State of Hawaii SARS-CoV-2 Sequencing and Variant Report

Hawaii Department of Health

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Introduction

Whole genome sequencing (WGS) involves a set of laboratory methods used to determine the full genome sequence of an organism or virus, which in the case of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the virus that causes Coronavirus Disease 2019 (COVID-19), is approximately 30,000 letters, each letter being one of A, C, G, or T.

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

Collecting the genome sequences of virus specimens can 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 also 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 the Centers for Disease Control and Prevention (CDC) as variants of concern and others as variants being monitored, because of their attributes, which, for example, can be increased transmissibility, decreased neutralization by antibodies generated during previous infection or vaccination, and/or increased severity of disease. The CDC has extensive information about SARS-CoV-2 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. Therefore, this report is limited to confirmed PCR-positives 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. Therefore, 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 5% of positive specimens since testing began, according to the CDC (https://covid.cdc.gov/covid-data-tracker/#published-sars-cov-2-sequences).

In February 2021, State Laboratories Division, Hawaii Department of Health increased sequencing efforts done on positive samples to improve the State's ability to detect new variants of concern and variants being monitored.

Acknowledgements

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

Institution	Program/partner	Count	Percent
Laboratory Preparedness and Response Branch, State Laboratories Division		7208	76.130%
Centers for Disease Control and Prevention	National SARS-CoV-2 Strain Surveillance (NS3)	312	3.295%
	Quest Diagnostics Incorporated	568	5.999%
	Laboratory Corporation of America	486	5.133%
	Aegis Sciences Corporation	330	3.485%
	Helix/Illumina	87	0.919%
	Infinity Biologix	16	0.169%
	Mako Medical	15	0.158%
	Fulgent Genetics	7	0.074%
Tripler Army Medical Center		439	4.637%
Total		**9468**	**100.000%**

Table Notes:

- The samples sequenced by the CDC for the National SARS-CoV-2 Strain Surveillance (NS3) program are collected, quality controlled, and shipped to the CDC by the Laboratory Preparedness and Response Branch (LPRB), State Laboratories Division, Hawaii Department of Health.

County distribution of genomes sequenced by State Laboratories Division since Jan 1st, 2021

Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
4258	1084	1172	360	334	7208

Table Notes:

- County information is unavailable or "unknown" for a number of samples sequenced by State Laboratories Division. Furthermore, county information is not provided for samples sequenced by the CDC and its commercial partners, and by Tripler Army Medical Center (TAMC).

Summary and key notes

- State Laboratories Division has reported 399 additional sequenced SARS-CoV-2 genomes since the previous report was generated (2/15/2022).
- The CDC and its commercial partners have reported 298 additional sequenced SARS-CoV-2 genomes from the State of Hawaii since the previous report was generated (2/15/2022).
- TAMC has reported 100 additional sequenced SARS-CoV-2 genomes from the State of Hawaii since the previous report was generated (2/15/2022).
- SARS-CoV-2 variant nomenclature is defined by a World Health Organization (WHO) label (letters of the Greek Alphabet, i.e., Alpha, Beta, Gamma, Delta, etc.), Pango lineage (alphabetical prefix and a numerical suffix), and/or Nextstrain clade (year of emergence followed by a letter ordered alphabetically by emergence, i.e., 20A, 20B, etc.). In this report, variant counts are reported using the WHO label and Pango lineage (or "Lineage") nomenclatures only.
- Classifications of Delta lineages are in flux. So far, there have been over 235 sub-lineages of Delta classified, 60 of which have been detected in the State of Hawaii. Sub-lineages of Delta have the AY.* designation. For simplicity, not all AY.* sub-lineages detected in the State of Hawaii or its counties are listed in the Tables on the following pages, and instead are included as "Other AY.*" under Lineage.
- Classifications of Omicron lineages are in flux. So far, there have been 20 sub-lineages of Omicron classified. Sub-lineages of Omicron have the BA.* designation. BA.1, BA.1.1, and BA.2 are the Omicron sub-lineages currently circulating in the State of Hawaii.

