

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 2599 viral genomes (1527 in Honolulu County, 416 in Maui County, 347 in Hawaii County, 90 in Kauai County and 219 lacking county information).
- This report also integrates 459 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 3086 genomes.
- Since the last version of this variant report was generated on 8/18/2021 reporting 582 Delta samples detected, 236 additional samples belonging to the Delta variant of concern have been detected and the Delta variant (the lineages B.1.617.2 and AY.*) now accounts for almost all the cases in Hawaii, with very few exceptions.
- In this report, we show the estimates of the variant proportions by adding up all the sub-lineages that make up one particular variant (e.g. B.1.617.2 and AY.* for Delta), but we show the absolute counts for each individual lineage separately in the total counts graph and in the variant of concern/interest tables. We also switched to a new color scheme, which is similar to the one used currently by CDC to show the different variants.

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

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)

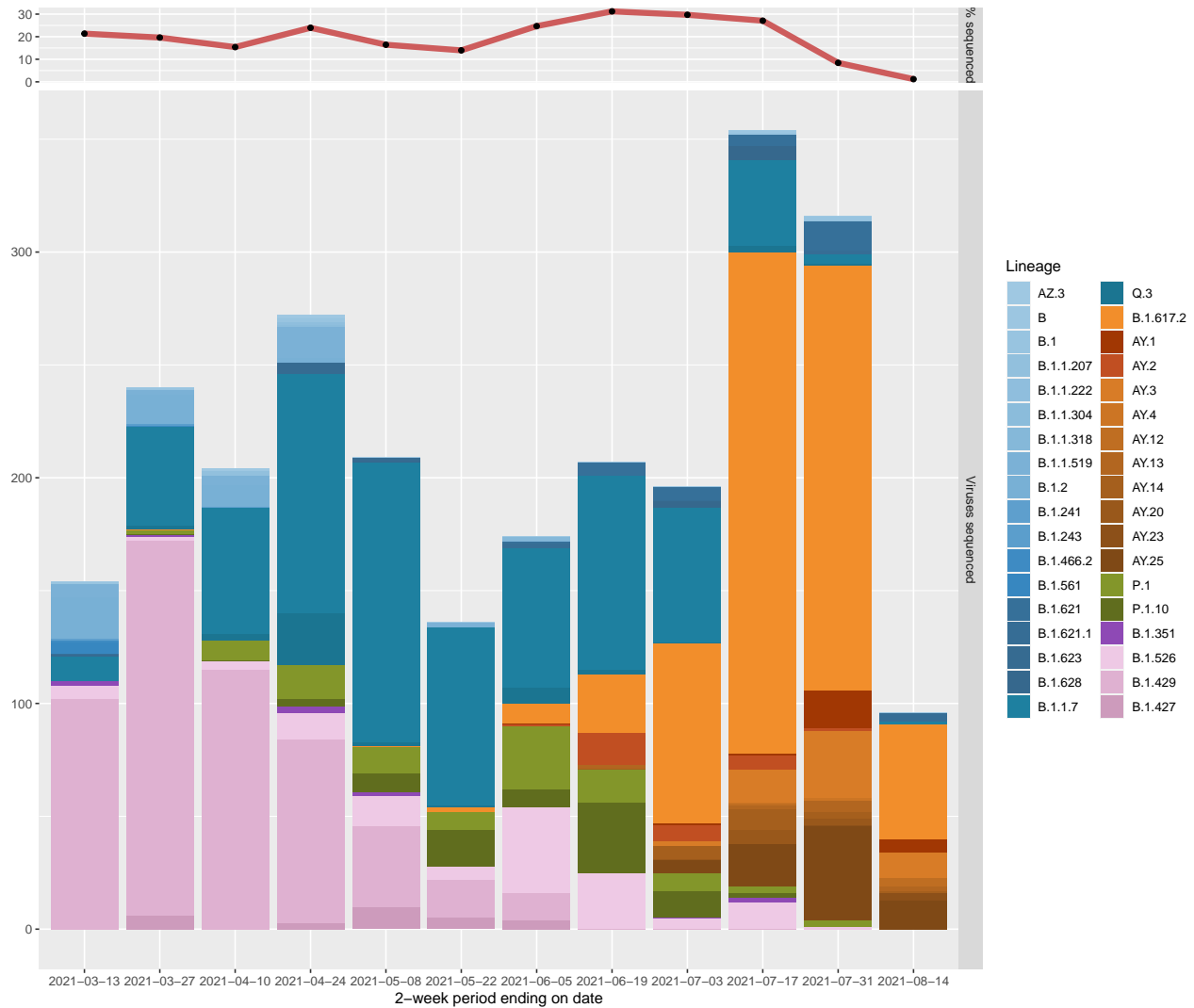
These closely related variants, B.1.429 and B.1.427, were first identified in California and designated initially as CA VUI1. WHO labeled them “Epsilon” on May 31, 2021. They can quickly spread from person-to-person, with an estimated ~20% higher efficiency than the original virus. CDC has deescalated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

