

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).

Acknowledgements

This report integrates genomes sequenced since Jan 1, 2021 by:

Institution	Program/partner	Count	Percent
Laboratory Preparedness and Response Branch, State Laboratories Division		2786	79.40%
Centers for Disease Control and Prevention	National SARS-CoV-2 Strain Surveillance (NS3)	228	6.50%
	Quest Diagnostics Incorporated	215	6.13%
	Laboratory Corporation of America	126	3.59%
	Aegis Sciences Corporation	65	1.85%
	Helix/Illumina	19	0.54%
	Infinity Biologix	12	0.34%
	Mako Medical	2	0.06%
	Fulgent Genetics	2	0.06%
Tripler Army Medical Center		54	1.54%
Total		3509	100.00%

Notes:

- the samples sequenced by CDC in the NS3 program are collected, quality controlled and shipped to CDC by Laboratory Preparedness and Response Branch, State Laboratory Division, Hawaii Department of Health

County distribution of genomes sequenced since Jan 1st, 20210

Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
1625	441	389	98	233	2786

Notes:

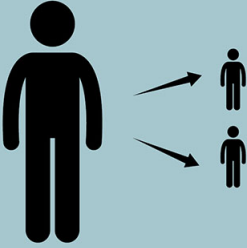
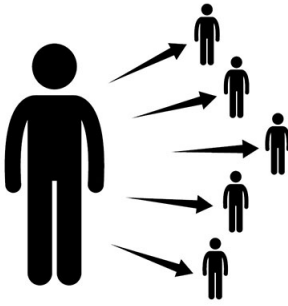
- County information is currently unavailable except for the samples sequenced by LPRB.

Short summary


- The vast majority of the genomes from Hawaii sequenced in the last 2 weeks belong the Delta variant, which accounts for the current surge in cases in Hawaii, as in the rest of US.
- The current surge in cases has put a strain on many components of the system that is required to do whole genome sequencing of the virus, including shortages of consumables (pipette tips, sequencing reagents), availability of lab personnel, which are overwhelmed with performing PCR testing and also receiving the samples from our clinical labs partners has been delayed, as they face similar issues caused by the surge.
- This has resulted in an increased lag from the time a sample is collected to the time it is sequenced and reported, with less data available for the most recent weeks.
- The Laboratory Preparedness and Response Branch within State Laboratories Division has taken steps to overcome these difficulties, including implementing a new protocol for genome sequencing, which allows faster turn-around times and increased throughput and it is not affected by the current nation-wide sequencing reagents backlog.

- As a result of these measures and also due to CDC and its commercial partners sequencing more genomes from Hawaii compared to previous months, the first half of August has been covered at levels comparable to the pre-surge intervals.

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://www.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

Mu variant (B.1.621)

Lineage B.1.621 was first identified in Columbia in January 2021 and it has a couple of mutations that are common with the Beta (B.1.351) and Gamma (P.1) variants, which have been associated with high transmissibility (N501Y) and a level of vaccine efficiency decrease (E484K). It has been designated by WHO as a variant of interest on Aug 30 (<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/>) and labeled “Mu”, but CDC has not included it in its variants of interests list (<https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html#Interest>), as its prevalence in US has been low (<0.1%) and hasn’t increased in the last few months and therefore, we are not showing it in the charts and tables below as a variant of interest. So far, this variant has been seen in 35 samples from Hawaii, the first one in the beginning of June 2021 and the last one at the end of July 2021.

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)

