

Hawaii sequencing and variants of SARS-Cov-2

Hawaii Department of Health

2021-10-27

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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 being monitored, 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 being monitored 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		4075	79.172%
Centers for Disease Control and Prevention	National SARS-CoV-2 Strain Surveillance (NS3)	228	4.430%
	Quest Diagnostics Incorporated	302	5.867%
	Laboratory Corporation of America	193	3.750%
	Aegis Sciences Corporation	85	1.651%
	Helix/Illumina	30	0.583%
	Infinity Biologix	15	0.291%
	Mako Medical	5	0.097%
	Fulgent Genetics	4	0.078%
Tripler Army Medical Center		210	4.080%
Total		5147	100.000%

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, 2021

Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
2403	575	644	177	276	4075

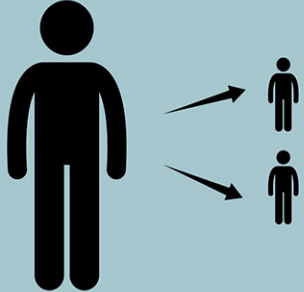
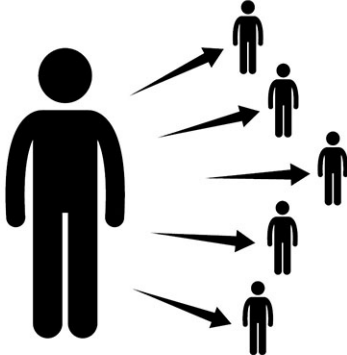
Notes:

- County information is currently unavailable for a number of samples that are sequenced by CDC and its commercial partners, as well as TAMC.


Short summary

- LPRB (Laboratory Preparedness and Response Division, State Laboratories Division, Hawaii Department of Health) has sequenced an additional 447 viral genomes since the last variant report was generated (10/13/2021).
- CDC and its commercial partners have sequenced an additional 39 viral genomes from Hawaii since the last variant report was generated (10/13/2021).
- Tripler Army Medical center has sequenced an additional 77 viral genomes from Hawaii since the last variant report was generated (10/13/2021).
- The vast majority of the genomes sequenced (>99%) belong to the Delta variant.
- In the last 2 weeks, several new Delta sublineages have been defined (AY.43, AY.44, AY.46.4, AY.47) by the Pango designation committee. Some of the Hawaii Delta samples have been re-classified into these sub-lineages. Their significance is the same as for all the other Delta sublineages.
- As a result of a decrease in the number of cases, a higher percentage of the positive samples have been sequenced (e.g. 14% for the week ending 10/09)

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 being monitored

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 being monitored 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 (VOC)

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>).

Variants being monitored (VBM)

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.

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).

Iota variant (B.1.526)

B.1.526 was first identified in New York and is classified by CDC as a variant being monitored, 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)

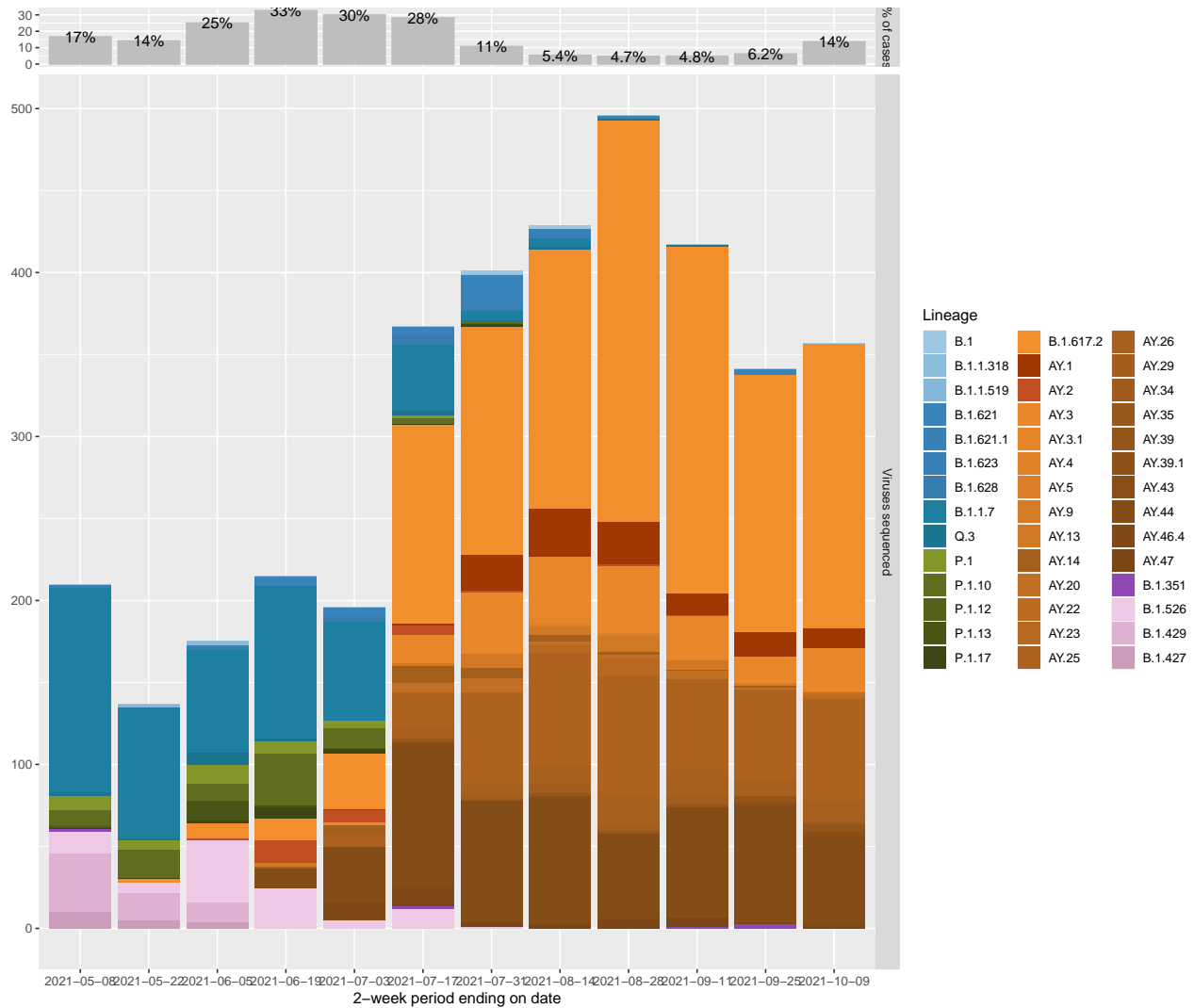
These closely related variants, B.1.429 and B.1.427, were first identified in California and designated initially as CA VUI1. WHO labeled them “Epsilon” on May 31, 2021. They can quickly spread from person-to-person, with an estimated ~20% higher efficiency than the original virus. CDC has deescalated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