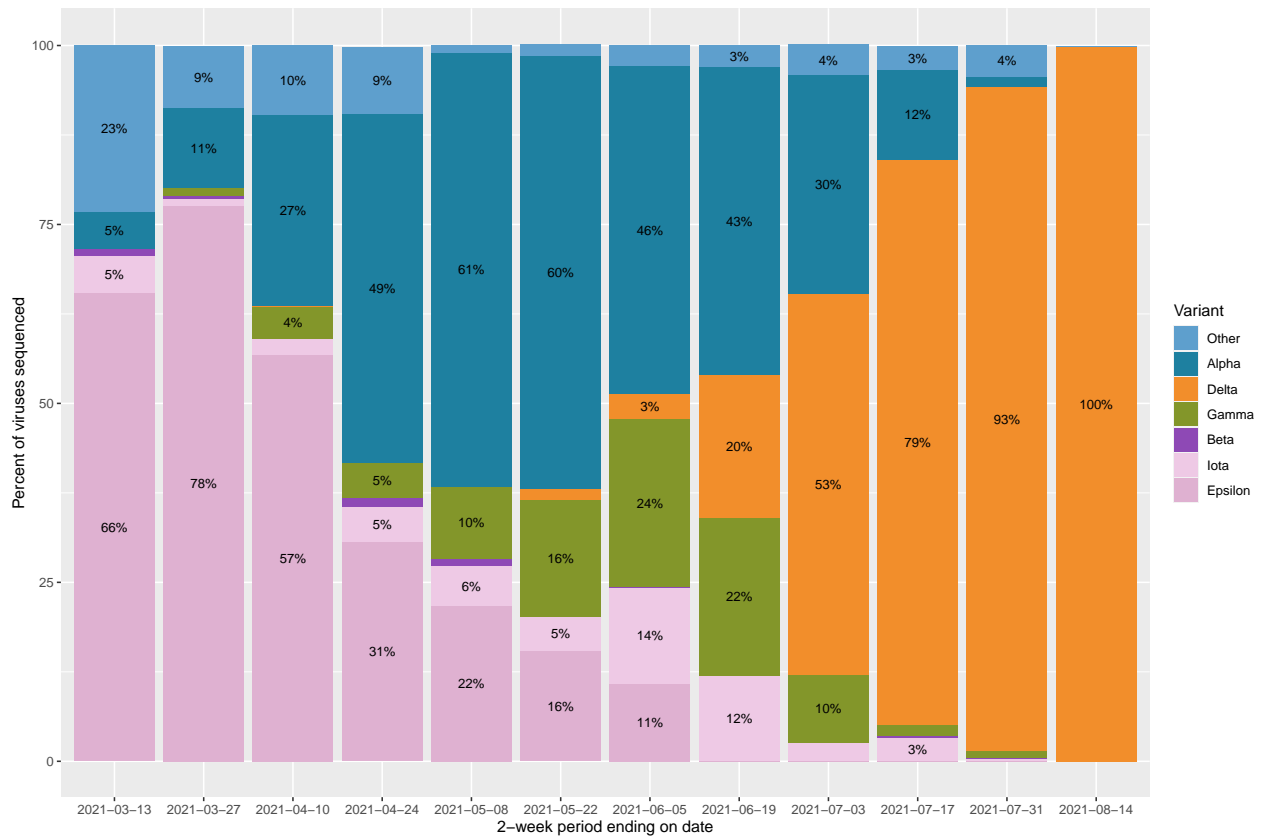
Total variants identified



Notes:

- The above bar graph shows the total number of variants by lineage 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 as follows orange/brown = Delta (lineages B.1.617.2 + AY.*), dark blue = Alpha (lineages B.1.1.7 + Q.*), purple = Beta (lineage B.1.351) and green = Gamma (lineages P.1 + P.1.*)
- Variants of interest are shown in pink: Epsilon (lineages B.1.429 and B.1.427) and Iota (lineage B.1.526)
- 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 variants 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, 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

