the same significance as the “main” variant from which they derive):
  - for Alpha (B.1.1.7) the sub-lineages Q.1, Q.2 and Q.3
  - for Gamma (P.1) the sub-lineages P.1.1, P.1.2, etc. up to P.1.10
  - for Beta (B.1.351) the sub-lineages B.1.351.1, B.1.351.2, B.1.351.3

The infographic is divided into several sections. At the top, a dark teal banner contains the text: "The Delta variant is more contagious than previous strains—it may cause more than 2x as many infections". Below this, two columns are separated by a dark teal header. The left column is titled "ORIGINAL COVID-19 STRAIN" and shows a large black silhouette of a person with two arrows pointing to two smaller black silhouettes of people. The right column is titled "DELTA VARIANT" and shows a large black silhouette of a person with five arrows pointing to five smaller black silhouettes of people, illustrating a higher transmission rate. Below the comparison, a dark teal banner contains the text: "Vaccines protect you from hospitalization, severe infections, and death". At the bottom left is the logo for the State of Hawaii Health Services Center and the CDC. At the bottom right is an orange banner with the text "cdc.gov/coronavirus". In the bottom right corner, there is a small text string: "CS 322041-AA 08/02/2021".

**The Delta variant is more contagious than previous strains—it may cause more than 2x as many infections**

ORIGINAL COVID-19 STRAIN      DELTA VARIANT

Vaccines protect you from hospitalization, severe infections, and death

 [cdc.gov/coronavirus](https://cdc.gov/coronavirus)

CS 322041-AA 08/02/2021

## 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

#### Delta variant (B.1.617.2 and AY.\* sub-lineages)

B.1.617.2 was first identified in India and it is also known as variant 21A. 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). The Delta variant is highly contagious, more than 2x as contagious as previous variants. For more information about Delta, go to (<https://www.cdc.gov/coronavirus/2019-ncov/variants/delta-variant.html>).

#### Alpha variant (B.1.1.7 and Q.\* sub-lineages)

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.

#### Gamma variant (P.1 and P.1.\* sub-lineages)

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.

#### Beta variant (B.1.351 and B.1.351.\* sub-lineages)

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.

## **Variants of interest**

### **Iota variant (B.1.526)**

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.

### **Epsilon variant (B.1.429 and B.1.427)**

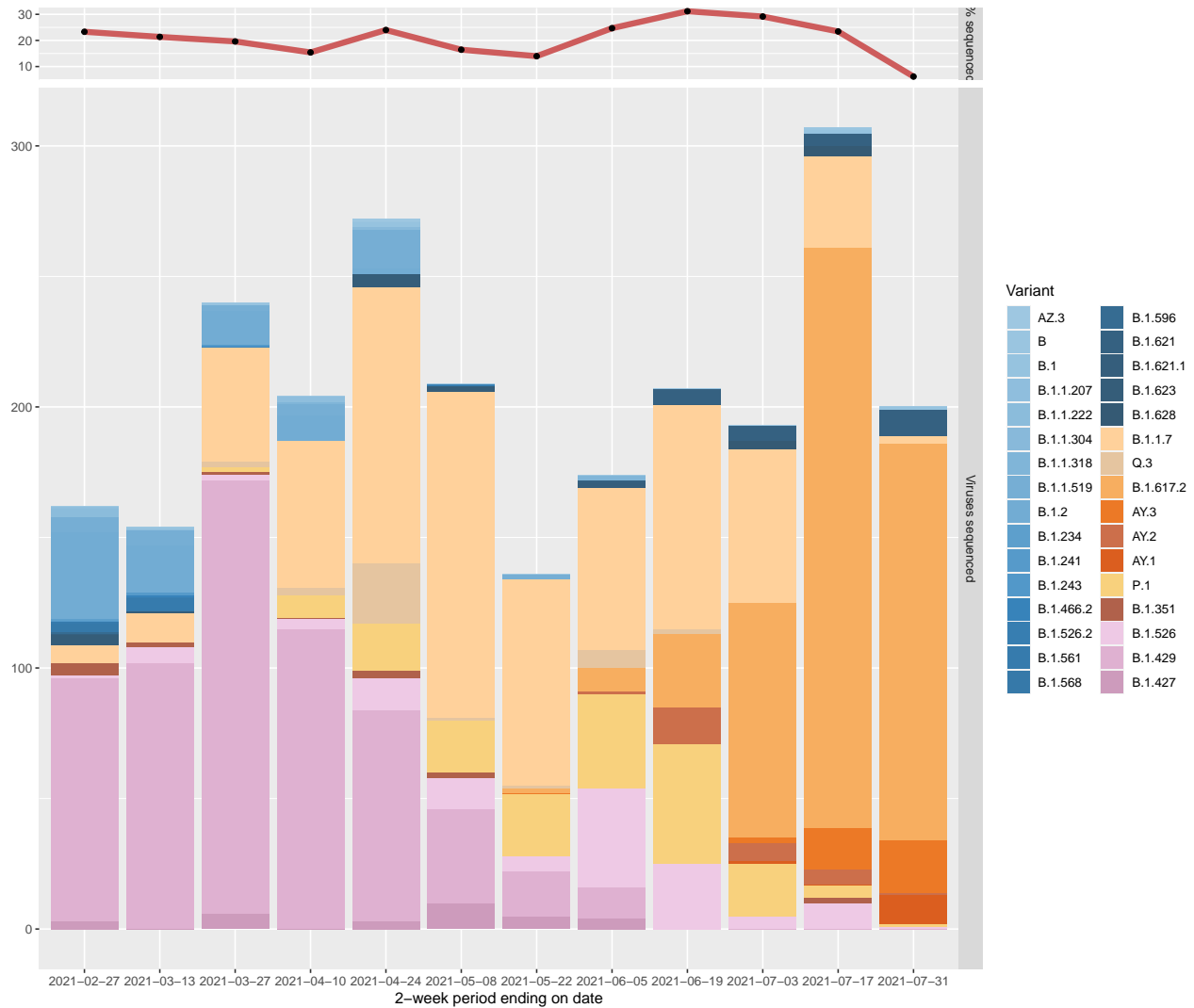
These closely related variants, B.1.429 and B.1.427, were first identified in California and designated initially as CA VUI1. WHO labeled them “Epsilon” on May 31, 2021. They can quickly spread from person-to-person, with an estimated ~20% higher efficiency than the original virus. CDC has deescalated “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. CDC has removed B.1.429 and B.1.427 from the “variants of interest” list in July 2021 due to declining prevalence and very few detections in recent months.