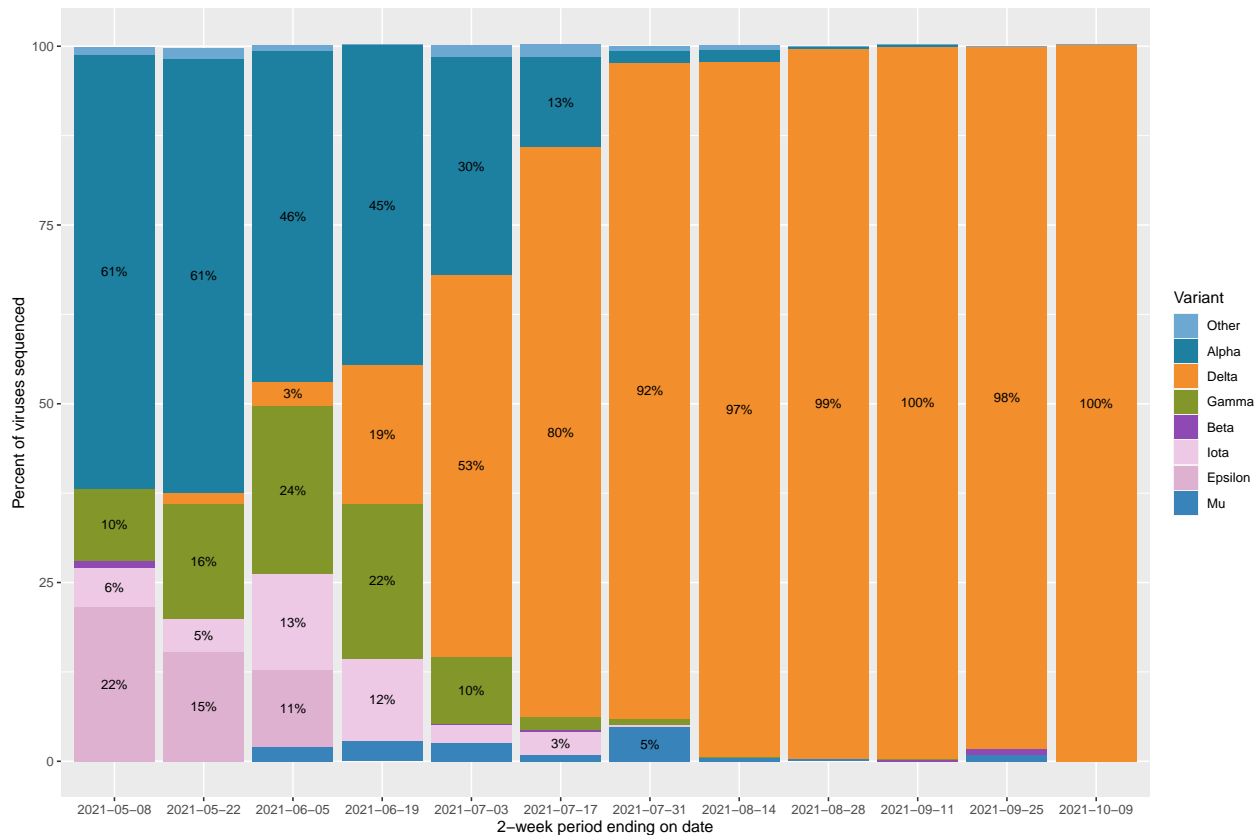
Total variants identified



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.*),
- Variants being monitored are shown as follows: dark blue = Alpha (lineages B.1.1.7 + Q.*), purple = Beta (lineage B.1.351), green = Gamma (lineages P.1 + P.1.*), pink = Epsilon (lineages B.1.429 and B.1.427) and Iota (lineage B.1.526)
- The gray bar 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