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 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) that have been detected in the State of Hawaii

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

B.1.617.2 was first identified in India and the WHO labeled it "Delta" on May 31, 2021. This variant contains the L452R mutation in the spike protein, which has been shown to escape neutralization by monoclonal antibodies and some convalescent sera, as well as 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. The Delta variant is also known as Nextstrain clades 21A, 21I, and 21J. For more information about Delta, go to (https://www.cdc.gov/coronavirus/2019-ncov/variants/delta-variant.html).

Omicron variant (B.1.1.529 and BA.* sub-lineages)

B.1.1.529 was reported to the WHO on November 24, 2021 and first detected in specimens collected on November 11, 2021 in Botswana and on November 14, 2021 in South Africa. The WHO named B.1.1.529 "Omicron" and classified it as a VOC on November 26, 2021. The United States designated Omicron as a VOC on November 30, 2021 and reported its first case on December 1, 2021. Omicron contains more changes in the spike protein than have been observed in other variants, including at least 30 amino acid substitutions (15 of these are in the receptor binding domain), three small deletions, and one small insertion. Several of these mutations, including S477N, N501Y, and E484K, have been associated with increased infectivity and decreased neutralizing activity of monoclonal antibodies and convalescent sera. Evidence indicates that Omicron spreads more easily than the original SARS-CoV-2 virus and the Delta variant, but generally causes less severe disease than infection with previous variants. The Omicron variant is also known as Nextstrain clades 21M, 21K, and 21L. For more information about Omicron, go to (https://www.cdc.gov/coronavirus/2019-ncov/variants/omicron-variant.html).

Variants being monitored (VBM) that have been detected in the State of Hawaii

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

B.1.1.7 was first identified in the United Kingdom and the WHO labeled it "Alpha" on May 31, 2021. This variant contains the N501Y mutation and a short deletion in the spike protein. This variant is concerning because it has been shown to be significantly more transmissible (~50%) than the original SARS-CoV-2 lineages and reports 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. The Alpha variant is also known as Nextstrain clade 20I.

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

P.1 was first identified in Brazil and the 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. The Gamma variant is also known as Nextstrain clade 20J.

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

B.1.351 was first identified in South Africa and the 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 due to presence of the E484K mutation in the spike protein. The Beta variant is also known as Nextstrain clade 20H.

Mu variant (B.1.621 and B.1.621.1)

Lineage B.1.621 was first identified in Columbia in January 2021 and it has a couple of mutations in common with the Beta (B.1.351) and Gamma (P.1) variants, which have been associated with high transmissibility (N501Y) and a level of decreased vaccine efficiency (E484K). The MU variant is also known as Nextstrain clade 21H.

Iota variant (B.1.526)

B.1.526 was first identified in New York and is classified by CDC as a VBM because of indications that it has increased transmissibility. The WHO labeled it "Iota" on May 31, 2021. Some of the samples (but not all) of this variant contain the E484K mutation. The Iota variant is also known as Nextstrain clade 21F.

Epsilon variant (B.1.429 and B.1.427)

The closely related lineages, B.1.429 and B.1.427, were first identified in California and designated initially as CA VUI1. The 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. The CDC has deescalated Epsilon from a VOC to VBM on June 29, 2021, due to the significant decrease in the proportion of B.1.429/B.1.427 lineage viruses circulating nationally, as well as the available data indicating that vaccines and treatments are effective against this variant. CDC removed B.1.429 and B.1.427 from the VBM list in July 2021 due to declining prevalence. The Epsilon variant is also known as Nextstrain clade 21C.