### **Zeta variant (P.2)**

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. This variant has been removed from the “variant of interest” list in July 2021 due to few detections in recent months.

# State of Hawaii

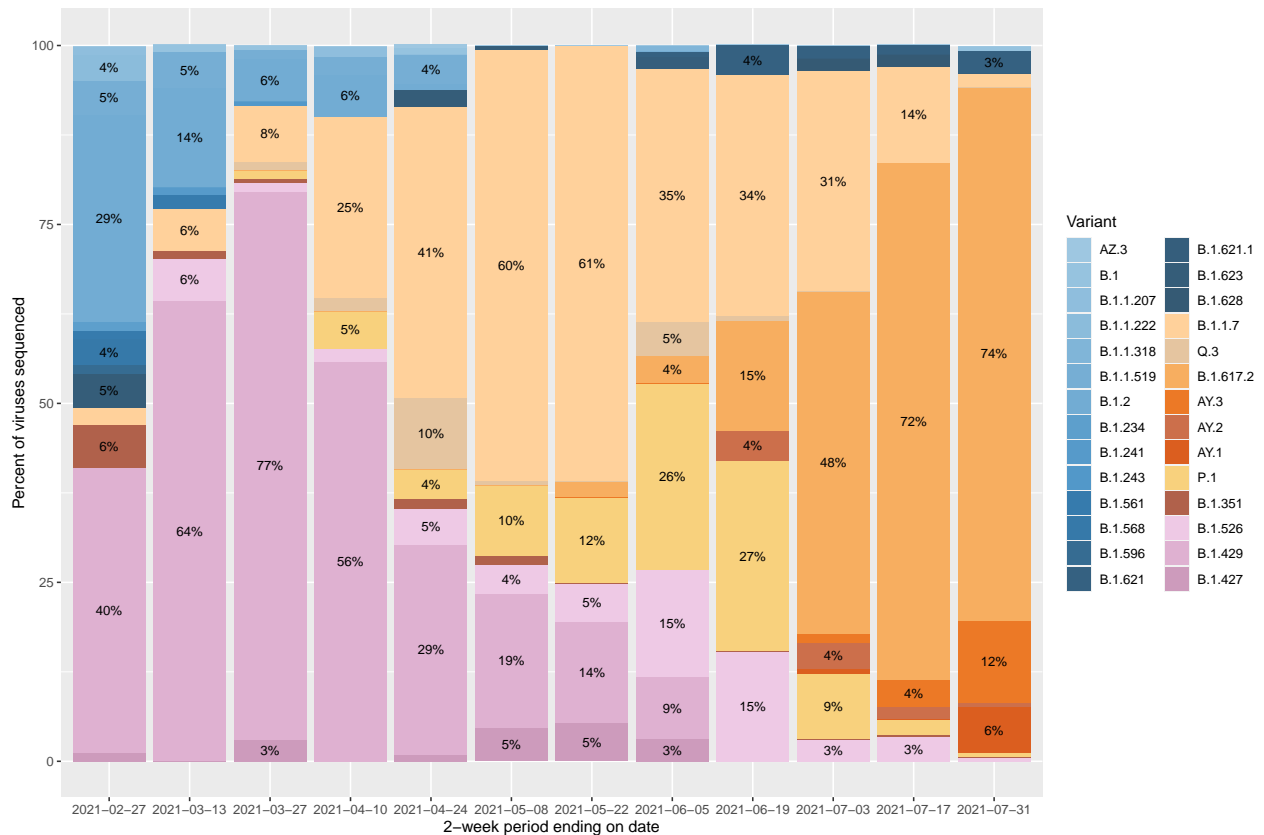
## Total variants identified



### 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 yellow/orange/brown colors (B.1.617.2 + AY.\*, B.1.1.7 + Q.\*, B.1.351, and P.1) 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.