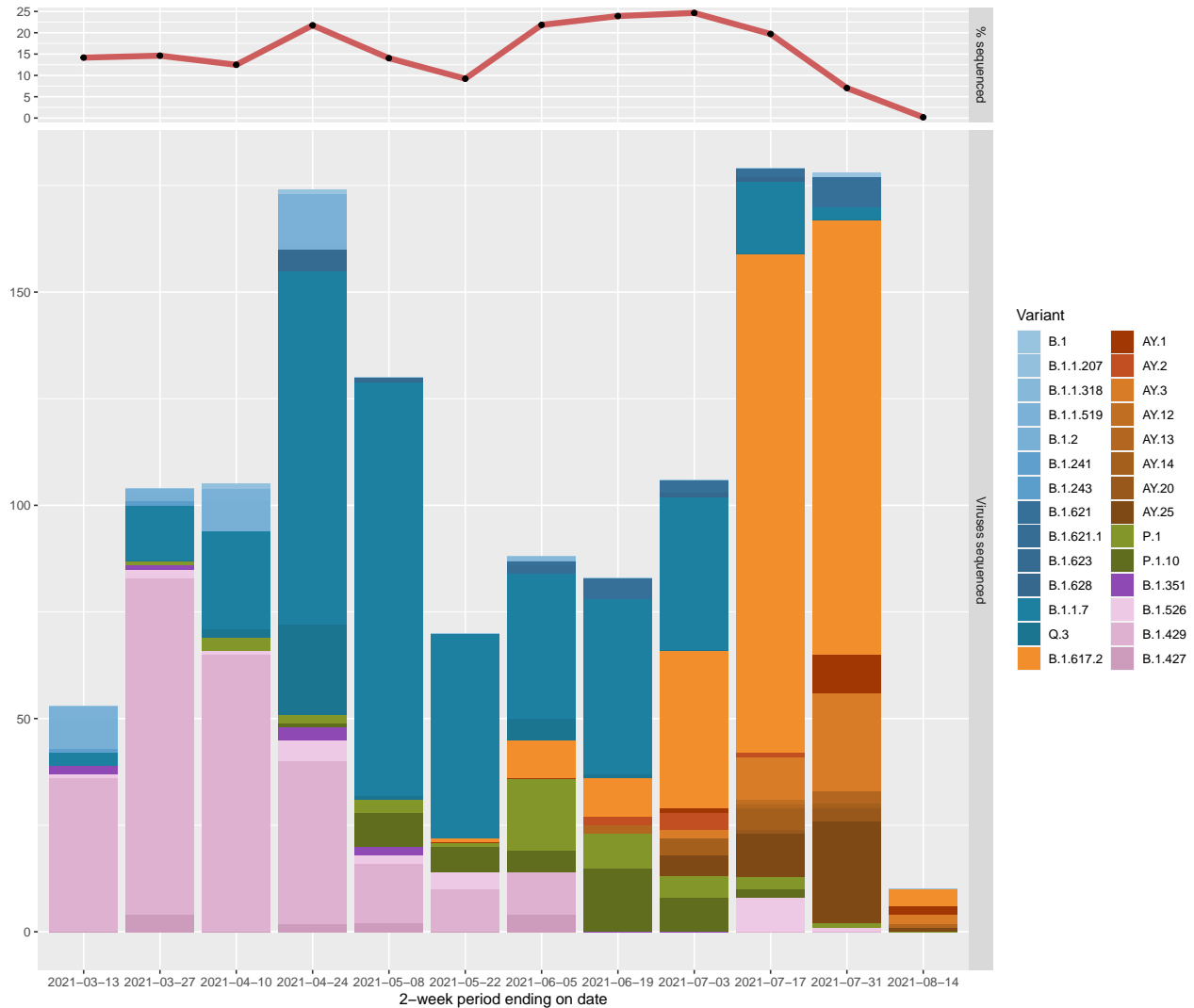
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			818		
	B.1.617.2	India	578	18 May 2021	14 Aug 2021
	AY.25	United States	80	21 Jun 2021	10 Aug 2021
	AY.3	United States	58	28 Jun 2021	09 Aug 2021
	AY.2	United States	29	01 Jun 2021	22 Jul 2021
	AY.1	Europe	25	30 Jun 2021	10 Aug 2021
	AY.14	United States	19	24 Jun 2021	02 Aug 2021
	AY.13	United States	11	09 Jun 2021	05 Aug 2021
	AY.20	United States/Mexico	9	10 Jul 2021	22 Jul 2021
	AY.12	Israel	5	09 Jul 2021	10 Aug 2021
	AY.23	Singapore/Indonesia	3	Aug 2021	Aug 2021
	AY.4	United Kingdom	1	Jul 2021	Jul 2021
Alpha			729		
	B.1.1.7	United Kingdom	685	21 Jan 2021	02 Aug 2021
	Q.3	United States	44	21 Mar 2021	18 Jul 2021
Gamma			183		
	P.1	Brazil	103	21 Mar 2021	21 Jul 2021
	P.1.10	United States	80	24 Apr 2021	13 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			771		
	B.1.429	California	712	31 Dec 2020	03 Jun 2021
	B.1.427	California	59	07 Dec 2020	05 Jun 2021
Iota	B.1.526	New York	128	06 Feb 2021	23 Jul 2021

Honolulu County

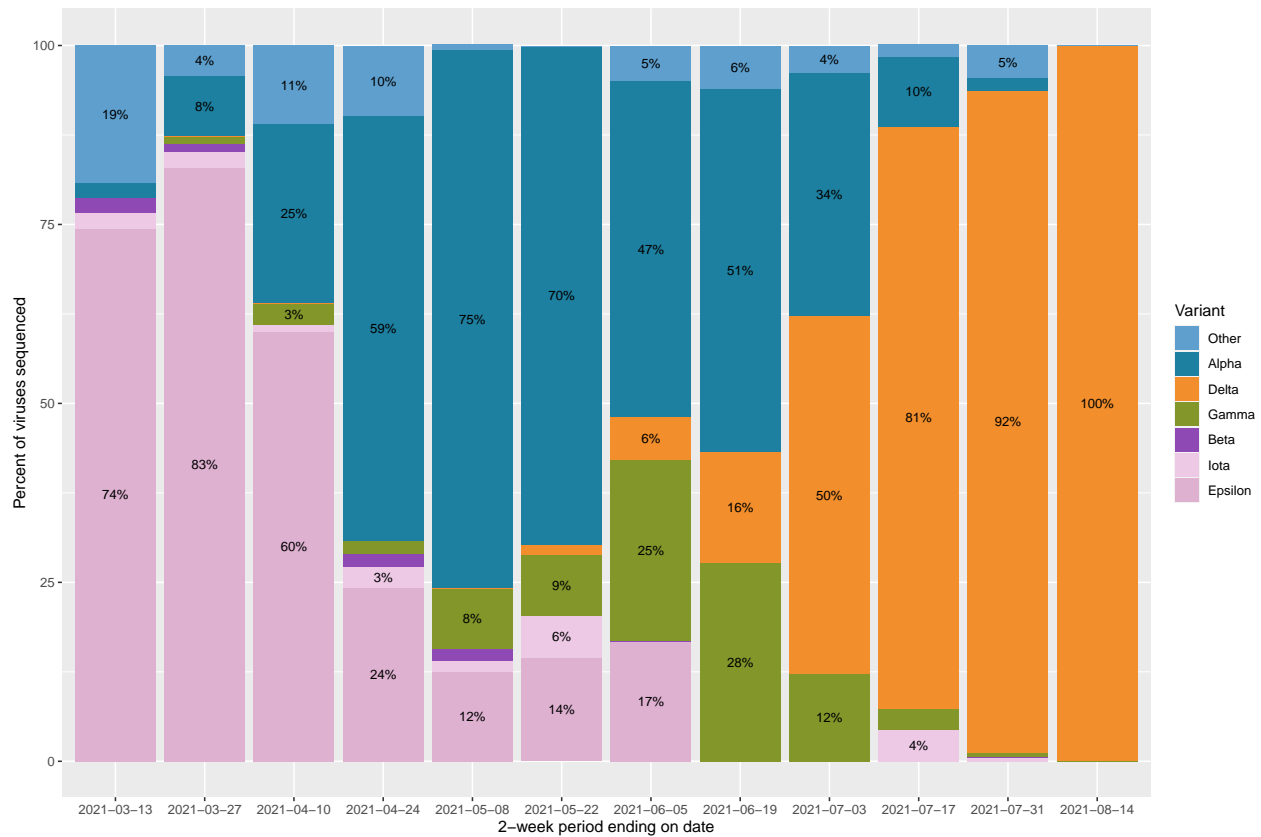
Total variants identified in Honolulu County