State of Hawaii

Total variants identified

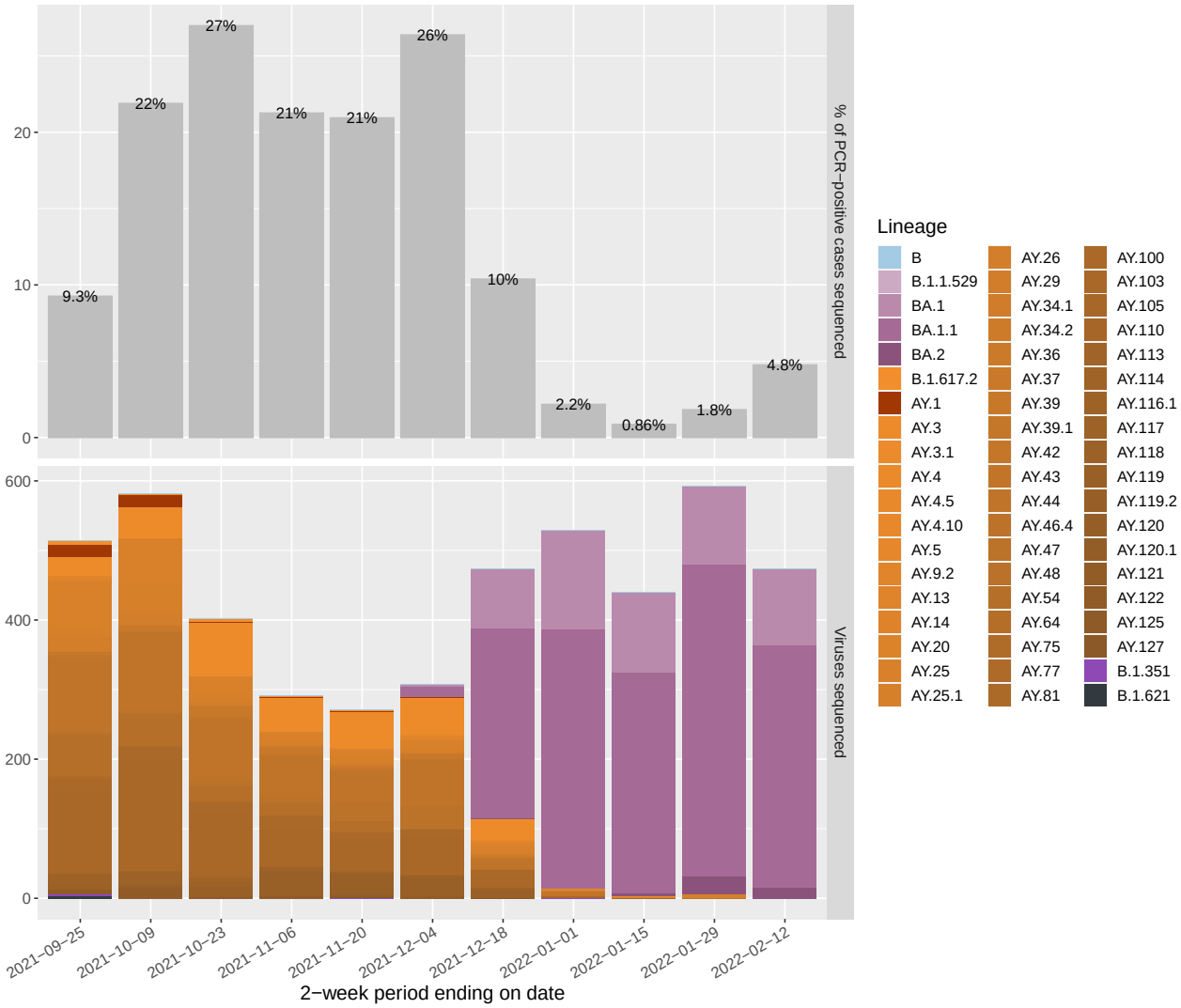

Figure Notes:

- The 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 shown are Delta (lineages B.1.617.2 + AY.*) and Omicron (lineages B.1.1.529 + BA.*).
- Variants being monitored shown are Beta (lineage B.1.351) and Mu (lineages B.1.621 + B.1.621.1).
- The gray bar graph (top) shows the percentage of PCR-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 graph does not estimate prevalence in the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.