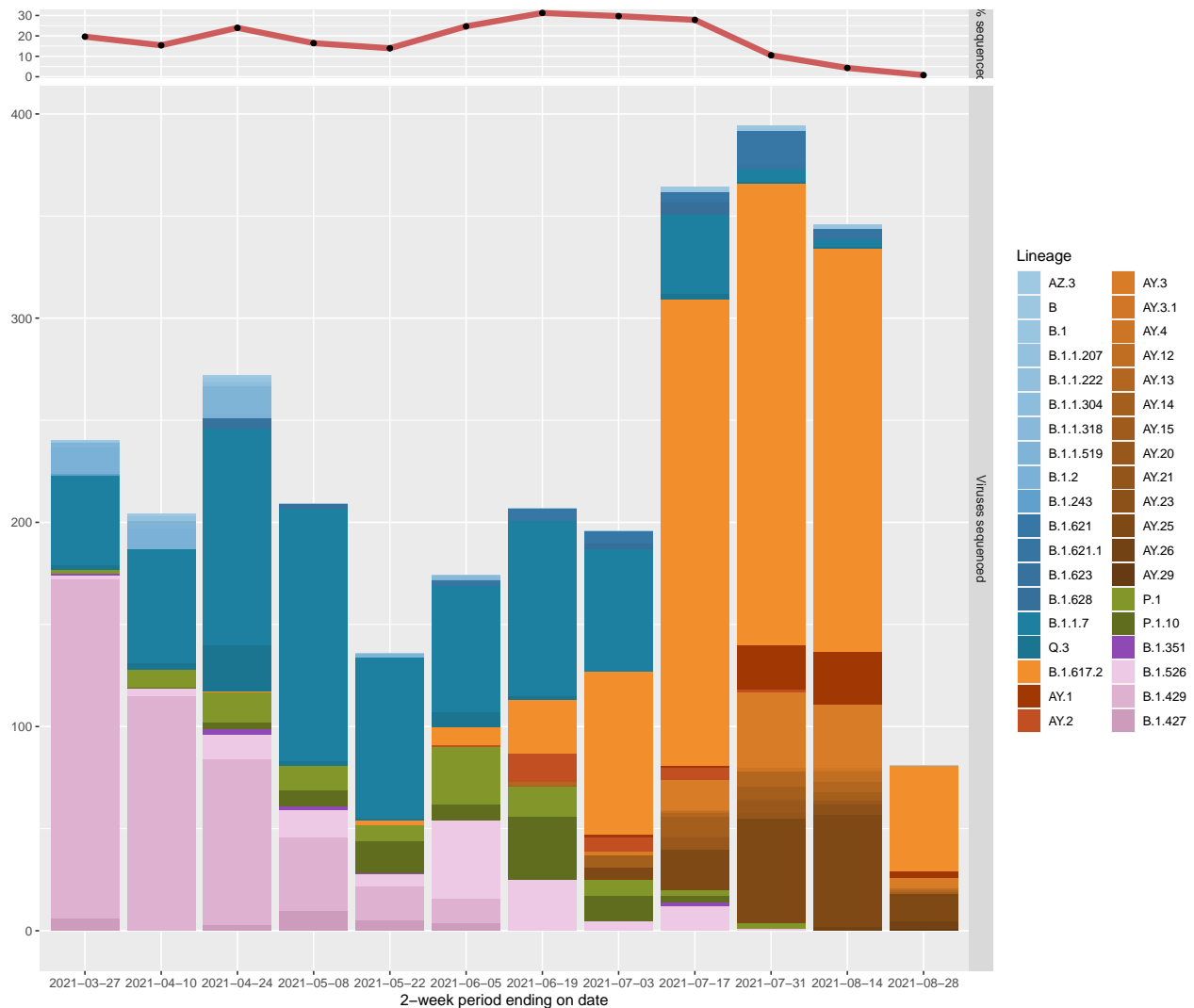
These closely related variants, B.1.429 and B.1.427, were first identified in California and designated initially as CA VUI1. WHO labeled them “Epsilon” on May 31, 2021. They can quickly spread from person-to-person, with an estimated ~20% higher efficiency than the original virus. CDC has deescalated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