## Variants of concern in the State of Hawaii

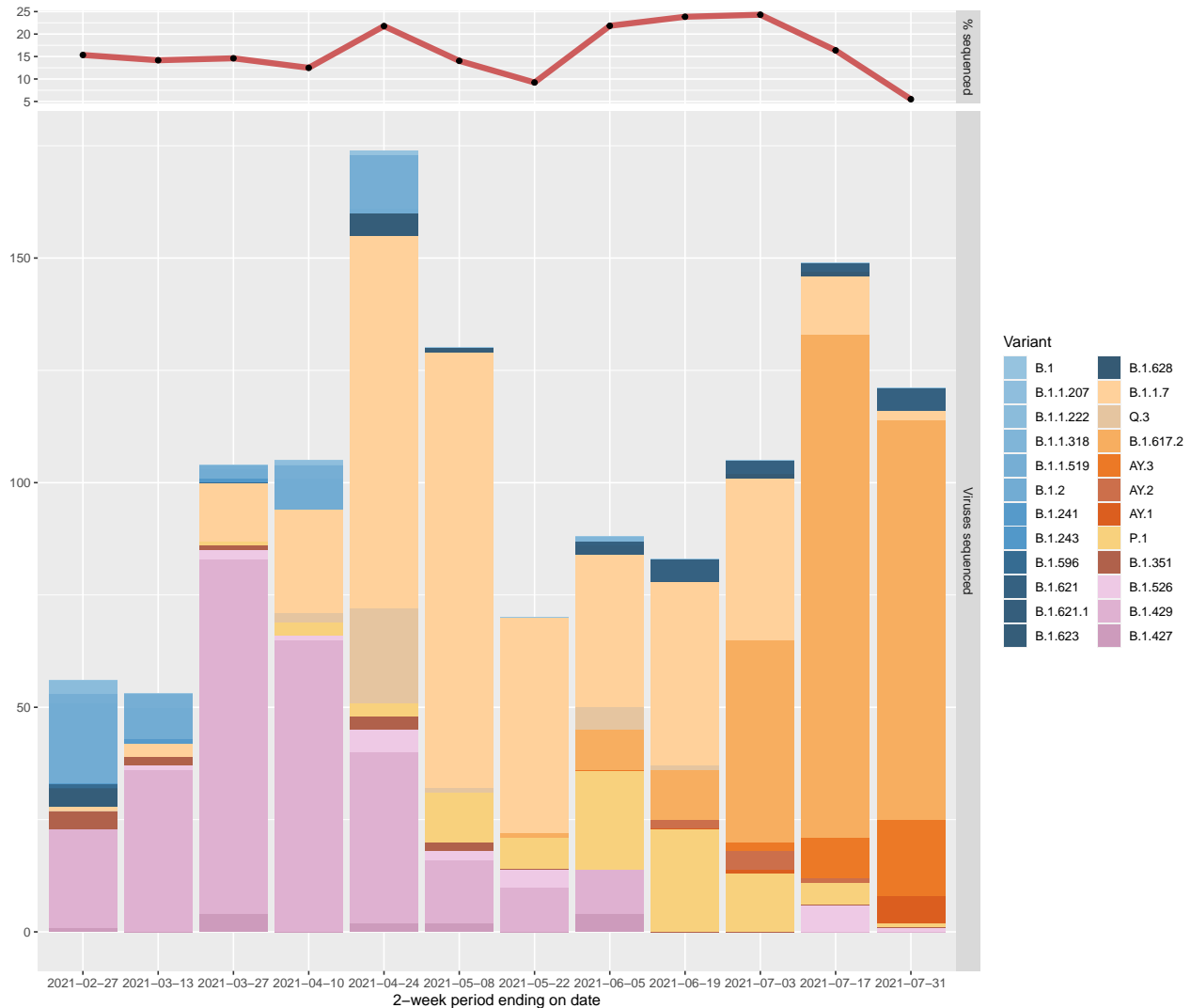
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			582		
	B.1.617.2	India	503	18 May 2021	29 Jul 2021
	AY.3	United States	38	28 Jun 2021	26 Jul 2021
	AY.2	United States	29	01 Jun 2021	22 Jul 2021
	AY.1	Europe	12	30 Jun 2021	29 Jul 2021
Alpha			719		
	B.1.1.7	United Kingdom	680	21 Jan 2021	24 Jul 2021
	Q.3	United States	39	21 Mar 2021	19 Jun 2021
Gamma	P.1	Brazil	181	21 Mar 2021	20 Jul 2021
Beta	B.1.351	South Africa	15	16 Feb 2021	08 Jul 2021

## Variants of interest in the State of Hawaii

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Epsilon	B.1.429	California	712	31 Dec 2020	03 Jun 2021
Iota	B.1.526	New York	125	06 Feb 2021	23 Jul 2021
Epsilon	B.1.427	California	59	07 Dec 2020	05 Jun 2021

# Honolulu County

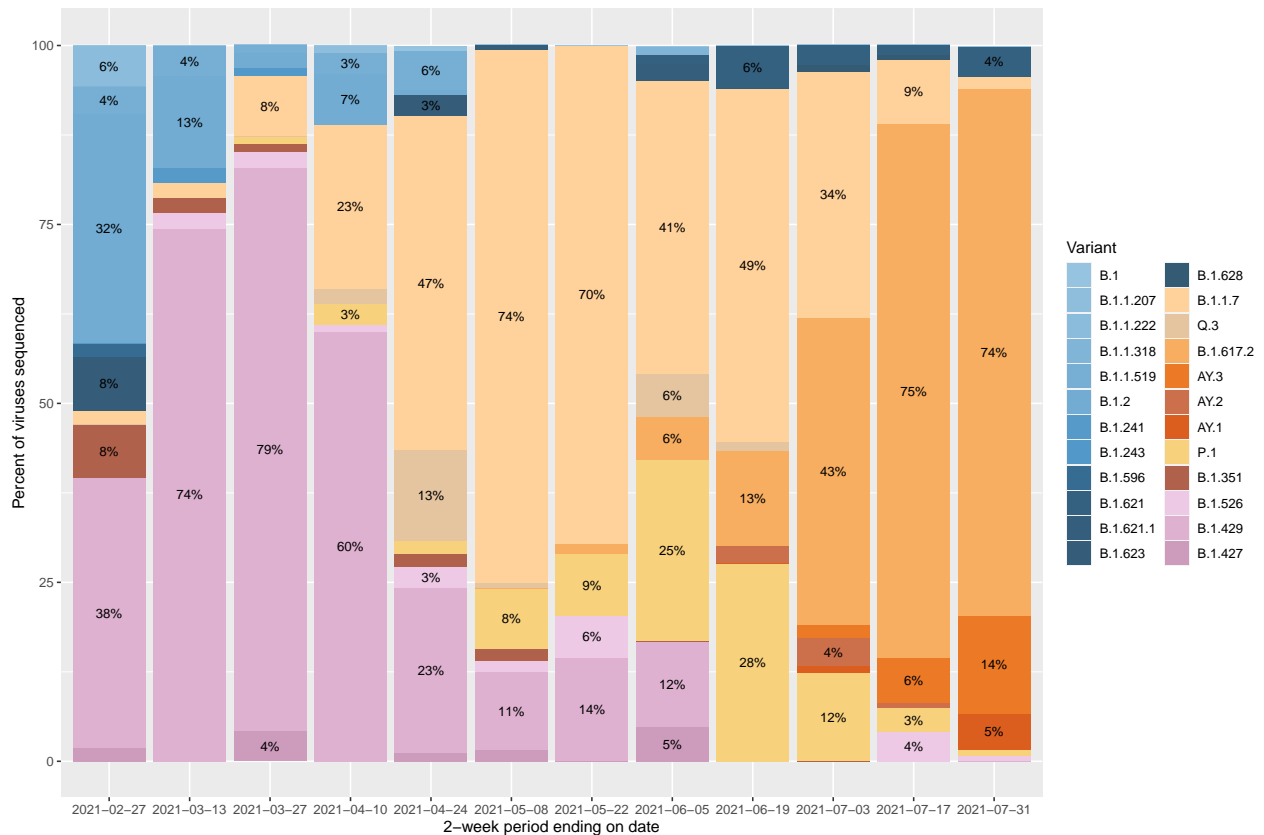
## Total variants identified in Honolulu County