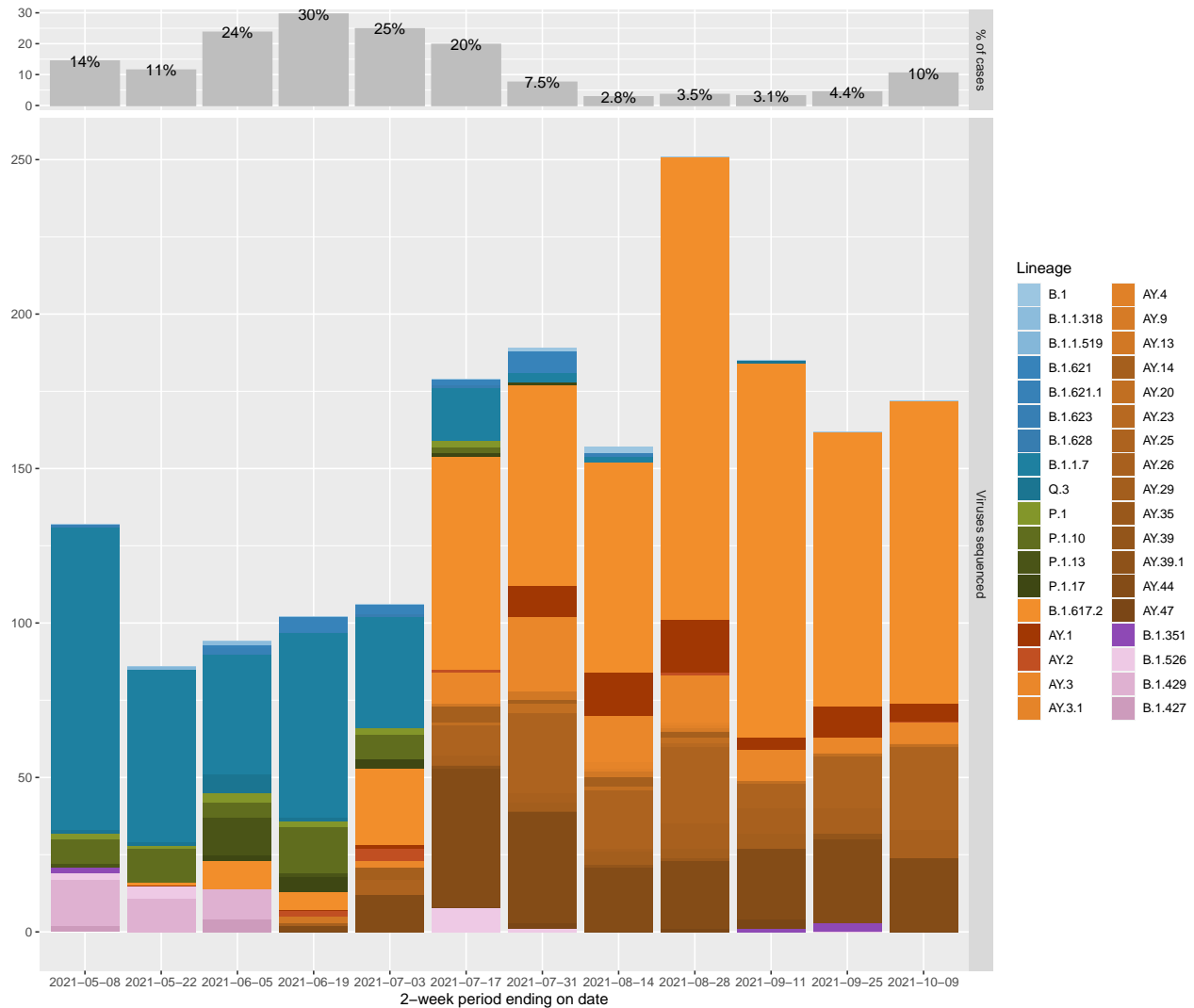
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			2837		
	B.1.617.2	India	1266	18 May 2021	11 Oct 2021
	AY.44	United States	531	07 Jun 2021	10 Oct 2021
	AY.25	United States	398	21 Jun 2021	13 Oct 2021
	AY.3	United States	202	28 Jun 2021	08 Oct 2021
	AY.1	Europe	119	30 Jun 2021	09 Oct 2021
	AY.26	United States/Mexico	82	07 Jun 2021	10 Oct 2021
	AY.13	United States	34	09 Jun 2021	12 Sep 2021
	AY.2	United States	30	01 Jun 2021	19 Aug 2021
	AY.14	United States	30	24 Jun 2021	22 Sep 2021
	AY.46.4	United States	28	21 Jun 2021	27 Sep 2021
	AY.20	United States/Mexico	27	10 Jul 2021	04 Oct 2021
	AY.29	Japan	18	23 Jul 2021	26 Sep 2021
	AY.47	United States	17	21 Jul 2021	01 Oct 2021
	AY.23	Singapore/Indonesia	16	11 Aug 2021	27 Aug 2021
	AY.39	United States	14	05 Aug 2021	04 Oct 2021
	AY.43	Europe	6	02 Aug 2021	04 Oct 2021
	AY.3.1	United States	5	01 Aug 2021	24 Aug 2021
	AY.35	United States	4	16 Jul 2021	27 Aug 2021
	AY.4	United Kingdom	3	Aug 2021	Sep 2021
	AY.5	United Kingdom	2	Aug 2021	Sep 2021
	AY.22	Portugal	2	Oct 2021	Oct 2021
	AY.39.1	Australia/United States	1	Jul 2021	Jul 2021
	AY.9	United Kingdom	1	Aug 2021	Aug 2021
	AY.34	United States	1	Oct 2021	Oct 2021

Variants being monitored in the State of Hawaii

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Alpha			753		
	B.1.1.7	United Kingdom	705	21 Jan 2021	14 Aug 2021
	Q.3	United States	48	21 Mar 2021	02 Sep 2021
Beta	B.1.351	South Africa	19	16 Feb 2021	22 Sep 2021
Gamma			185		
	P.1.10	United States	87	24 Apr 2021	21 Jul 2021
	P.1	Brazil	46	24 Mar 2021	11 Jul 2021
	P.1.12	Peru	20	21 Mar 2021	28 Apr 2021
	P.1.17	United States/Mexico	18	29 Mar 2021	21 Jul 2021
	P.1.13	United States	14	03 May 2021	07 Jun 2021
Epsilon			772		
	B.1.429	California	714	31 Dec 2020	03 Jun 2021
	B.1.427	California	58	07 Dec 2020	05 Jun 2021
Iota	B.1.526	New York	128	06 Feb 2021	23 Jul 2021
Mu			53		
	B.1.621	Columbia	43	03 Jun 2021	17 Sep 2021
	B.1.621.1	United States	10	27 May 2021	11 Aug 2021