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 as follows orange/brown = Delta (lineages B.1.617.2 + AY.*), dark blue = Alpha (lineages B.1.1.7 + Q.*), purple = Beta (lineage B.1.351) and green = Gamma (lineages P.1 + P.1.*)
- Variants of interest are shown in pink: Epsilon (lineages B.1.429 and B.1.427) and Iota (lineage B.1.526)
- 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 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.
- 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 Honolulu County

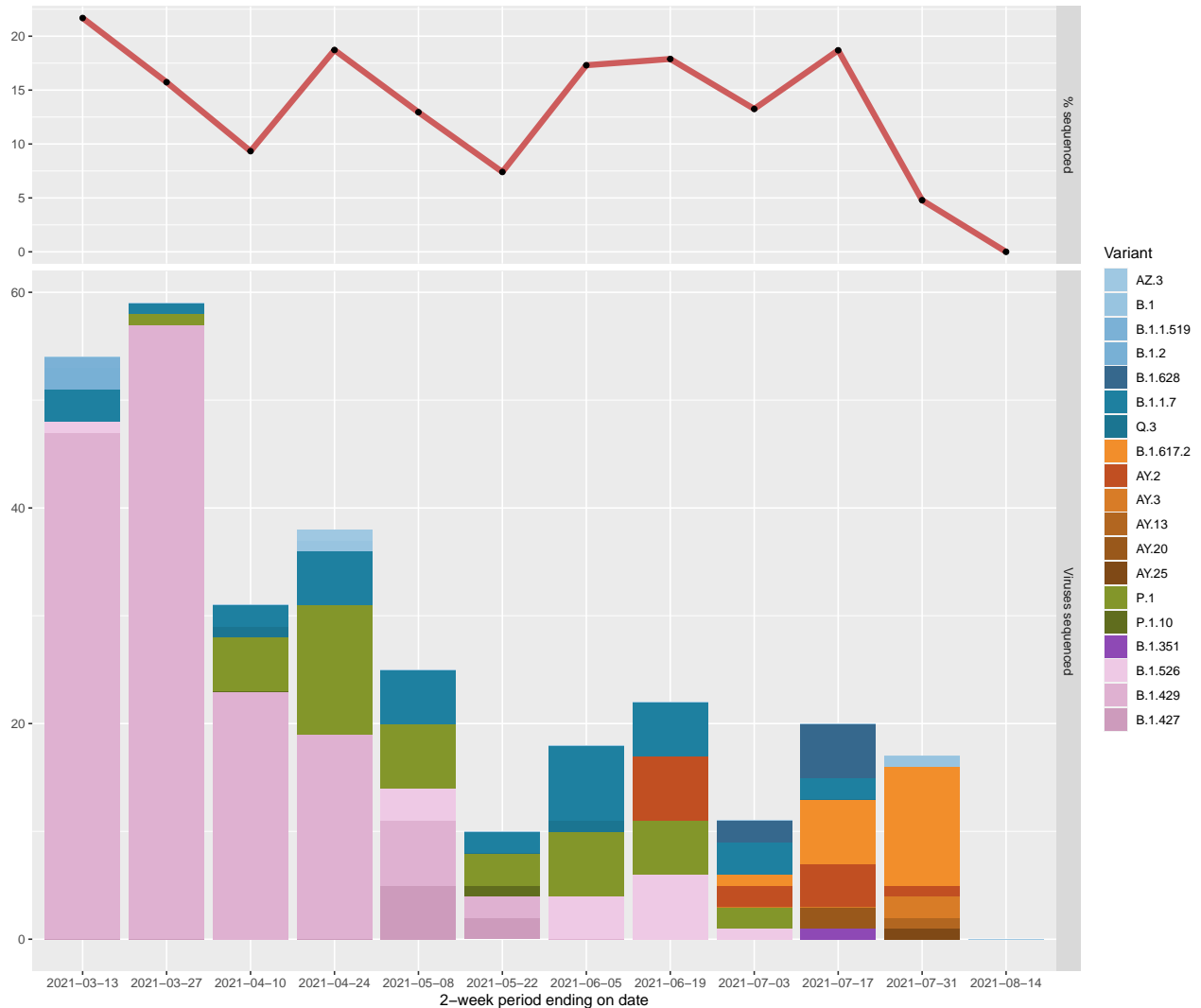
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			397		
	B.1.617.2	India	279	18 May 2021	05 Aug 2021
	AY.25	United States	40	21 Jun 2021	02 Aug 2021
	AY.3	United States	37	28 Jun 2021	04 Aug 2021
	AY.1	Europe	12	30 Jun 2021	03 Aug 2021
	AY.14	United States	10	29 Jun 2021	23 Jul 2021
	AY.13	United States	7	09 Jun 2021	04 Aug 2021
	AY.2	United States	7	12 Jun 2021	17 Jul 2021
	AY.20	United States/Mexico	4	15 Jul 2021	22 Jul 2021
	AY.12	Israel	1	Jul 2021	Jul 2021
Alpha			435		
	B.1.1.7	United Kingdom	405	21 Jan 2021	28 Jul 2021
	Q.3	United States	30	03 Apr 2021	19 Jun 2021
Gamma			89		
	P.1.10	United States	45	24 Apr 2021	13 Jul 2021
	P.1	Brazil	44	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			326		
	B.1.429	California	297	05 Jan 2021	29 May 2021
	B.1.427	California	29	07 Jan 2021	05 Jun 2021
Iota	B.1.526	New York	26	08 Feb 2021	23 Jul 2021