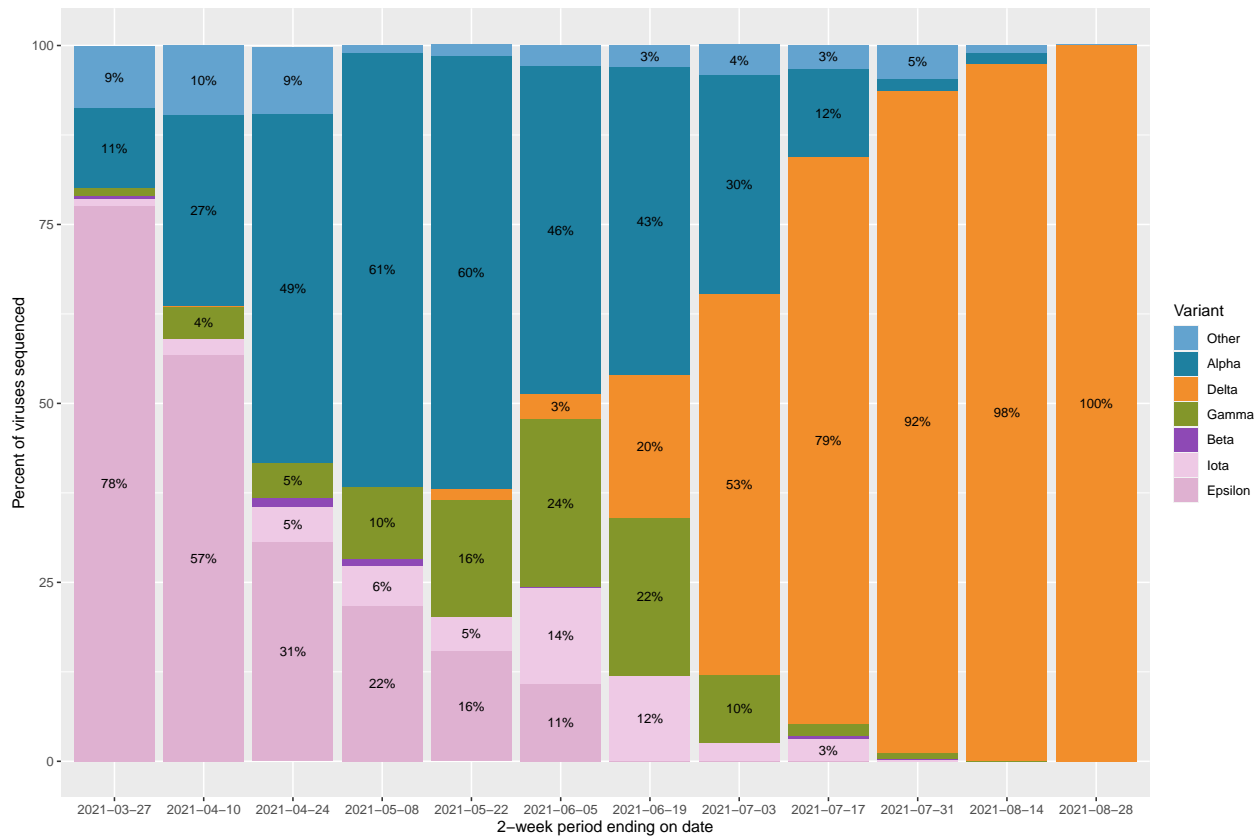
Total variants identified



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

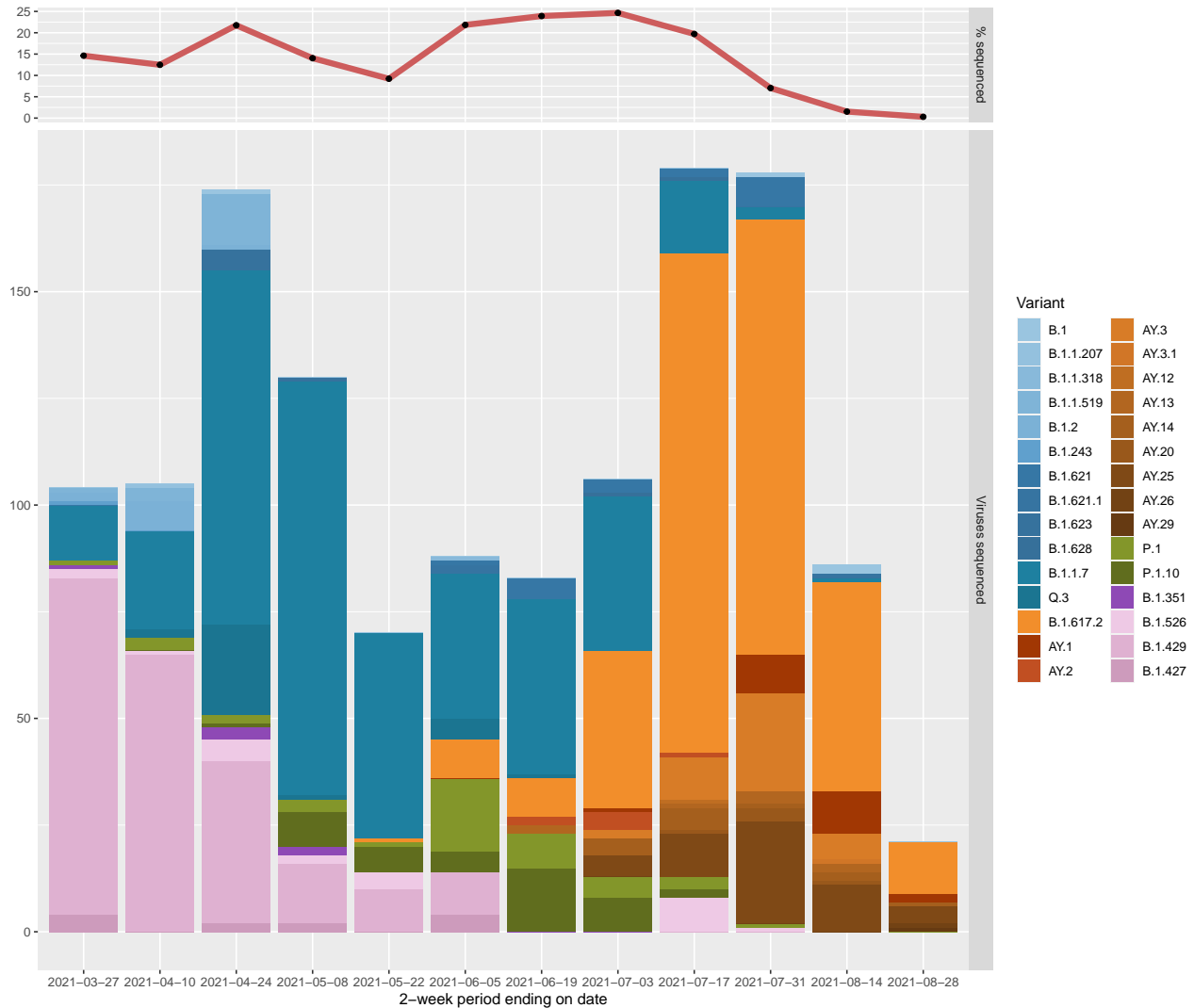
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			1226		
	B.1.617.2	India	822	18 May 2021	05 Sep 2021
	AY.25	United States	146	21 Jun 2021	07 Sep 2021
	AY.3	United States	90	28 Jun 2021	25 Aug 2021
	AY.1	Europe	53	30 Jun 2021	23 Aug 2021
	AY.2	United States	29	01 Jun 2021	22 Jul 2021
	AY.14	United States	27	24 Jun 2021	19 Aug 2021
	AY.13	United States	17	09 Jun 2021	19 Aug 2021
	AY.20	United States/Mexico	15	10 Jul 2021	02 Sep 2021
	AY.12	Israel	7	09 Jul 2021	21 Aug 2021
	AY.26	United States/Mexico	6	01 Aug 2021	21 Aug 2021
	AY.23	Singapore/Indonesia	5	11 Aug 2021	11 Aug 2021
	AY.21	Italy/Switzerland	3	Jul 2021	Jul 2021
	AY.4	United Kingdom	3	Jul 2021	Aug 2021
	AY.29	Japan	1	Aug 2021	Aug 2021
	AY.3.1	United States	1	Aug 2021	Aug 2021
	AY.15	Canada	1	Jul 2021	Jul 2021
Alpha			736		
	B.1.1.7	United Kingdom	691	21 Jan 2021	04 Aug 2021
	Q.3	United States	45	21 Mar 2021	03 Aug 2021
Gamma			184		
	P.1	Brazil	103	21 Mar 2021	21 Jul 2021
	P.1.10	United States	81	24 Apr 2021	14 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