Honolulu County

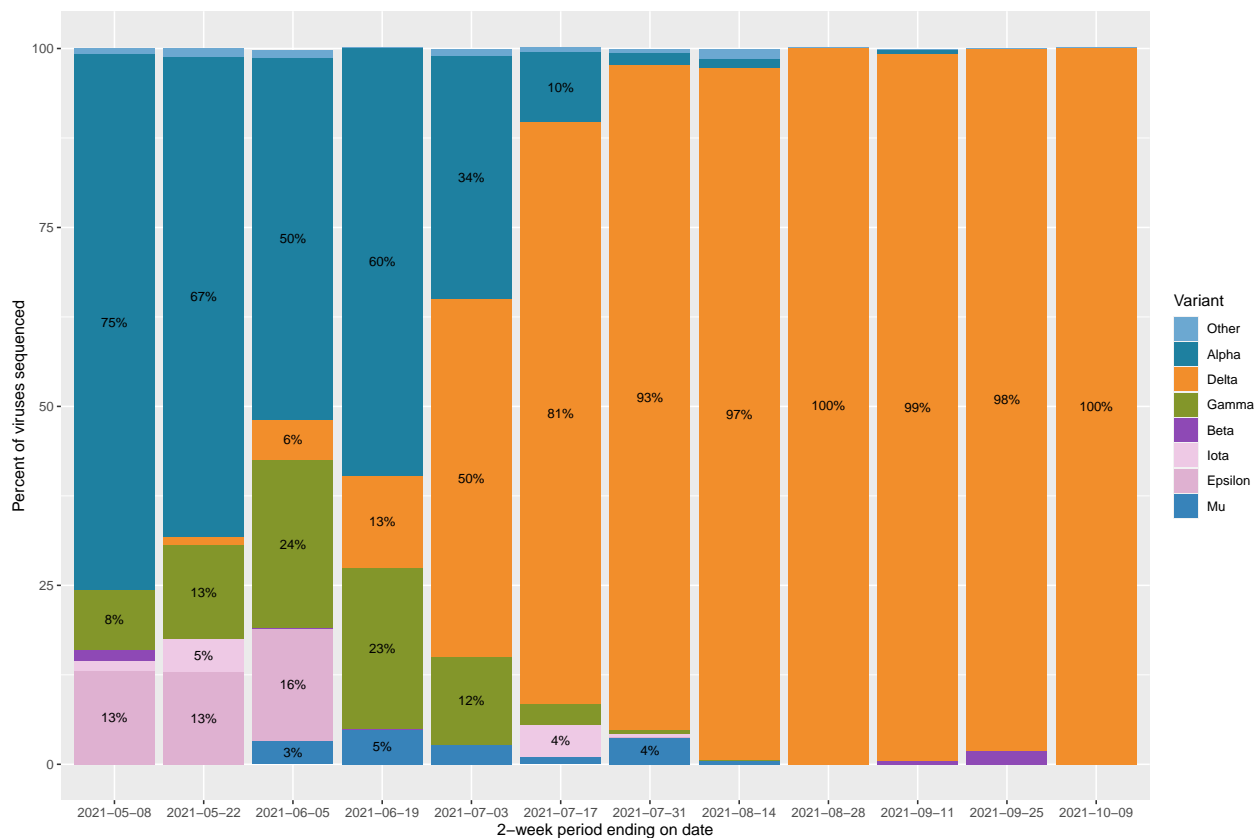
Total variants identified in Honolulu County



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.*),
- Variants being monitored are shown as follows: dark blue = Alpha (lineages B.1.1.7 + Q.*), purple = Beta (lineage B.1.351), green = Gamma (lineages P.1 + P.1.*), pink = Epsilon (lineages B.1.429 and B.1.427) and Iota (lineage B.1.526)
- 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

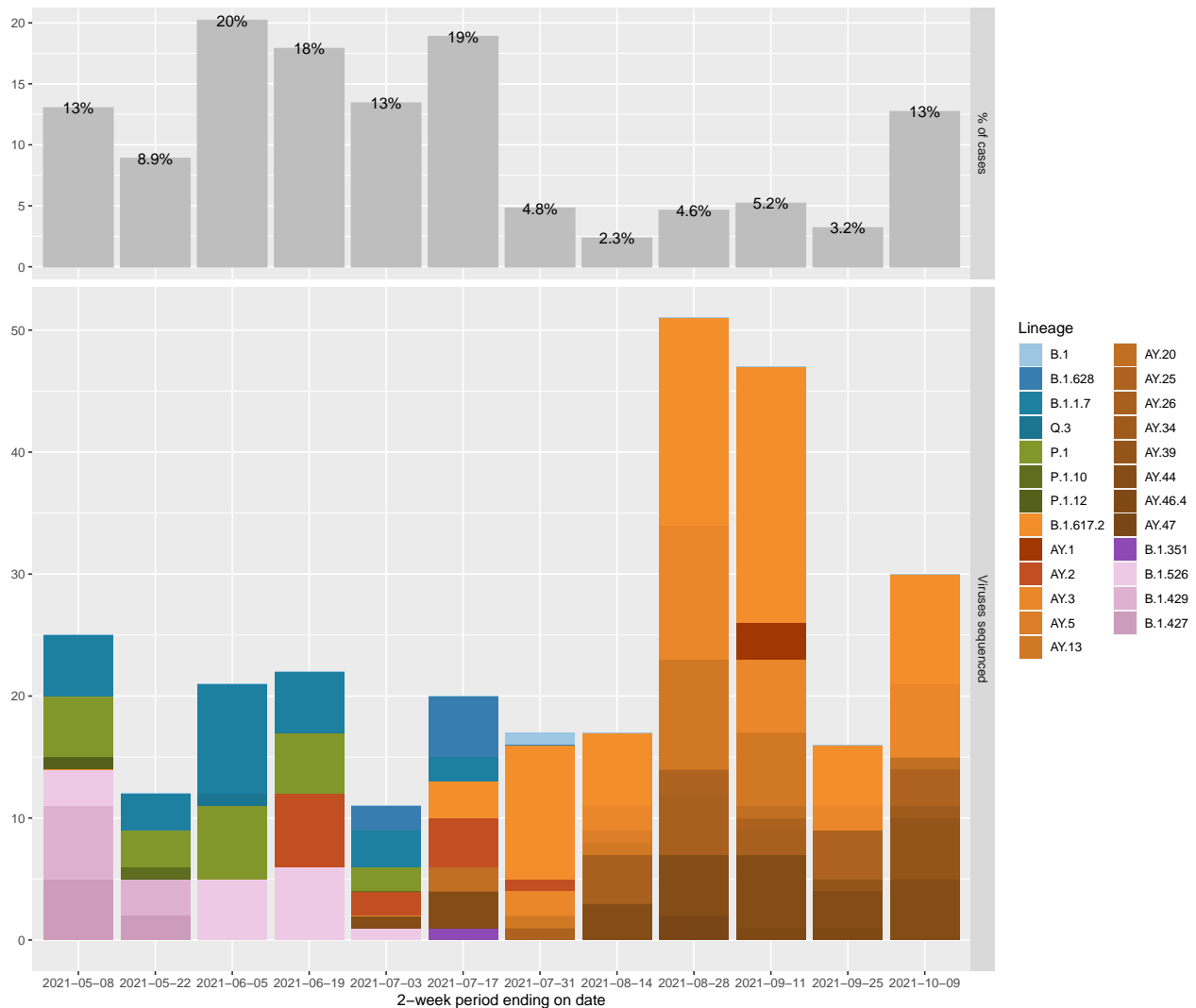
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			1320		
	B.1.617.2	India	701	18 May 2021	09 Oct 2021
	AY.44	United States	216	07 Jun 2021	10 Oct 2021
	AY.25	United States	137	21 Jun 2021	09 Oct 2021
	AY.3	United States	88	28 Jun 2021	07 Oct 2021
	AY.1	Europe	62	30 Jun 2021	09 Oct 2021
	AY.26	United States/Mexico	42	07 Jun 2021	10 Oct 2021
	AY.29	Japan	15	23 Jul 2021	08 Sep 2021
	AY.14	United States	15	29 Jun 2021	27 Aug 2021
	AY.20	United States/Mexico	10	15 Jul 2021	04 Oct 2021
	AY.2	United States	8	12 Jun 2021	19 Aug 2021
	AY.13	United States	8	09 Jun 2021	04 Aug 2021
	AY.47	United States	6	21 Jul 2021	04 Sep 2021
	AY.3.1	United States	3	Aug 2021	Aug 2021
	AY.39	United States	3	Aug 2021	Sep 2021
	AY.4	United Kingdom	2	Aug 2021	Aug 2021
	AY.23	Singapore/Indonesia	1	Aug 2021	Aug 2021
	AY.35	United States	1	Aug 2021	Aug 2021
	AY.39.1	Australia/United States	1	Jul 2021	Jul 2021
	AY.9	United Kingdom	1	Aug 2021	Aug 2021