Maui County

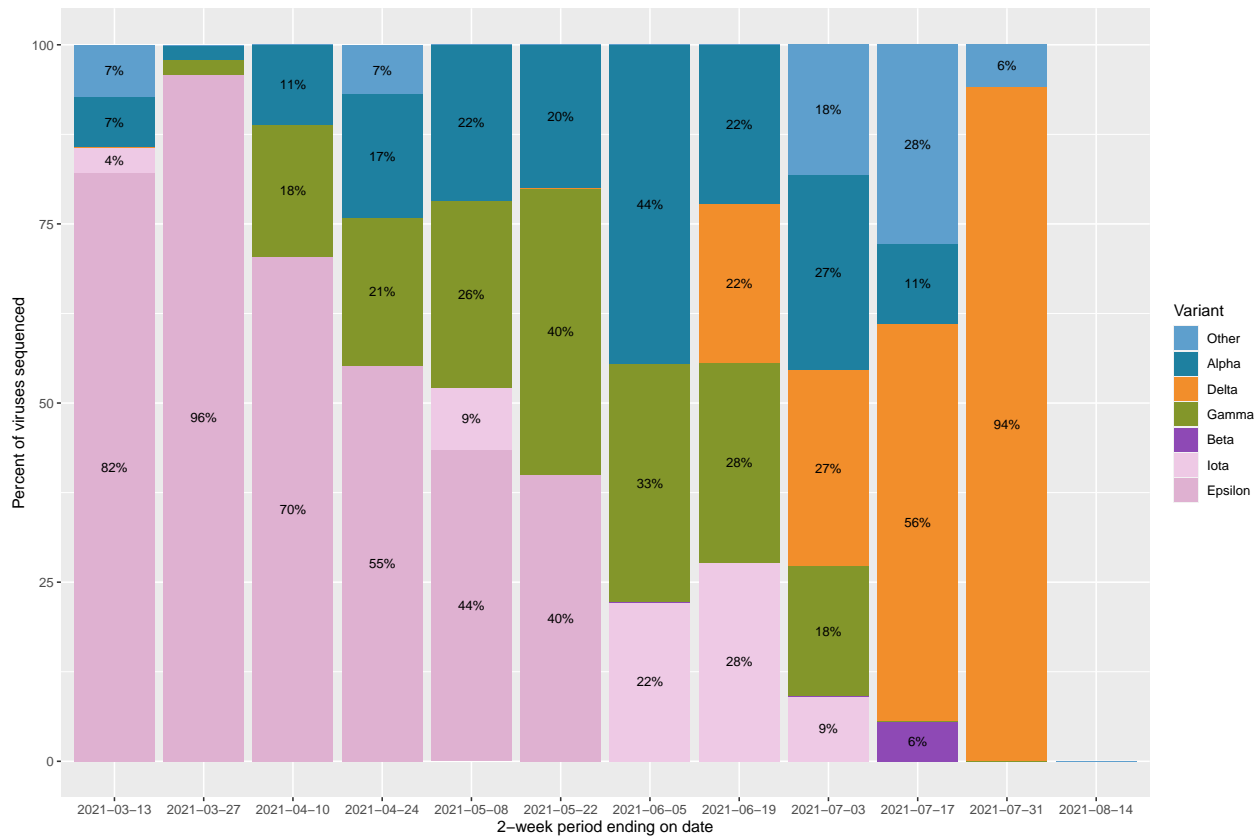
Total variants identified in Maui County



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 as follows orange/brown = Delta (lineages B.1.617.2 + AY.*), dark blue = Alpha (lineages B.1.1.7 + Q.*), purple = Beta (lineage B.1.351) and green = Gamma (lineages P.1 + P.1.*)
- Variants of interest are shown in pink: Epsilon (lineages B.1.429 and B.1.427) and Iota (lineage B.1.526)
- 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 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.
- 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 Maui County