**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.1.617.2 + AY.\*, B.1.1.7 + Q.\*, B.1.351, and P.1) 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.
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## Estimate of proportion of variants circulating in Honolulu County



### Notes:

- The chart above shows the estimate of biweekly percentages of the SARS-CoV-2 lineages circulating in Honolulu County, 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.
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## Variants of concern in Honolulu County

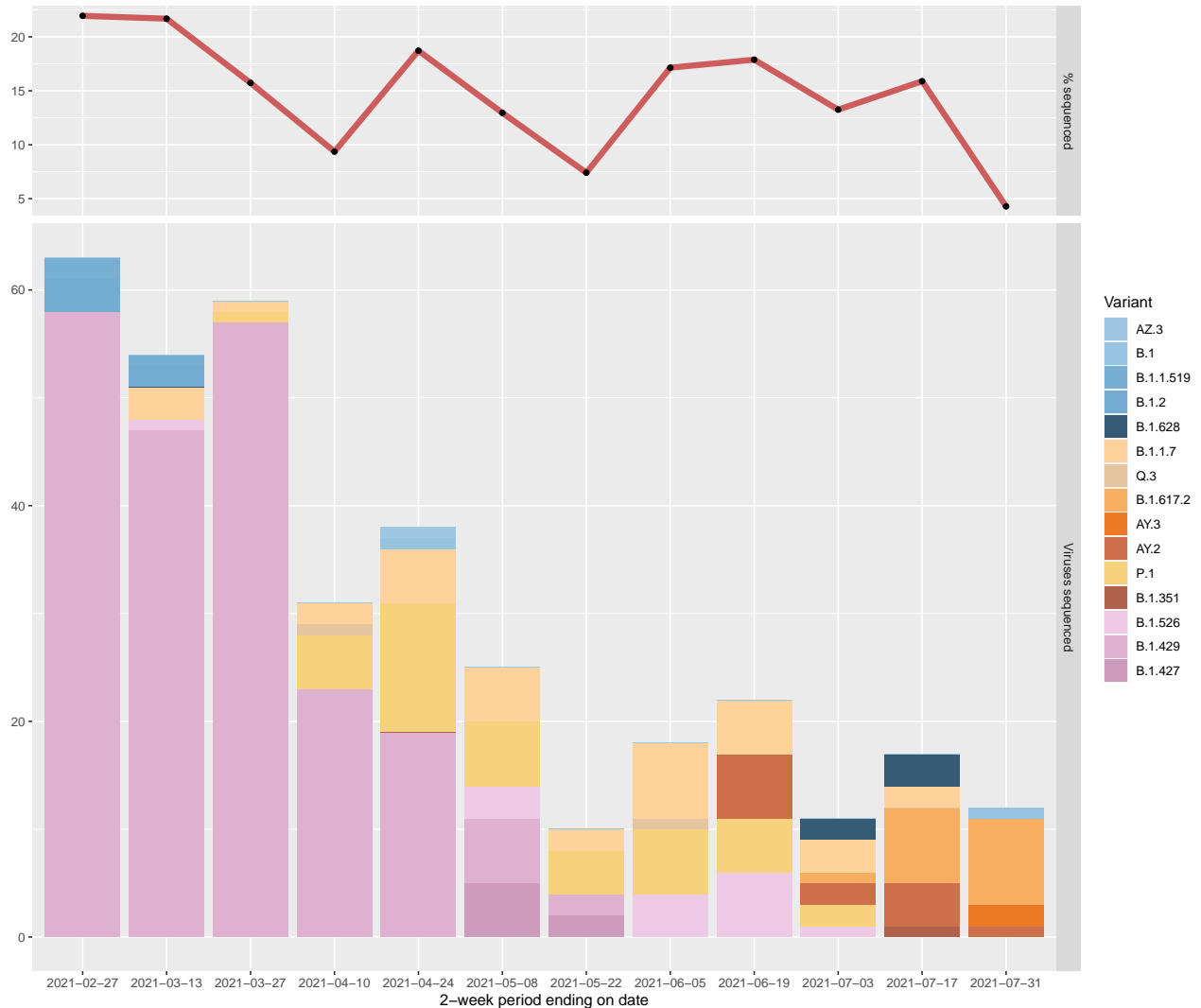
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			309		
	B.1.617.2	India	267	18 May 2021	27 Jul 2021
	AY.3	United States	28	28 Jun 2021	26 Jul 2021
	AY.1	Europe	7	30 Jun 2021	29 Jul 2021
	AY.2	United States	7	12 Jun 2021	17 Jul 2021
Alpha			430		
	B.1.1.7	United Kingdom	400	21 Jan 2021	24 Jul 2021
	Q.3	United States	30	03 Apr 2021	19 Jun 2021
Gamma	P.1	Brazil	89	24 Mar 2021	20 Jul 2021
Beta	B.1.351	South Africa	12	16 Feb 2021	02 May 2021