Variants being monitored in Honolulu County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Alpha			477		
	B.1.1.7	United Kingdom	444	21 Jan 2021	14 Aug 2021
	Q.3	United States	33	03 Apr 2021	02 Sep 2021
Beta	B.1.351	South Africa	16	16 Feb 2021	22 Sep 2021
Gamma			94		
	P.1.10	United States	50	24 Apr 2021	13 Jul 2021
	P.1	Brazil	15	24 Mar 2021	11 Jul 2021
	P.1.13	United States	14	03 May 2021	07 Jun 2021
	P.1.17	United States/Mexico	14	29 Mar 2021	20 Jul 2021
	P.1.12	Peru	1	Apr 2021	Apr 2021
Epsilon			346		
	B.1.429	California	315	05 Jan 2021	29 May 2021
	B.1.427	California	31	07 Jan 2021	05 Jun 2021
Iota	B.1.526	New York	26	08 Feb 2021	23 Jul 2021
Mu			21		
	B.1.621	Columbia	18	03 Jun 2021	28 Jul 2021
	B.1.621.1	United States	3	May 2021	Aug 2021

Maui County

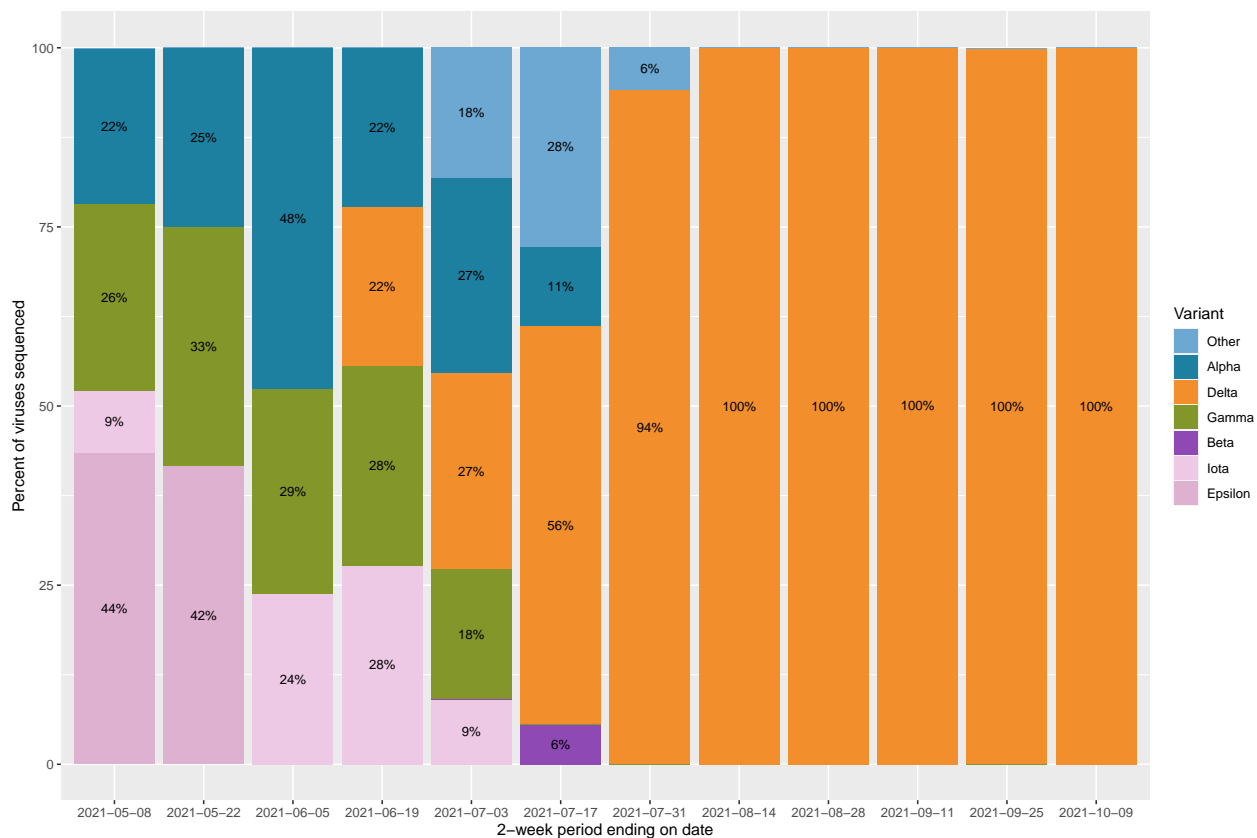
Total variants identified in Maui County



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.*),
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- SARS-CoV-2 genome sequencing may not be a random sample of all cases. This figure does not estimate the prevalence of the population.
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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.
- 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