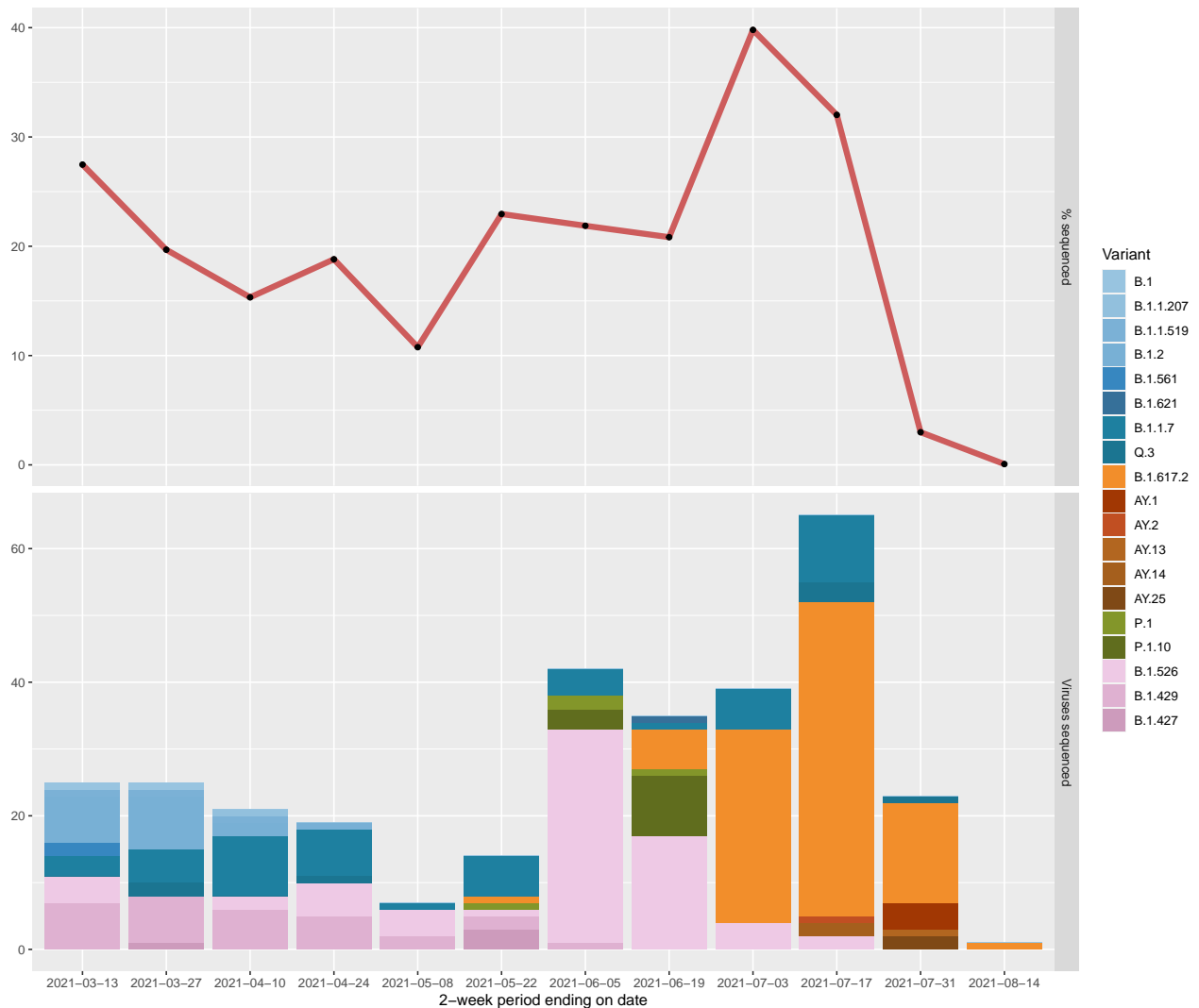
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			37		
	B.1.617.2	India	18	27 Jun 2021	28 Jul 2021
	AY.2	United States	13	07 Jun 2021	22 Jul 2021
	AY.20	United States/Mexico	2	Jul 2021	Jul 2021
	AY.3	United States	2	Jul 2021	Jul 2021
	AY.13	United States	1	Jul 2021	Jul 2021
	AY.25	United States	1	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			41		
	P.1	Brazil	40	21 Mar 2021	20 Jun 2021
	P.1.10	United States	1	May 2021	May 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			253		
	B.1.429	California	246	08 Jan 2021	18 May 2021
	B.1.427	California	7	27 Apr 2021	10 May 2021
Iota	B.1.526	New York	15	12 Mar 2021	25 Jun 2021

Hawaii County

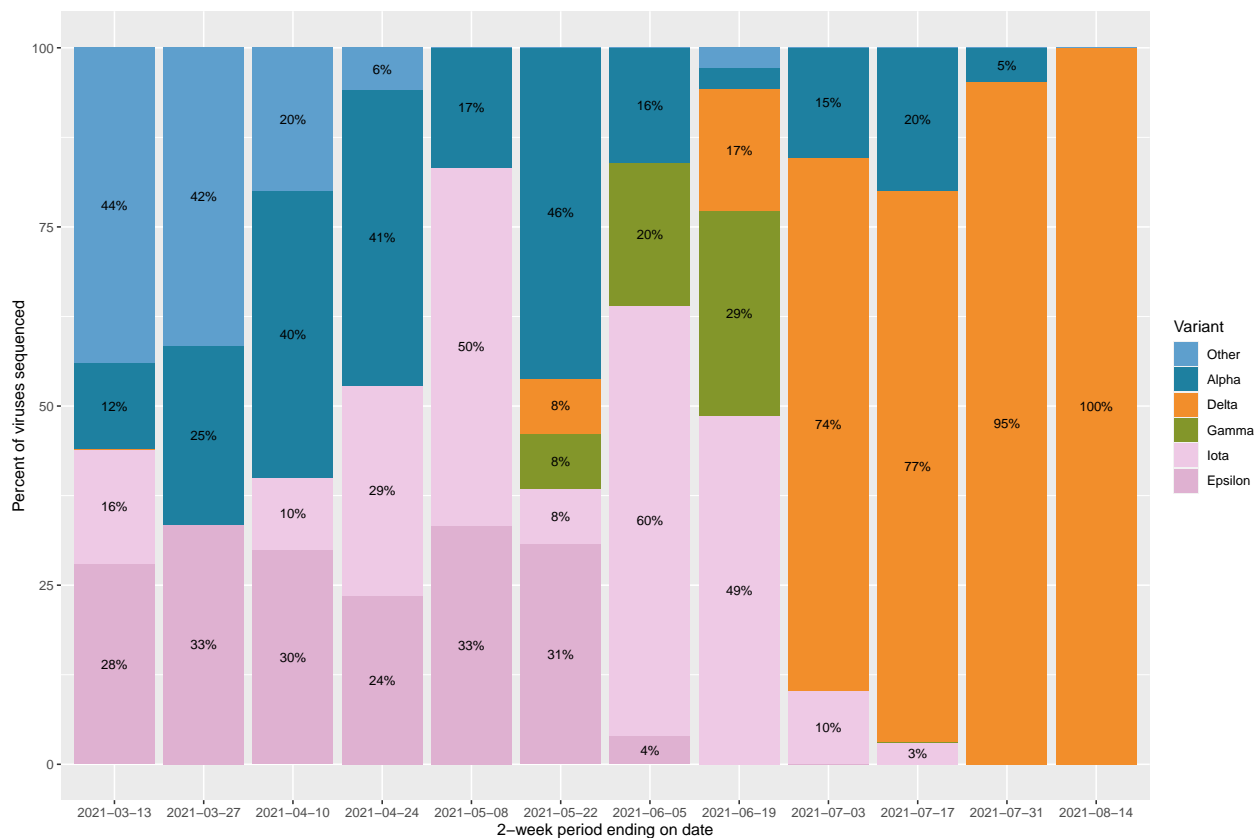
Total variants identified in Hawaii County