## Variants of interest in Honolulu County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Epsilon	B.1.429	California	297	05 Jan 2021	29 May 2021
Epsilon	B.1.427	California	29	07 Jan 2021	05 Jun 2021
Iota	B.1.526	New York	24	08 Feb 2021	23 Jul 2021

# Maui County

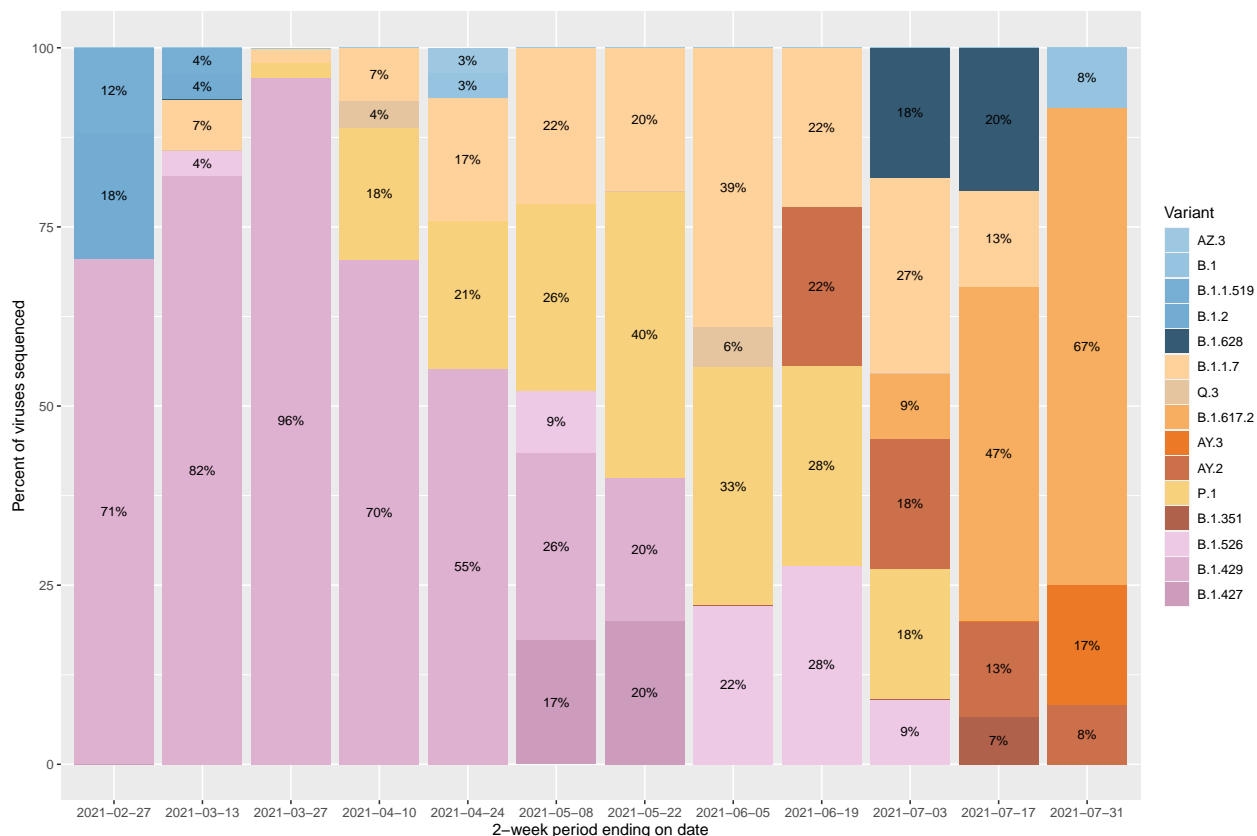
## Total variants identified in Maui County



### 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)
- Variants of concern are shown in orange/brown colors (B.1.617.2 + AY.\*, B.1.1.7 + Q.\*, B.1.351, and P.1) 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.
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## Estimate of proportion of variants circulating in Maui County



### Notes:

- The chart above shows the estimate of biweekly percentages of the SARS-CoV-2 lineages circulating in Maui County, 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.
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## Variants of concern in Maui County