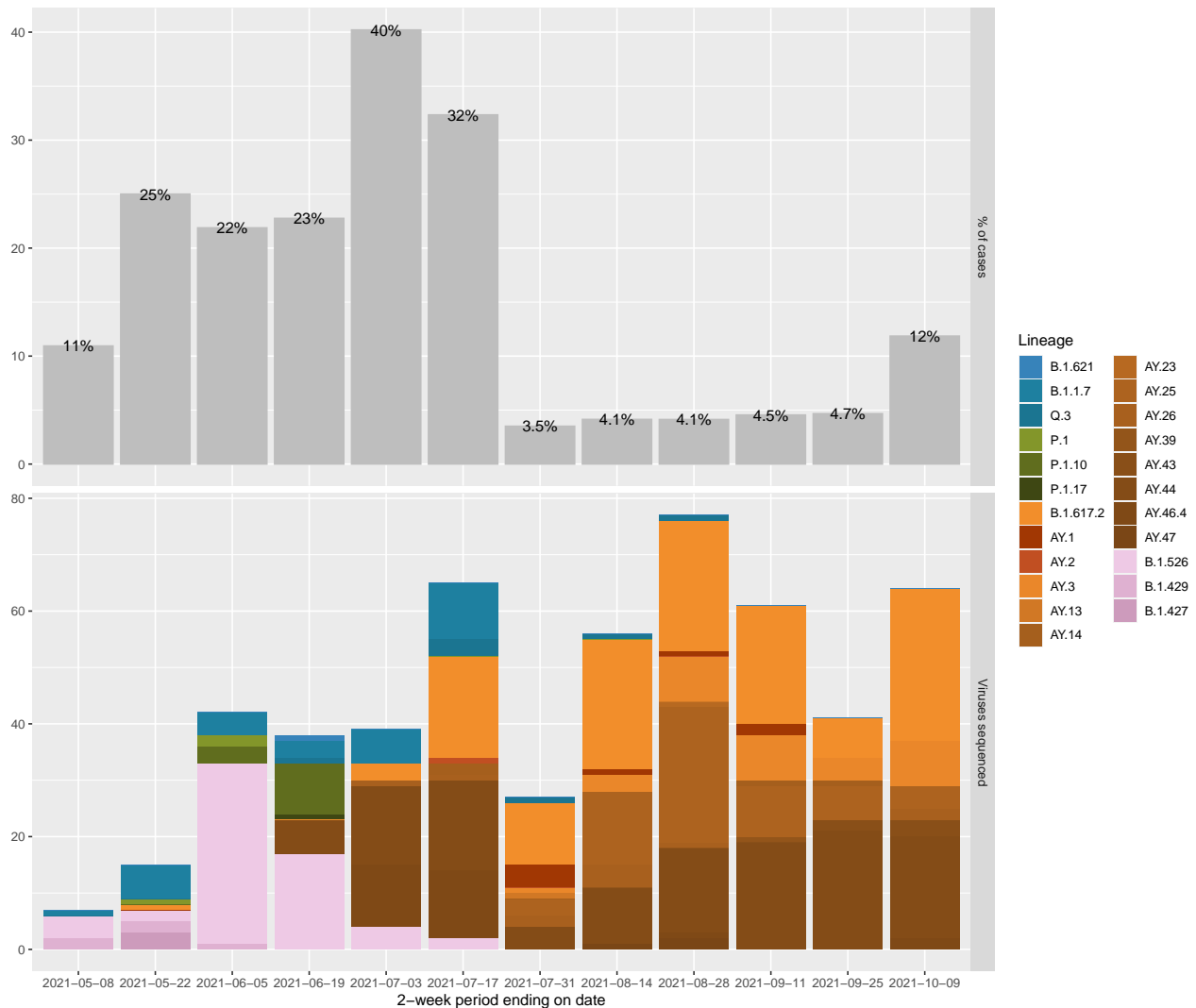
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			198		
	B.1.617.2	India	72	06 Jul 2021	08 Oct 2021
	AY.3	United States	29	19 Jul 2021	07 Oct 2021
	AY.44	United States	26	27 Jun 2021	04 Oct 2021
	AY.13	United States	17	21 Jul 2021	08 Sep 2021
	AY.2	United States	13	07 Jun 2021	22 Jul 2021
	AY.25	United States	11	24 Jul 2021	04 Oct 2021
	AY.26	United States/Mexico	11	03 Aug 2021	04 Sep 2021
	AY.39	United States	6	25 Sep 2021	04 Oct 2021
	AY.20	United States/Mexico	4	14 Jul 2021	30 Sep 2021
	AY.1	Europe	3	Aug 2021	Sep 2021
	AY.46.4	United States	2	Aug 2021	Sep 2021
	AY.47	United States	2	Aug 2021	Aug 2021
	AY.34	United States	1	Oct 2021	Oct 2021
	AY.5	United Kingdom	1	Aug 2021	Aug 2021

Variants being monitored in Maui County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Alpha			41		
	B.1.1.7	United Kingdom	39	01 Mar 2021	11 Jul 2021
	Q.3	United States	2	Apr 2021	May 2021
Beta	B.1.351	South Africa	1	Jul 2021	Jul 2021
Gamma			42		
	P.1	Brazil	22	18 Apr 2021	20 Jun 2021
	P.1.12	Peru	19	21 Mar 2021	28 Apr 2021
	P.1.10	United States	1	May 2021	May 2021
Epsilon			272		
	B.1.429	California	265	08 Jan 2021	18 May 2021
	B.1.427	California	7	27 Apr 2021	10 May 2021
Iota	B.1.526	New York	16	12 Mar 2021	25 Jun 2021