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 as follows orange/brown = Delta (lineages B.1.617.2 + AY.*), dark blue = Alpha (lineages B.1.1.7 + Q.*), purple = Beta (lineage B.1.351) and green = Gamma (lineages P.1 + P.1.*)
- Variants of interest are shown in pink: Epsilon (lineages B.1.429 and B.1.427) and Iota (lineage B.1.526)
- 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 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.
- 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 Hawaii County

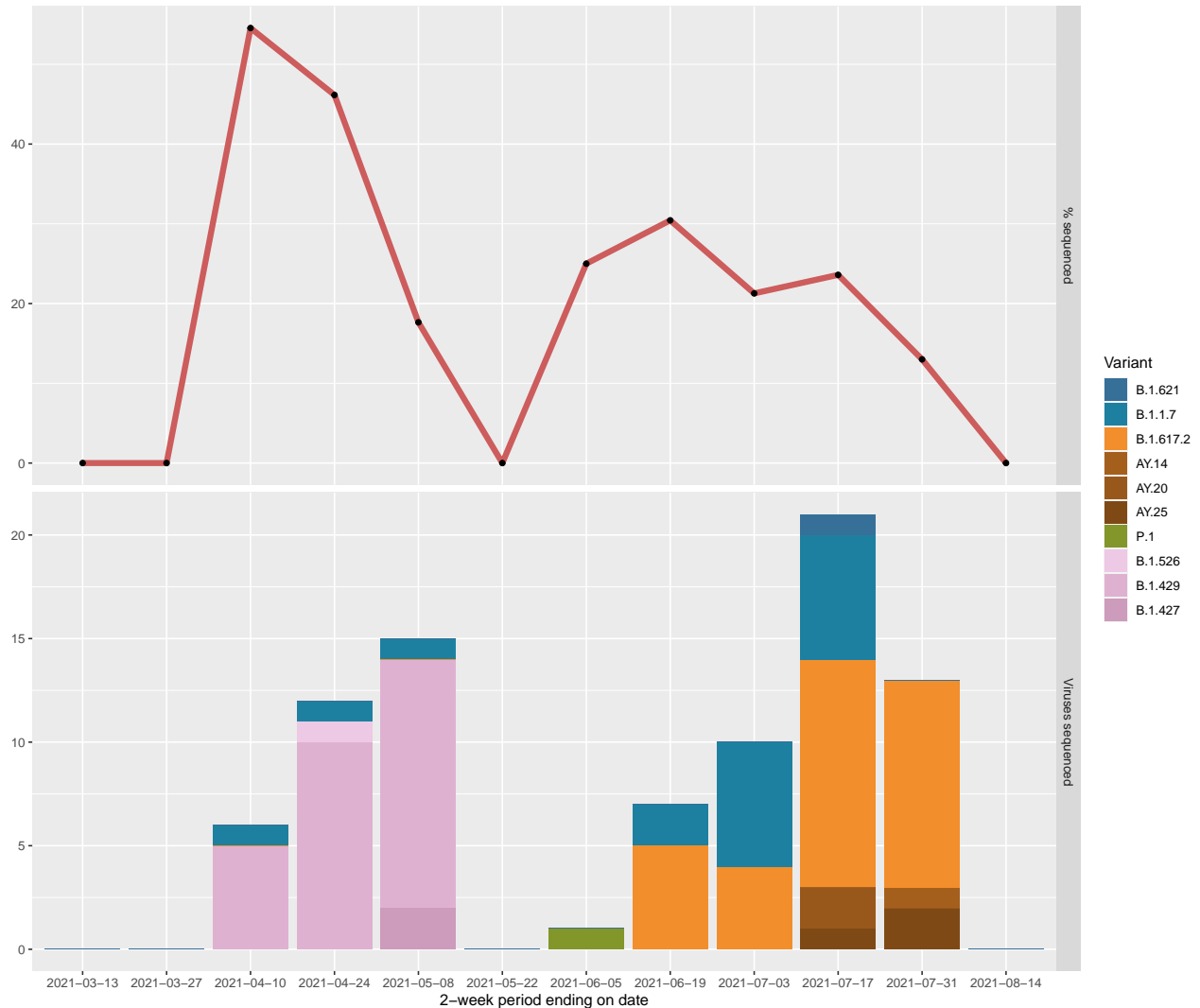
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			109		
	B.1.617.2	India	99	21 May 2021	03 Aug 2021
	AY.1	Europe	4	20 Jul 2021	22 Jul 2021
	AY.14	United States	2	Jul 2021	Jul 2021
	AY.25	United States	2	Jul 2021	Jul 2021
	AY.13	United States	1	Jul 2021	Jul 2021
	AY.2	United States	1	Jul 2021	Jul 2021
Alpha			60		
	B.1.1.7	United Kingdom	53	22 Feb 2021	16 Jul 2021
	Q.3	United States	7	21 Mar 2021	18 Jul 2021
Gamma			16		
	P.1.10	United States	12	27 May 2021	13 Jun 2021
	P.1	Brazil	4	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
Epsilon			39		
	B.1.429	California	34	25 Jan 2021	26 May 2021
	B.1.427	California	5	04 Feb 2021	17 May 2021
Iota	B.1.526	New York	72	06 Feb 2021	07 Jul 2021