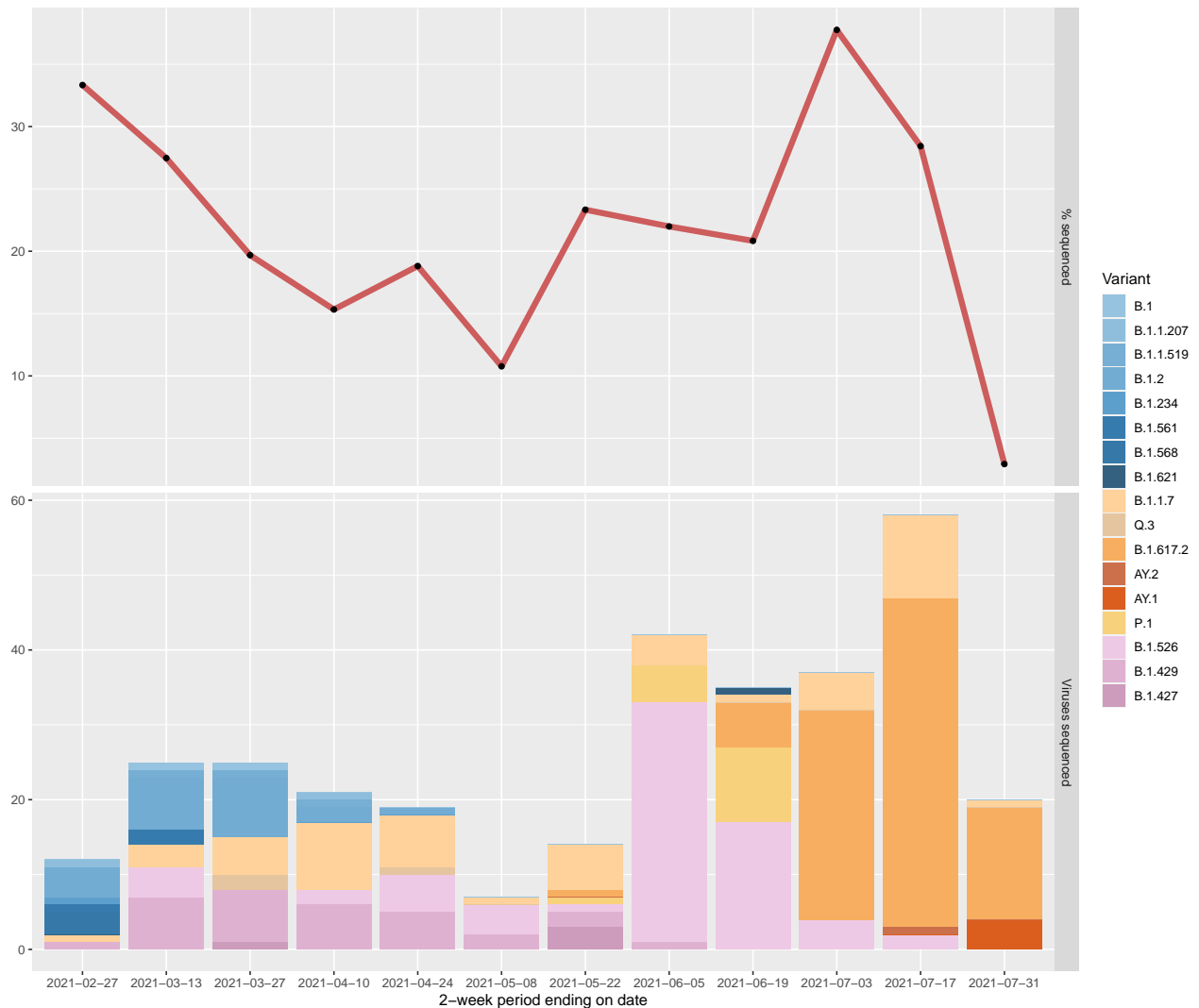
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			31		
	B.1.617.2	India	16	27 Jun 2021	23 Jul 2021
	AY.2	United States	13	07 Jun 2021	22 Jul 2021
	AY.3	United States	2	Jul 2021	Jul 2021
Alpha			37		
	B.1.1.7	United Kingdom	35	01 Mar 2021	11 Jul 2021
	Q.3	United States	2	Apr 2021	May 2021
Gamma	P.1	Brazil	41	21 Mar 2021	20 Jun 2021
Beta	B.1.351	South Africa	1	Jul 2021	Jul 2021

## Variants of interest in Maui County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Epsilon	B.1.429	California	246	08 Jan 2021	18 May 2021
Iota	B.1.526	New York	15	12 Mar 2021	25 Jun 2021
Epsilon	B.1.427	California	7	27 Apr 2021	10 May 2021