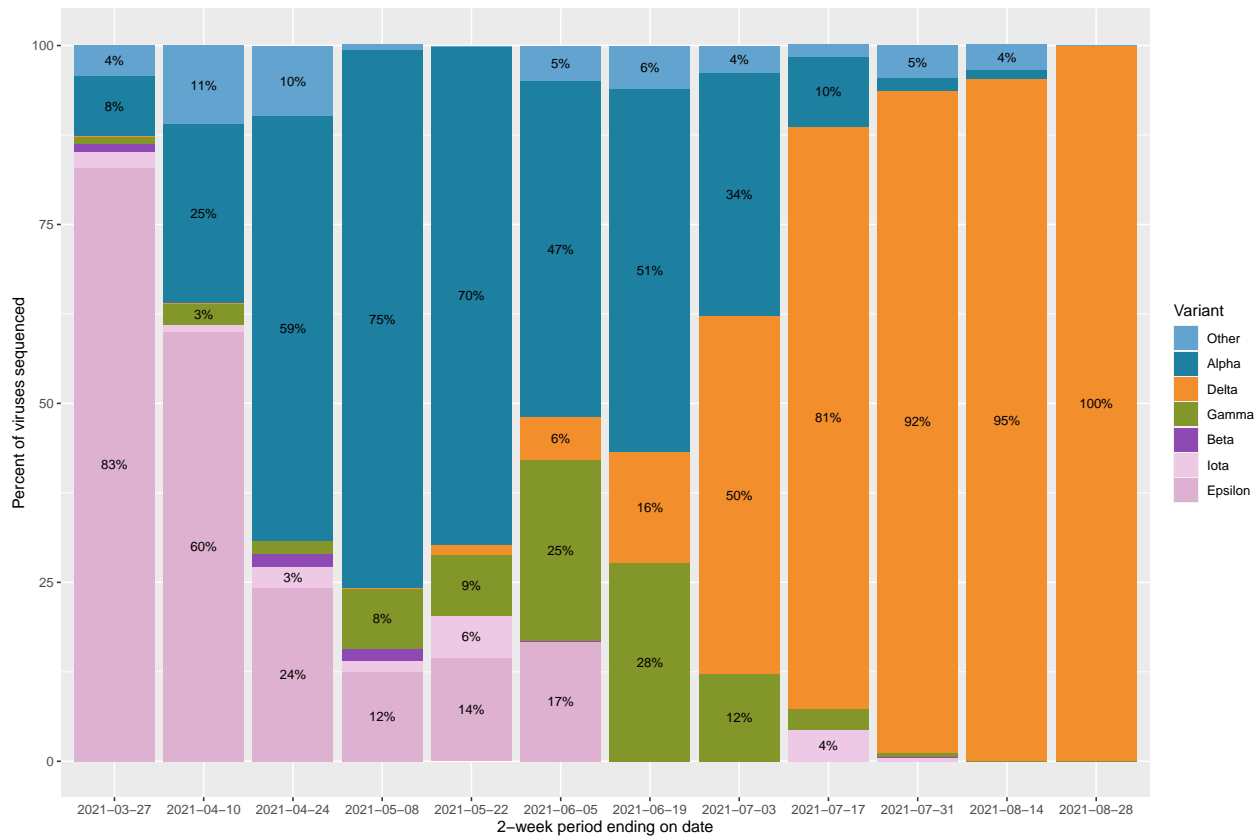
Total variants identified in Honolulu County



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.*)
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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