Estimated proportions of variants circulating in the State of Hawaii

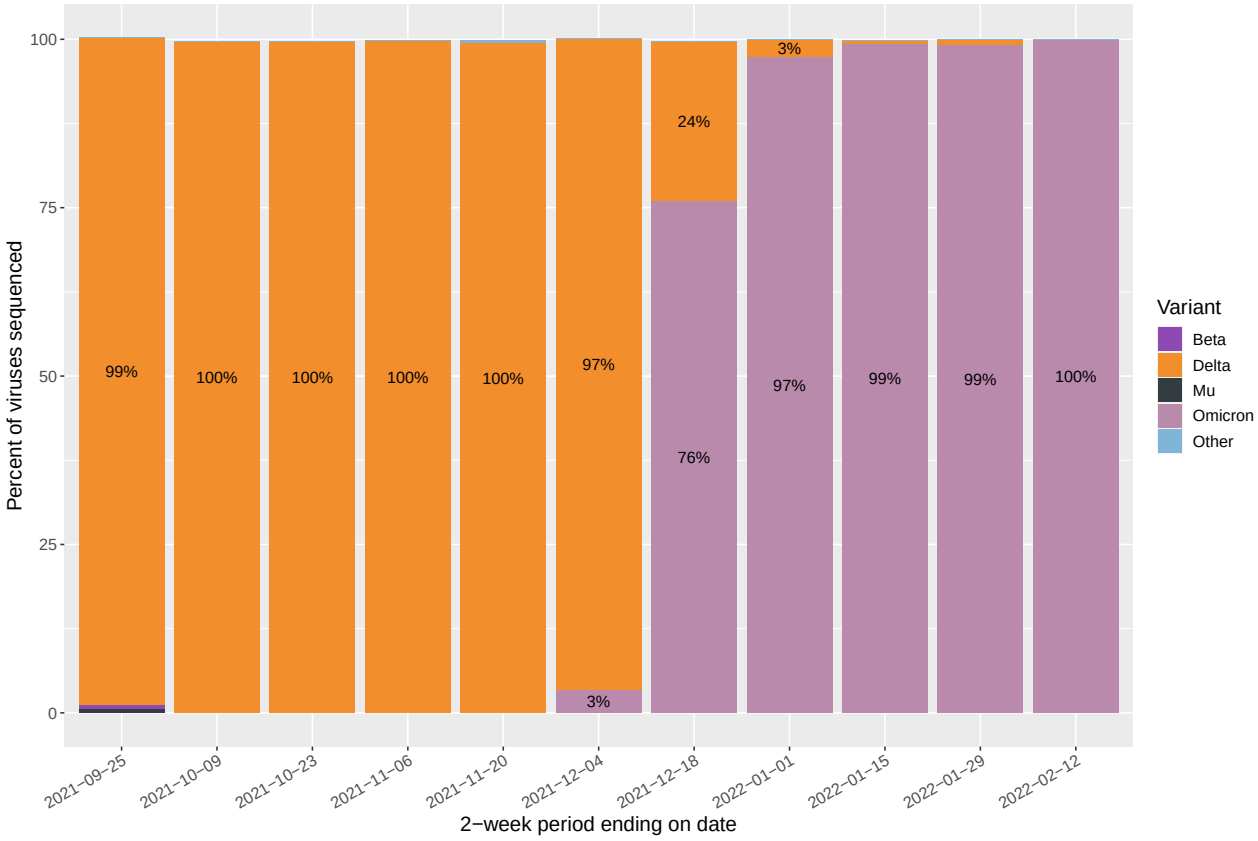

Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in the State of Hawaii, grouped in two-week intervals (based on the date of sample collection).
- Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases in the State of Hawaii. This graph 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. Therefore, 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			4751		
	AY.103	United States	1017	21 May 2021	12 Jan 2022
	AY.44	United States	922	07 Jun 2021	19 Jan 2022
	AY.3	United States	487	28 Jun 2021	02 Jan 2022
	AY.25	United States	422	21 Jun 2021	20 Jan 2022
	AY.54	United States	339	28 May 2021	21 Nov 2021
	Other AY.*	Various	199	01 Aug 2021	Sep 2021
	AY.100	South Africa/Botswana	169	17 Jul 2021	12 Dec 2021
	AY.25.1	South Africa/Botswana	158	08 Jul 2021	27 Jan 2022
	AY.1	Europe	136	30 Jun 2021	30 Nov 2021
	AY.119	United States	133	06 Jul 2021	18 Dec 2021
	AY.26	United States/Mexico	116	07 Jun 2021	28 Dec 2021
	AY.117	United States	97	15 Jul 2021	17 Dec 2021
	AY.47	United States	94	21 Jul 2021	07 Dec 2021
	AY.122	South Africa/Botswana	74	09 Jul 2021	26 Nov 2021
	AY.39	United States	56	05 Aug 2021	15 Dec 2021
	AY.118	United States	55	08 Jul 2021	17 Dec 2021
	B.1.617.2	India	53	04 Jun 2021	16 Dec 2021