# Hawaii County

## Total variants identified in Hawaii County

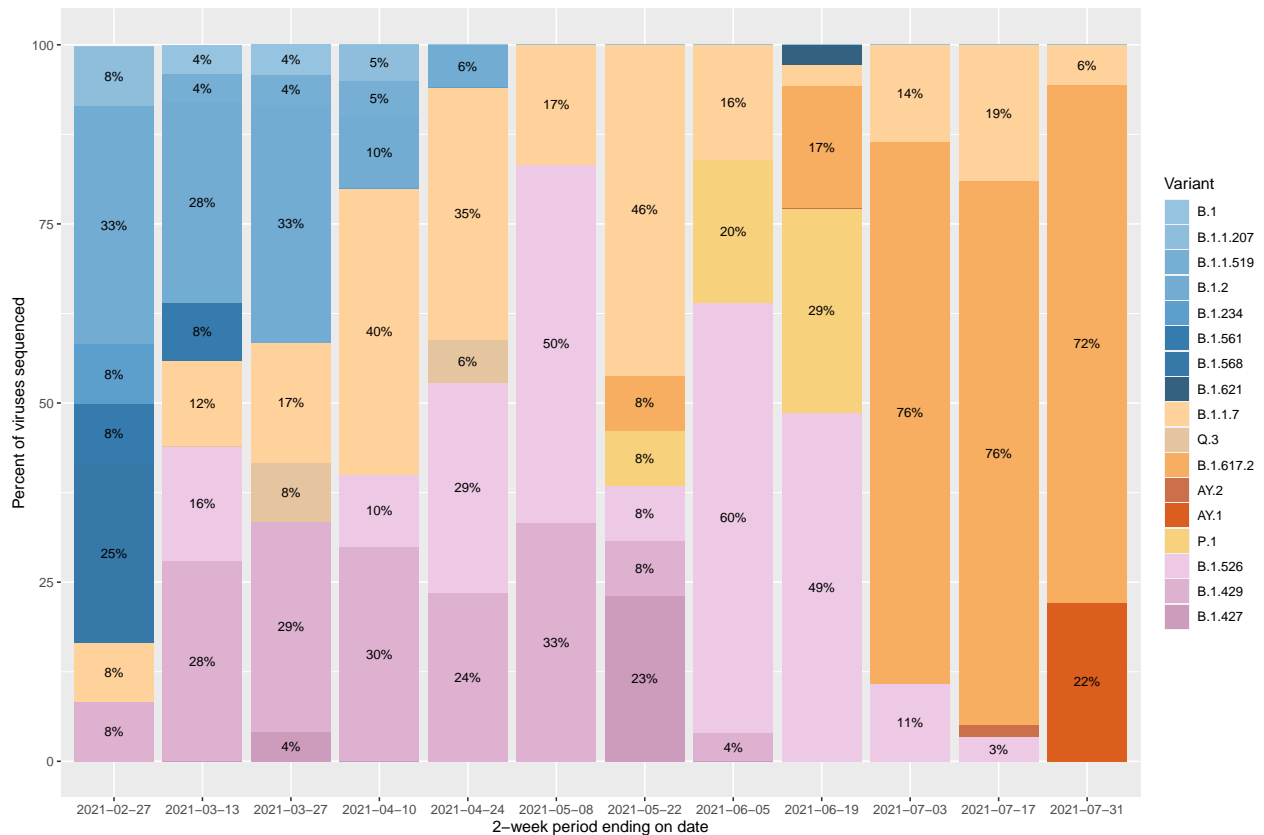


### Notes:

- The above graph shows the total number of variants detected in Hawaii 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.1.617.2 + AY.\*, B.1.1.7 + Q.\*, B.1.351, and P.1) and variants of interest are shown in pink (B.1.429, B.1.427, B.1.526 and P.2)
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## Estimate of proportion of variants circulating in Hawaii County



### Notes:

- The chart above shows the biweekly percentages of the SARS-CoV-2 lineages circulating in Hawaii County, 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.
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## Variants of concern in Hawaii County

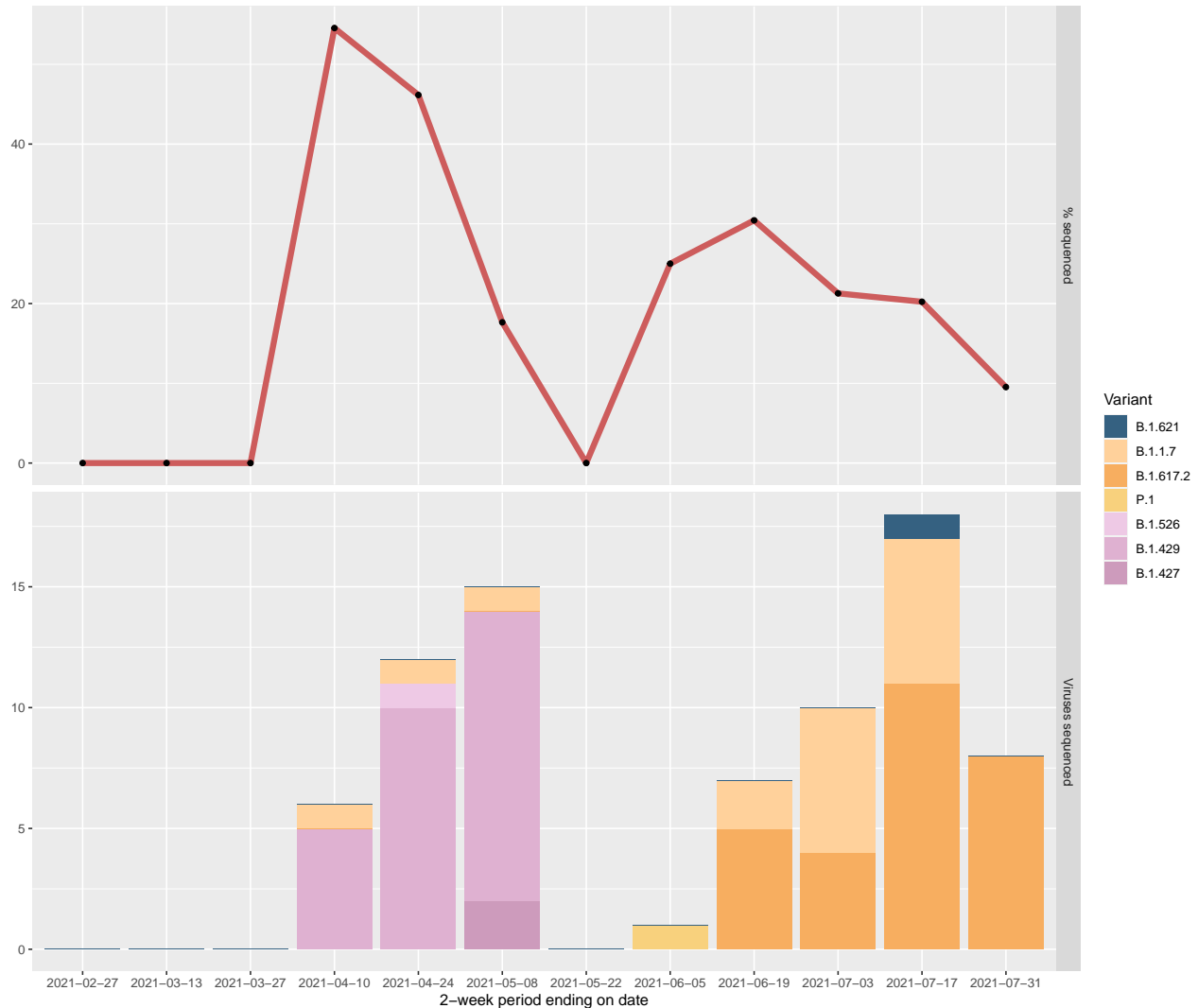
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			99		
	B.1.617.2	India	94	21 May 2021	28 Jul 2021
	AY.1	Europe	4	20 Jul 2021	22 Jul 2021
	AY.2	United States	1	Jul 2021	Jul 2021
Alpha			57		
	B.1.1.7	United Kingdom	54	22 Feb 2021	18 Jul 2021
	Q.3	United States	3	Mar 2021	Apr 2021
Gamma	P.1	Brazil	16	10 May 2021	14 Jun 2021