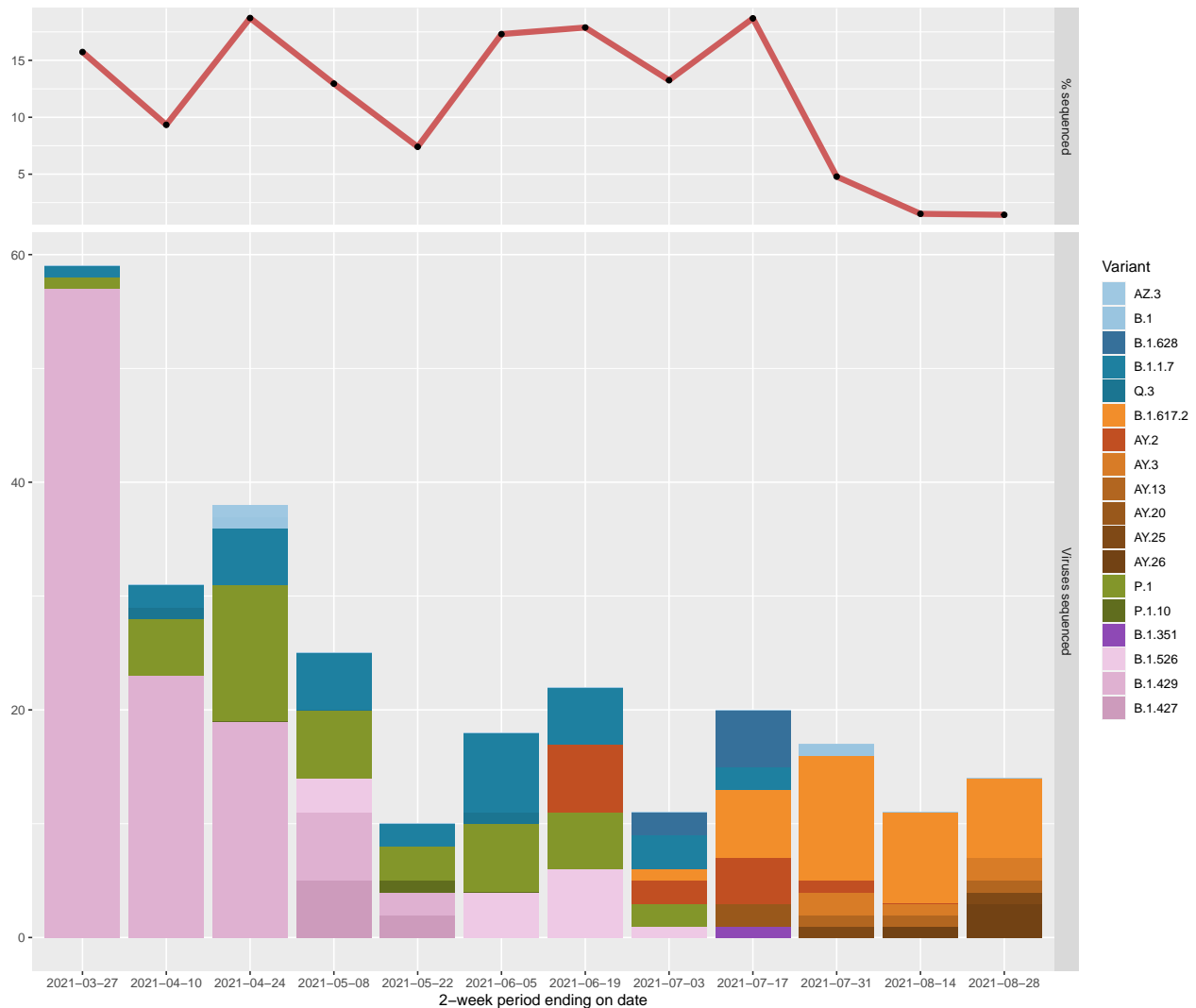
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			490		
	B.1.617.2	India	336	18 May 2021	23 Aug 2021
	AY.25	United States	54	21 Jun 2021	23 Aug 2021
	AY.3	United States	41	28 Jun 2021	14 Aug 2021
	AY.1	Europe	22	30 Jun 2021	23 Aug 2021
	AY.14	United States	13	29 Jun 2021	19 Aug 2021
	AY.13	United States	8	09 Jun 2021	04 Aug 2021
	AY.2	United States	7	12 Jun 2021	17 Jul 2021
	AY.20	United States/Mexico	5	15 Jul 2021	10 Aug 2021
	AY.12	Israel	1	Jul 2021	Jul 2021
	AY.26	United States/Mexico	1	Aug 2021	Aug 2021
	AY.3.1	United States	1	Aug 2021	Aug 2021
	AY.29	Japan	1	Aug 2021	Aug 2021
Alpha			436		
	B.1.1.7	United Kingdom	406	21 Jan 2021	02 Aug 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

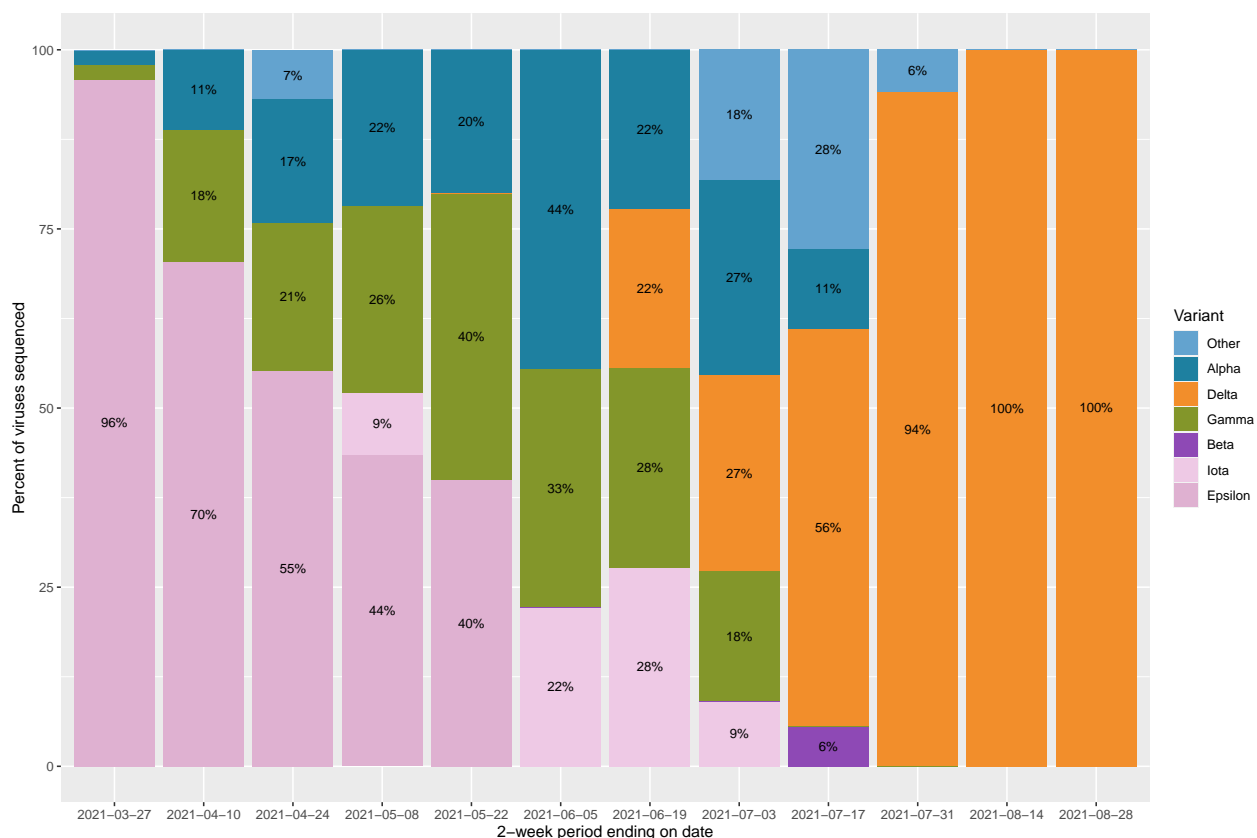
Total variants identified in Maui County