Hawaii County

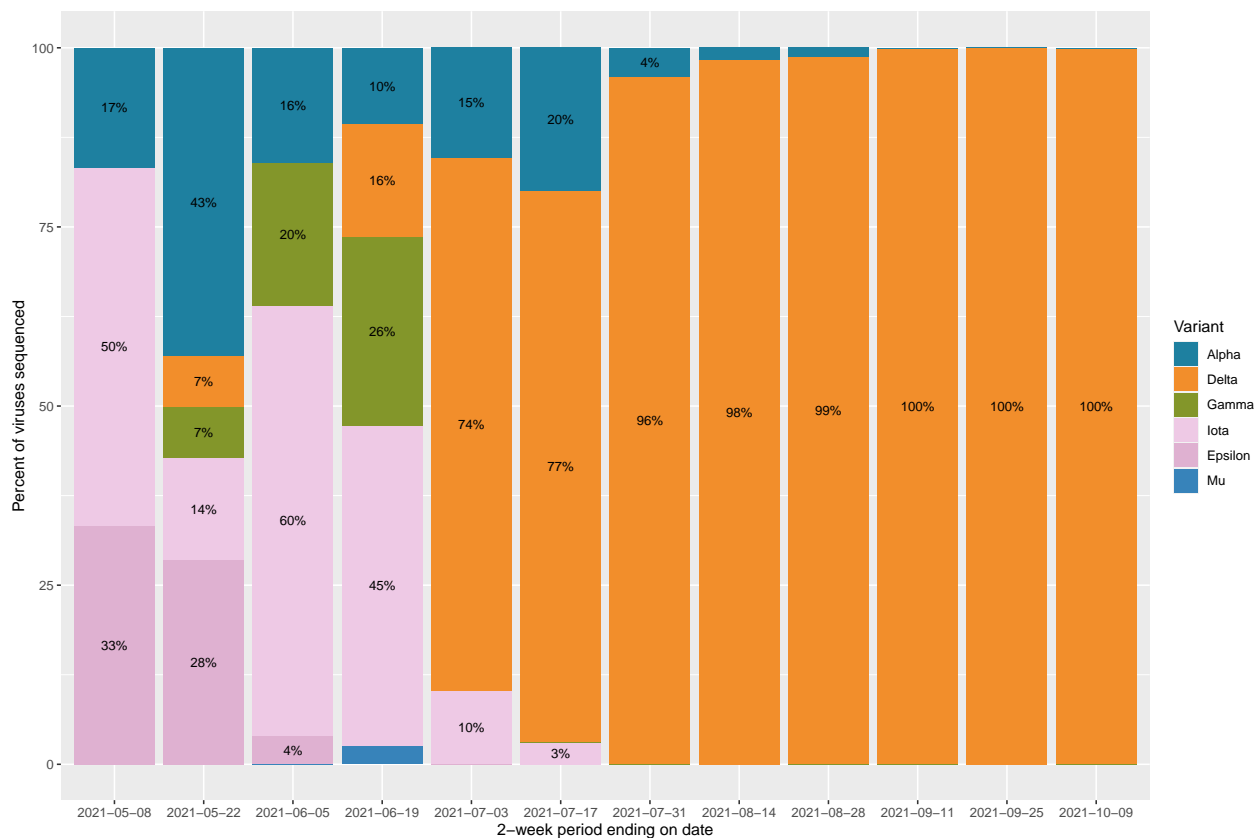
Total variants identified in Hawaii County



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

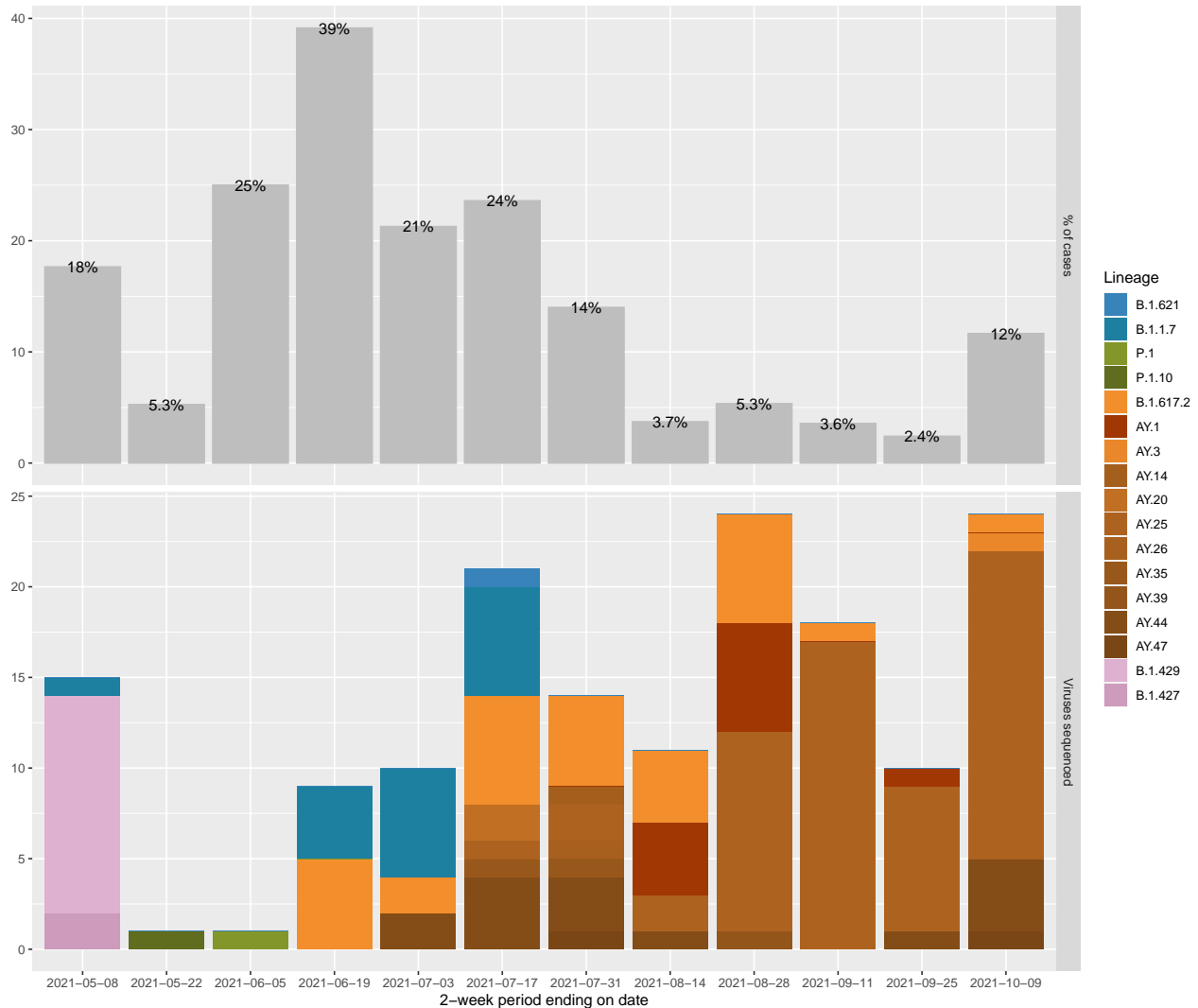
Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Delta			409		
	B.1.617.2	India	134	21 May 2021	08 Oct 2021
	AY.44	United States	123	11 Jun 2021	06 Oct 2021
	AY.25	United States	59	19 Jul 2021	06 Oct 2021
	AY.3	United States	32	31 Jul 2021	08 Oct 2021
	AY.46.4	United States	26	21 Jun 2021	27 Sep 2021
	AY.26	United States/Mexico	11	24 Jun 2021	29 Sep 2021
	AY.1	Europe	8	20 Jul 2021	03 Sep 2021
	AY.43	Europe	5	19 Sep 2021	04 Oct 2021
	AY.14	United States	4	12 Jul 2021	22 Sep 2021
	AY.47	United States	3	Aug 2021	Aug 2021
	AY.13	United States	1	Jul 2021	Jul 2021
	AY.2	United States	1	Jul 2021	Jul 2021
	AY.23	Singapore/Indonesia	1	Aug 2021	Aug 2021
	AY.39	United States	1	Aug 2021	Aug 2021