## Variants of interest in Hawaii County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Iota	B.1.526	New York	72	06 Feb 2021	07 Jul 2021
Epsilon	B.1.429	California	34	25 Jan 2021	26 May 2021
Epsilon	B.1.427	California	5	04 Feb 2021	17 May 2021

# Kauai County

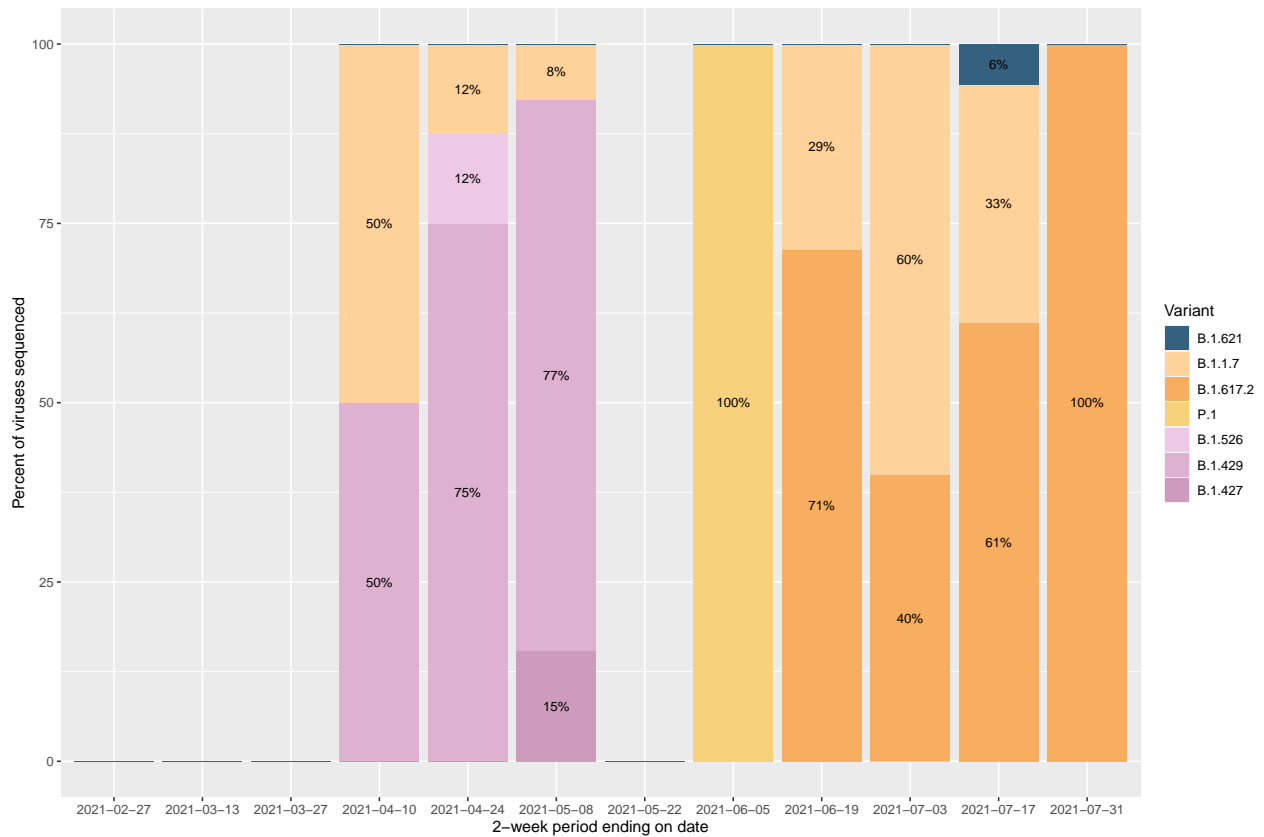
## Total variants identified in Kauai County



### Notes:

- The above graph shows the total number of variants detected in Kauai 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.1.617.2 + AY.\*, B.1.1.7 + Q.\*, B.1.351, and P.1) and variants of interest are shown in pink (B.1.429, B.1.427, B.1.526 and P.2)
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## Estimate of proportion of variants circulating in Kauai County



### Notes:

- The chart above shows the estimate of biweekly percentages of the SARS-CoV-2 lineages circulating in Kauai County, 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.
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## Variants of concern in Kauai County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta	B.1.617.2	India	28	06 Jun 2021	24 Jul 2021
Alpha	B.1.1.7	United Kingdom	17	05 Apr 2021	13 Jul 2021
Gamma	P.1	Brazil	1	May 2021	May 2021

## Variants of interest in Kauai County

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