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

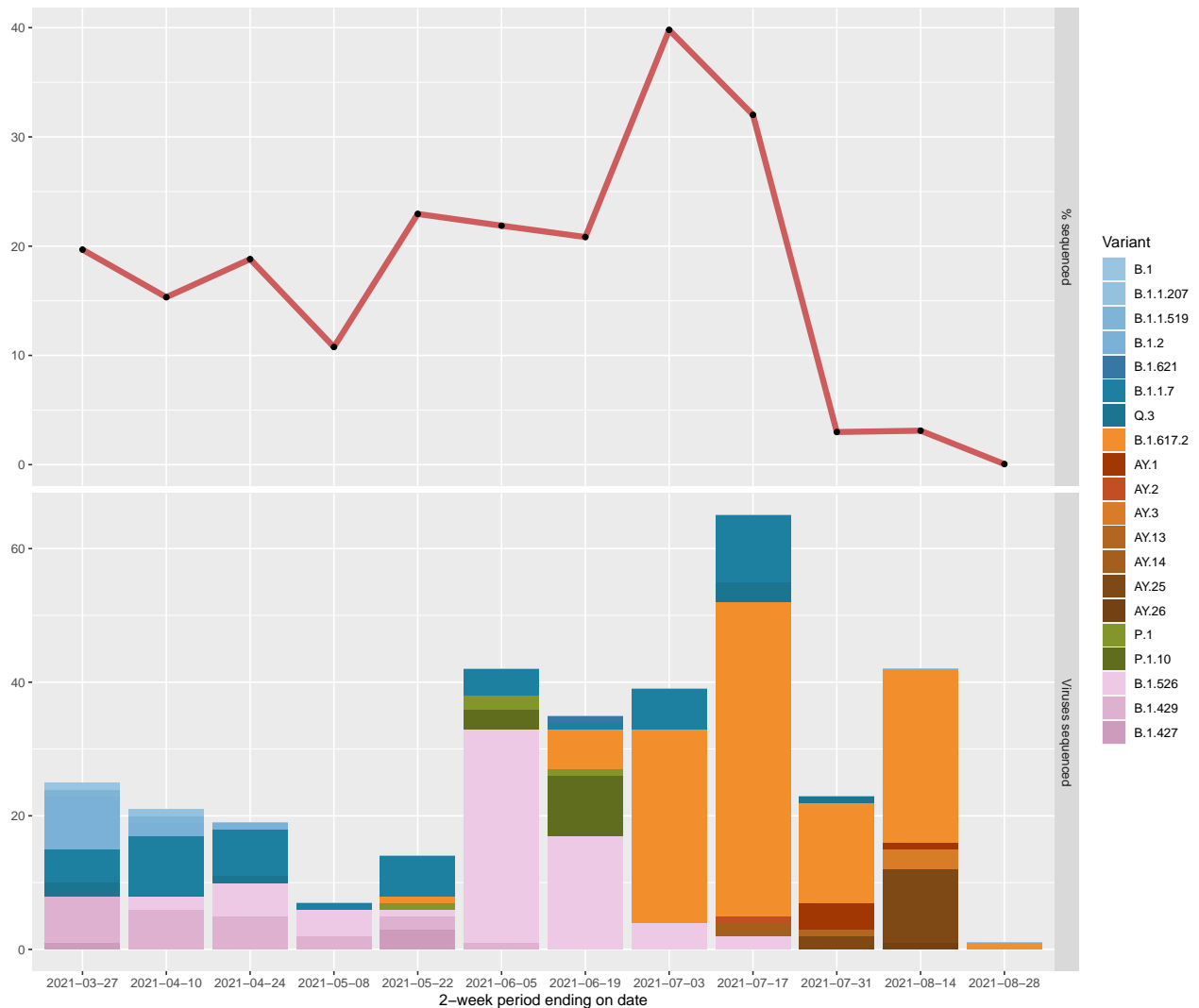
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			62		
	B.1.617.2	India	33	27 Jun 2021	26 Aug 2021
	AY.2	United States	13	07 Jun 2021	22 Jul 2021
	AY.3	United States	5	19 Jul 2021	23 Aug 2021
	AY.26	United States/Mexico	4	09 Aug 2021	21 Aug 2021
	AY.13	United States	3	Jul 2021	Aug 2021
	AY.20	United States/Mexico	2	Jul 2021	Jul 2021
	AY.25	United States	2	Jul 2021	Aug 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