Kauai County

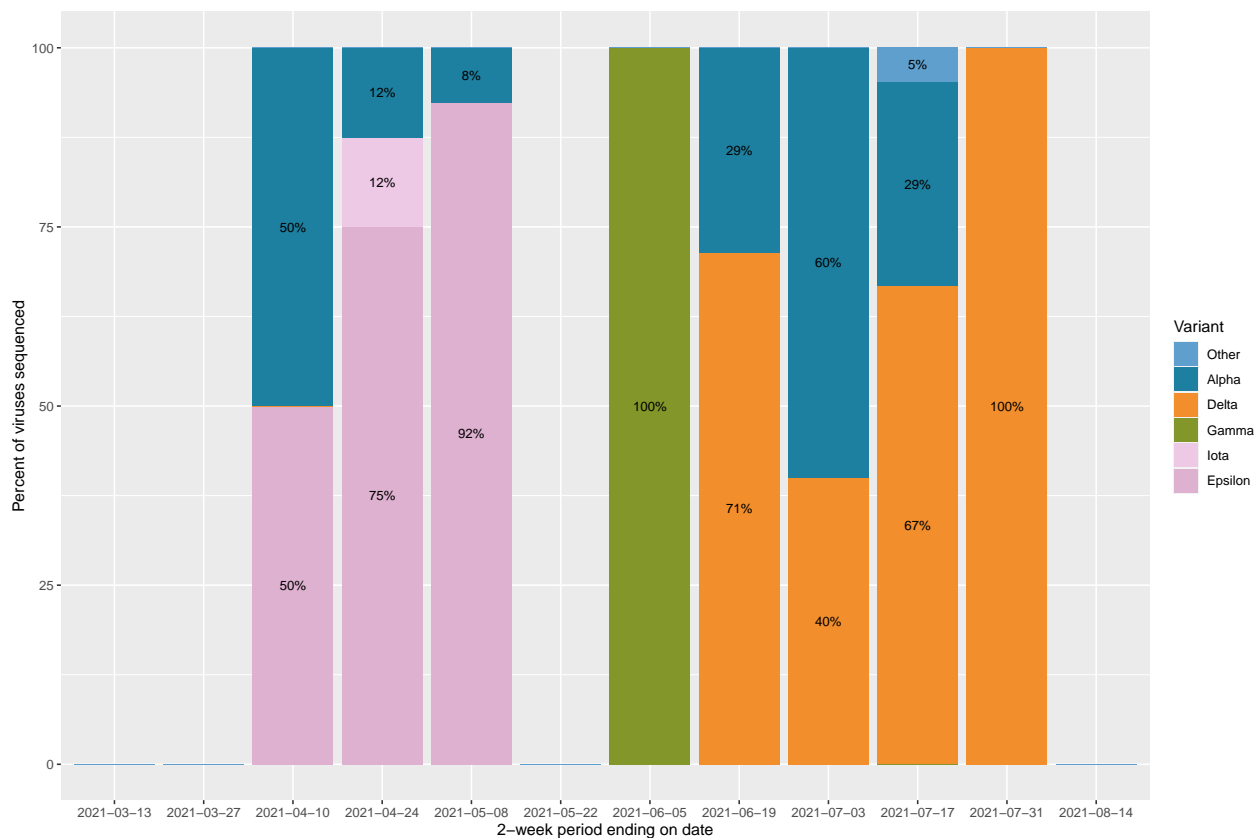
Total variants identified in Kauai County



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 as follows orange/brown = Delta (lineages B.1.617.2 + AY.*), dark blue = Alpha (lineages B.1.1.7 + Q.*), purple = Beta (lineage B.1.351) and green = Gamma (lineages P.1 + P.1.*)
- Variants of interest are shown in pink: Epsilon (lineages B.1.429 and B.1.427) and Iota (lineage B.1.526)
- 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 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.
- 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 Kauai County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			36		
	B.1.617.2	India	30	06 Jun 2021	27 Jul 2021
	AY.25	United States	3	Jul 2021	Jul 2021
	AY.20	United States/Mexico	2	Jul 2021	Jul 2021
	AY.14	United States	1	Jul 2021	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			30		
	B.1.429	California	28	07 Jan 2021	08 May 2021
	B.1.427	California	2	Apr 2021	Apr 2021
Iota	B.1.526	New York	1	Apr 2021	Apr 2021