	AY.13	United States	38	09 Jun 2021	16 Sep 2021
	AY.20	United States/Mexico	37	10 Jul 2021	12 Dec 2021
	AY.46.4	United States	35	21 Jun 2021	06 Dec 2021
	AY.14	United States	33	24 Jun 2021	17 Nov 2021
	AY.2	United States	31	01 Jun 2021	19 Aug 2021
	AY.75	United States/Europe	30	09 Jul 2021	04 Nov 2021
	AY.29	Japan	20	23 Jul 2021	26 Sep 2021
Omicron			2457		
	BA.1.1	South Africa/Botswana	1825	27 Nov 2021	19 Feb 2022
	BA.1	South Africa/Botswana	577	30 Nov 2021	18 Feb 2022
	BA.2	South Africa/Botswana	54	06 Jan 2022	17 Feb 2022
	B.1.1.529	South Africa/Botswana	1	Jan 2022	Jan 2022

Table Notes:

- Lineage "Other AY.*" represents an aggregate of different AY.* sub-lineages, each with less than 20 sequenced genomes, from the State of Hawaii.

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			754		
	B.1.1.7	United Kingdom	703	21 Jan 2021	14 Aug 2021
	Q.3	United States	49	21 Mar 2021	02 Sep 2021
	Q.4	South Africa/Botswana	2	Apr 2021	Apr 2021
Beta	B.1.351	South Africa	19	16 Feb 2021	22 Sep 2021
Gamma			185		
	P.1.10	United States	81	24 Apr 2021	14 Jul 2021
	P.1	Brazil	52	24 Mar 2021	21 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			774		
	B.1.429	California	715	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
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