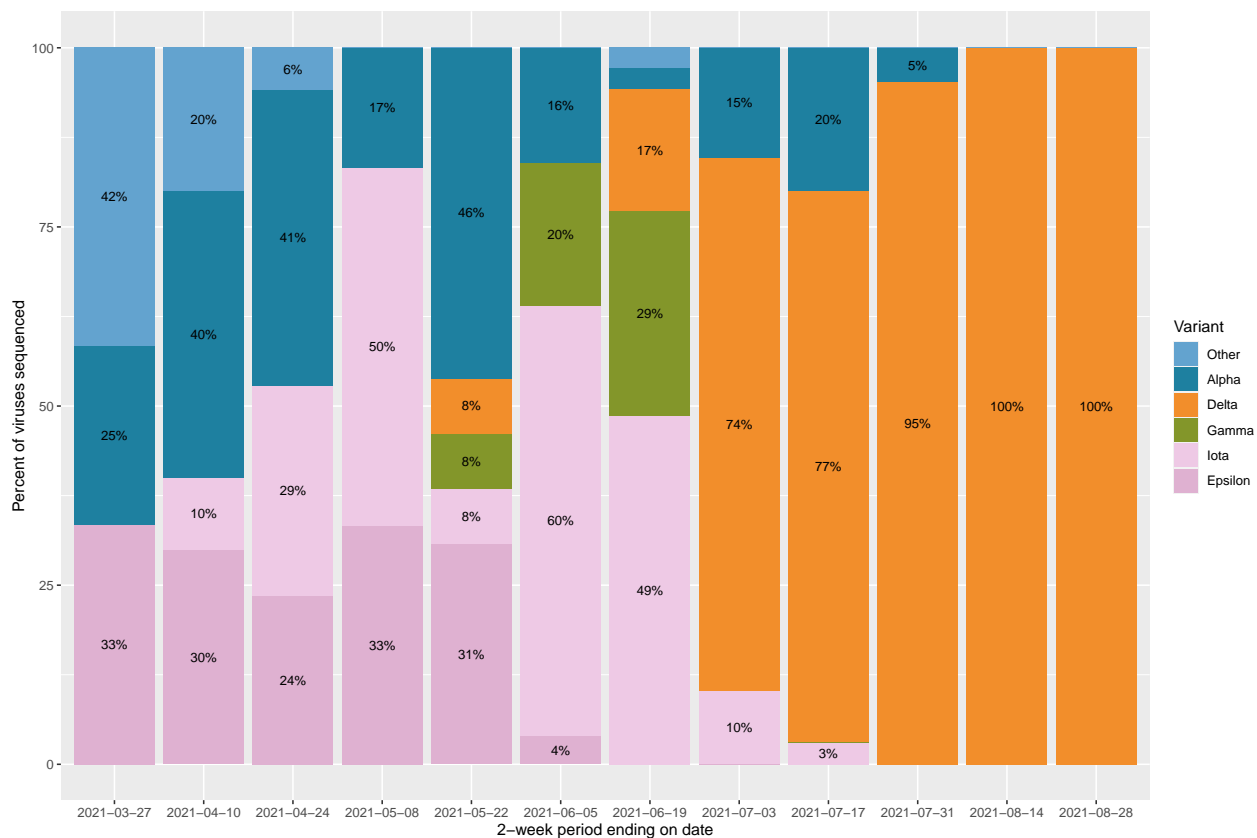
Total variants identified in Hawaii County



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

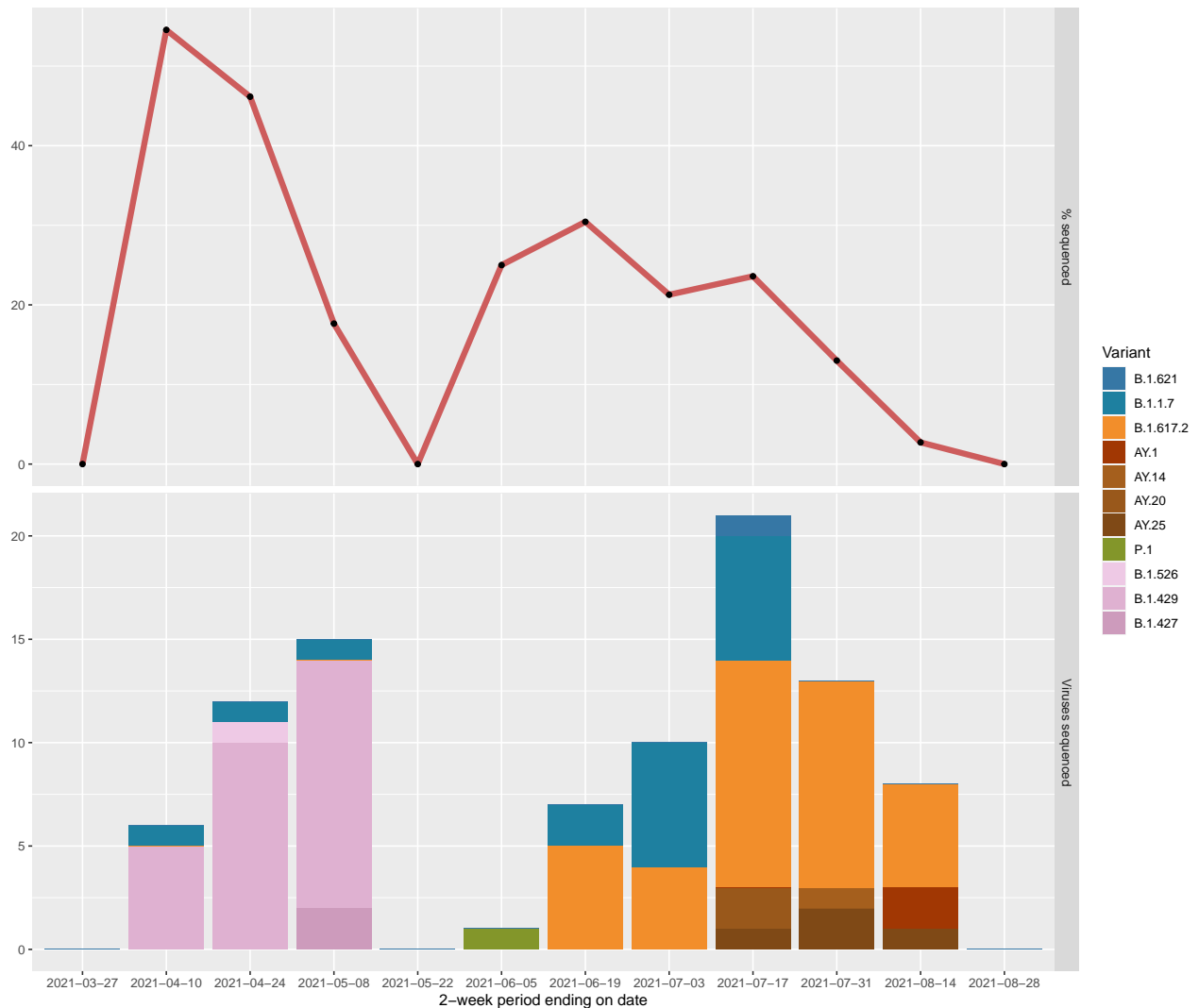
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			151		
	B.1.617.2	India	125	21 May 2021	17 Aug 2021
	AY.25	United States	13	19 Jul 2021	11 Aug 2021
	AY.1	Europe	5	20 Jul 2021	02 Aug 2021
	AY.3	United States	3	Aug 2021	Aug 2021
	AY.14	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
	AY.26	United States/Mexico	1	Aug 2021	Aug 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