Variants being monitored in Hawaii County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Alpha			65		
	B.1.1.7	United Kingdom	55	22 Feb 2021	16 Jul 2021
	Q.3	United States	10	21 Mar 2021	20 Aug 2021
Gamma			16		
	P.1.10	United States	12	27 May 2021	13 Jun 2021
	P.1	Brazil	3	May 2021	Jun 2021
	P.1.17	United States/Mexico	1	Jun 2021	Jun 2021
Epsilon			43		
	B.1.429	California	37	25 Jan 2021	26 May 2021
	B.1.427	California	6	04 Feb 2021	17 May 2021
Iota	B.1.526	New York	73	06 Feb 2021	07 Jul 2021
Mu	B.1.621	Columbia	1	Jun 2021	Jun 2021

Kauai County

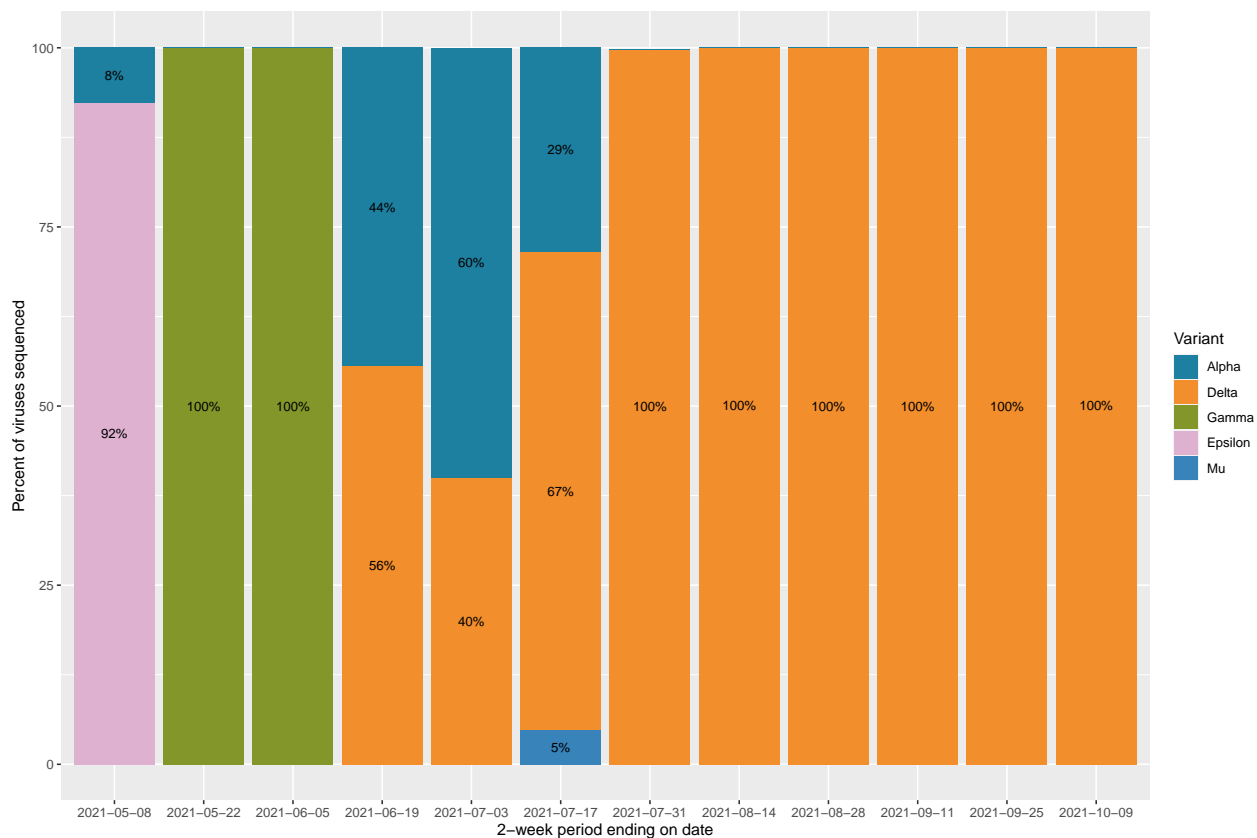
Total variants identified in Kauai County



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.*),
- Variants being monitored are shown as follows: dark blue = Alpha (lineages B.1.1.7 + Q.*), purple = Beta (lineage B.1.351), green = Gamma (lineages P.1 + P.1.*), pink = Epsilon (lineages B.1.429 and B.1.427) and Iota (lineage B.1.526)
- 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			124		
	AY.25	United States	58	16 Jul 2021	04 Oct 2021
	B.1.617.2	India	30	06 Jun 2021	04 Oct 2021
	AY.44	United States	15	01 Jul 2021	04 Oct 2021
	AY.1	Europe	11	09 Aug 2021	21 Sep 2021
	AY.20	United States/Mexico	2	Jul 2021	Jul 2021
	AY.35	United States	2	Jul 2021	Jul 2021
	AY.47	United States	2	Jul 2021	Oct 2021
	AY.14	United States	1	Jul 2021	Jul 2021
	AY.26	United States/Mexico	1	Jul 2021	Jul 2021
	AY.3	United States	1	Sep 2021	Sep 2021
	AY.39	United States	1	Aug 2021	Aug 2021

Variants being monitored in Kauai County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Alpha	B.1.1.7	United Kingdom	19	05 Apr 2021	13 Jul 2021
Gamma			2		
	P.1	Brazil	1	May 2021	May 2021
	P.1.10	United States	1	May 2021	May 2021
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
Mu	B.1.621	Columbia	1	Jul 2021	Jul 2021