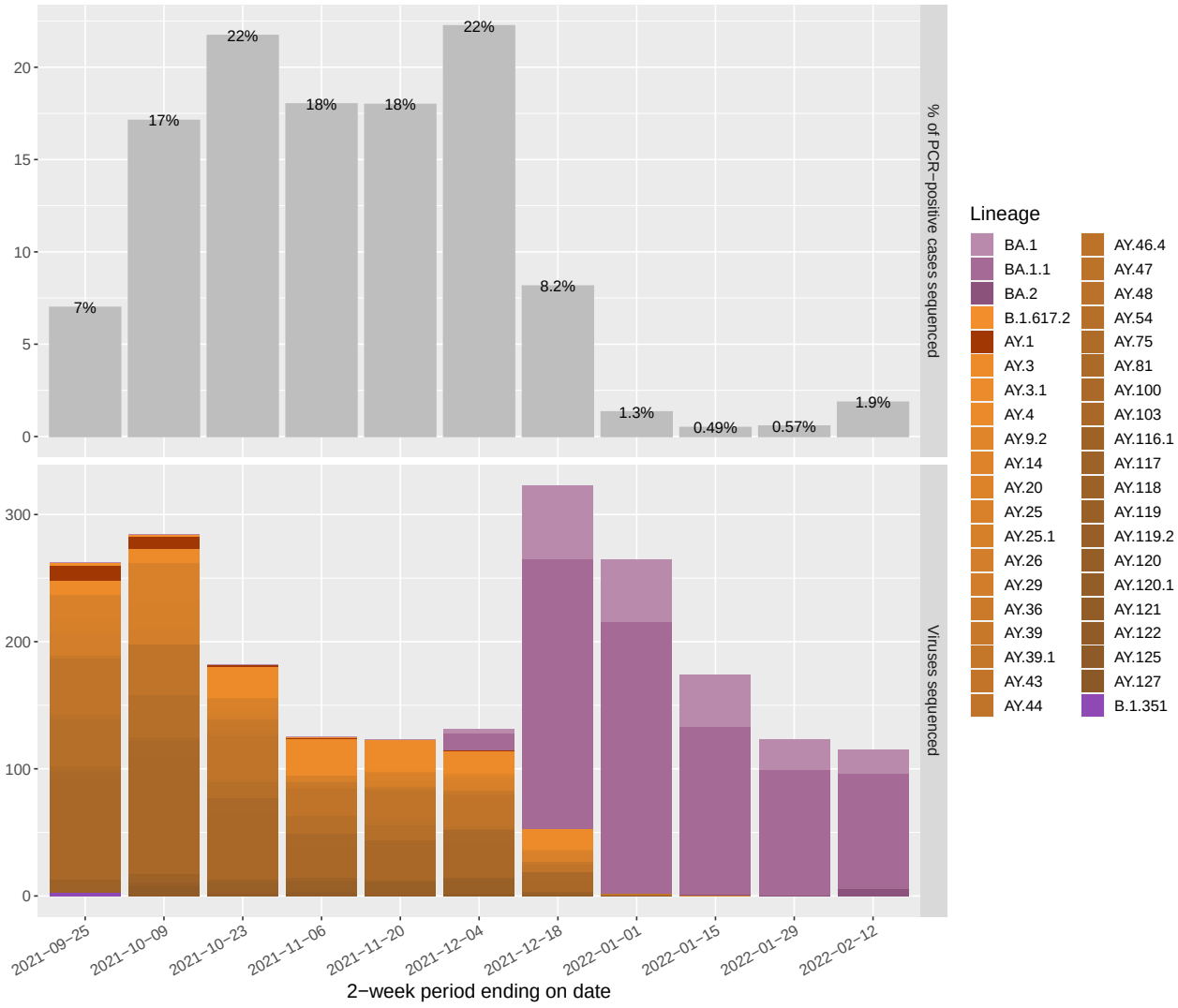

Figure Notes:

- The 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 shown are Delta (lineages B.1.617.2 + AY.*) and Omicron (lineages B.1.1.529 + BA.*).
- Variants being monitored shown is Beta (lineage B.1.351).
- The gray bar graph (top) shows the percentage of PCR-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 graph does not estimate prevalence in the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.