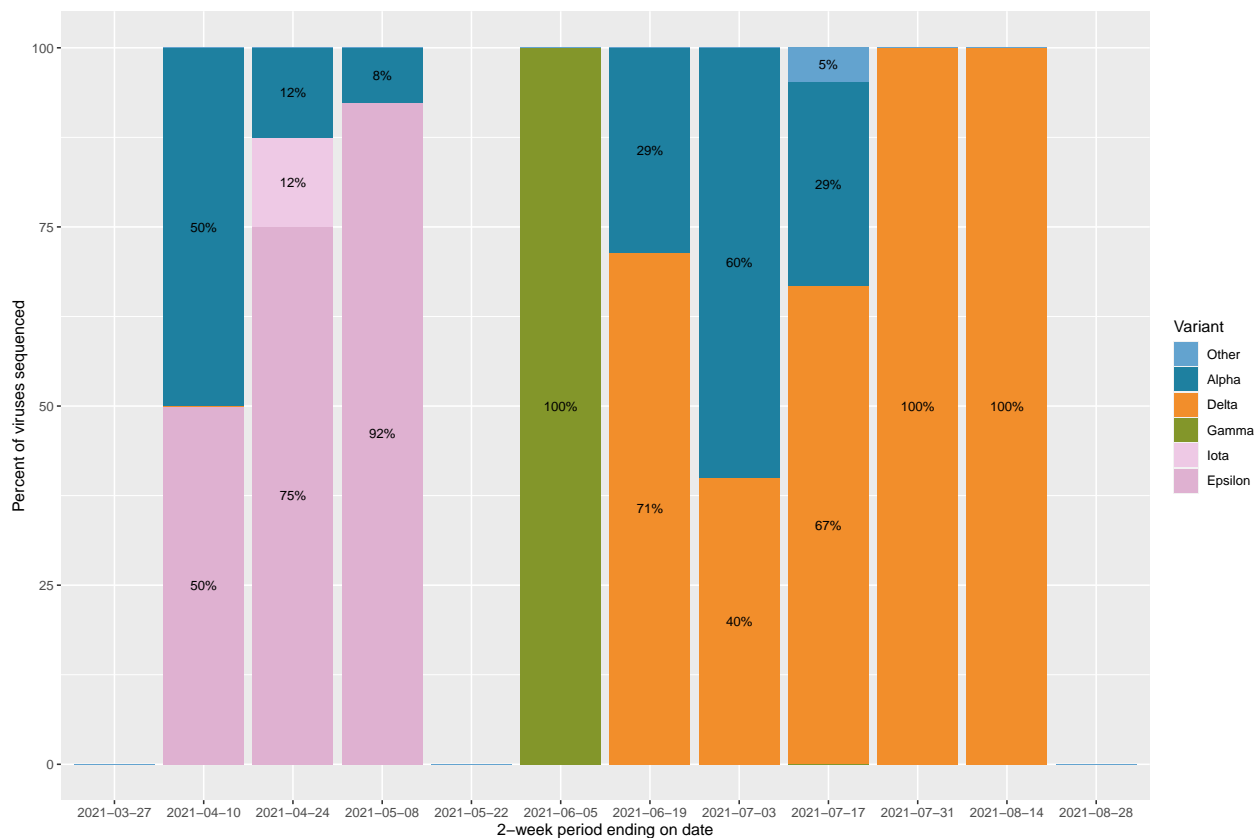
Total variants identified in Kauai County



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			44		
	B.1.617.2	India	35	06 Jun 2021	12 Aug 2021
	AY.25	United States	4	16 Jul 2021	09 Aug 2021
	AY.1	Europe	2	Aug 2021	Aug 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