Estimated proportions of variants circulating in Honolulu County

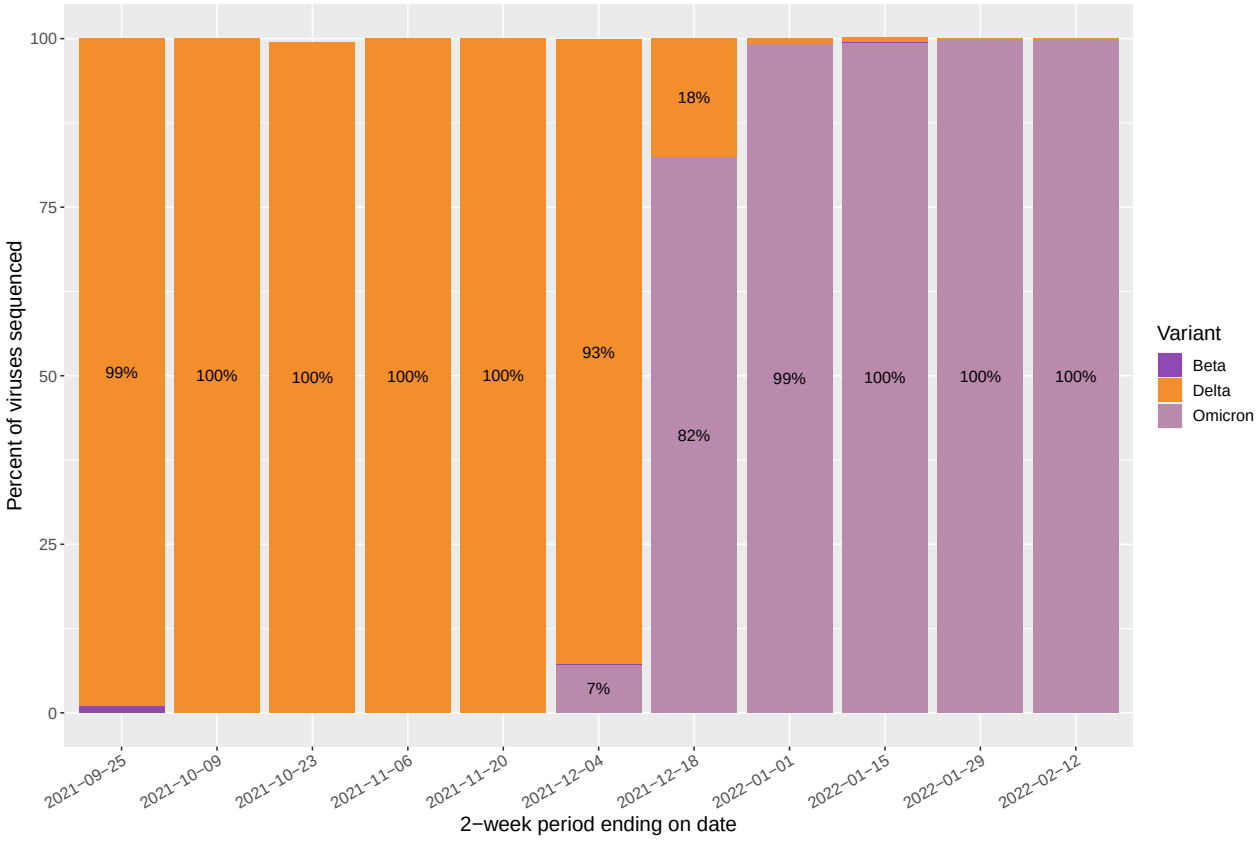

Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Honolulu County, grouped in two-week intervals (based on the date of sample collection).
- Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases in Honolulu County. This graph 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. Therefore, 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			2181		
	AY.103	United States	582	20 Jun 2021	18 Dec 2021
	AY.44	United States	362	07 Jun 2021	13 Dec 2021
	AY.54	United States	235	28 May 2021	21 Nov 2021
	AY.3	United States	202	28 Jun 2021	17 Dec 2021
	AY.25	United States	161	21 Jun 2021	04 Jan 2022
	AY.100	South Africa/Botswana	81	23 Jul 2021	12 Dec 2021
	Other AY.*	Various	80	01 Aug 2021	Sep 2021
	AY.1	Europe	74	30 Jun 2021	30 Nov 2021
	AY.26	United States/Mexico	60	07 Jun 2021	21 Nov 2021
	AY.25.1	South Africa/Botswana	57	18 Jul 2021	11 Dec 2021
	AY.117	United States	50	15 Jul 2021	11 Nov 2021
	AY.119	United States	48	06 Jul 2021	13 Dec 2021
	AY.122	South Africa/Botswana	28	09 Jul 2021	26 Nov 2021
	AY.75	United States/Europe	22	09 Jul 2021	02 Oct 2021
	AY.39	United States	21	05 Aug 2021	09 Dec 2021
	B.1.617.2	India	19	04 Jun 2021	25 Oct 2021
	AY.14	United States	17	29 Jun 2021	17 Nov 2021
	AY.118	United States	16	12 Jul 2021	30 Nov 2021
	AY.29	Japan	16	23 Jul 2021	16 Sep 2021
	AY.20	United States/Mexico	14	15 Jul 2021	07 Dec 2021
	AY.116.1	United States	13	02 Jul 2021	23 Oct 2021
	AY.47	United States	13	21 Jul 2021	01 Dec 2021
	AY.52	South Africa/Botswana	10	18 May 2021	03 Jul 2021
Omicron			994		
	BA.1.1	South Africa/Botswana	788	27 Nov 2021	19 Feb 2022
	BA.1	South Africa/Botswana	195	30 Nov 2021	13 Feb 2022
	BA.2	South Africa/Botswana	11	27 Jan 2022	17 Feb 2022

Table Notes:

- Lineage "Other AY.*" represents an aggregate of different AY.* sub-lineages, each with less than 10 sequenced genomes, from Honolulu County.

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

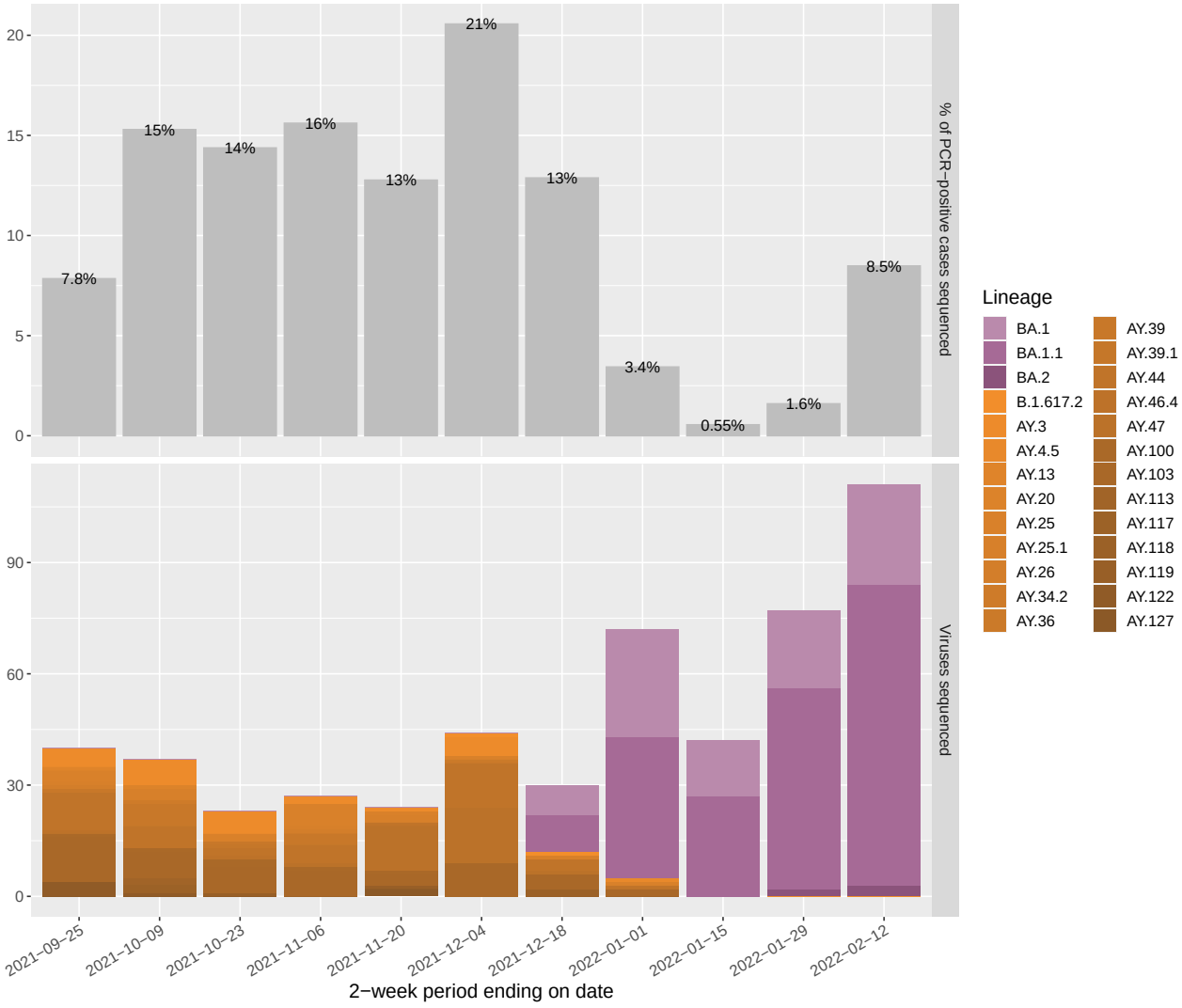

Figure Notes:

- The 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 shown are Delta (lineages B.1.617.2 + AY.*) and Omicron (lineages B.1.1.529 + BA.*).
- None of the variants being monitored were detected during the time periods shown.
- The gray bar graph (top) shows the percentage of PCR-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 graph does not estimate prevalence in the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.

Estimated proportions of variants circulating in Maui County

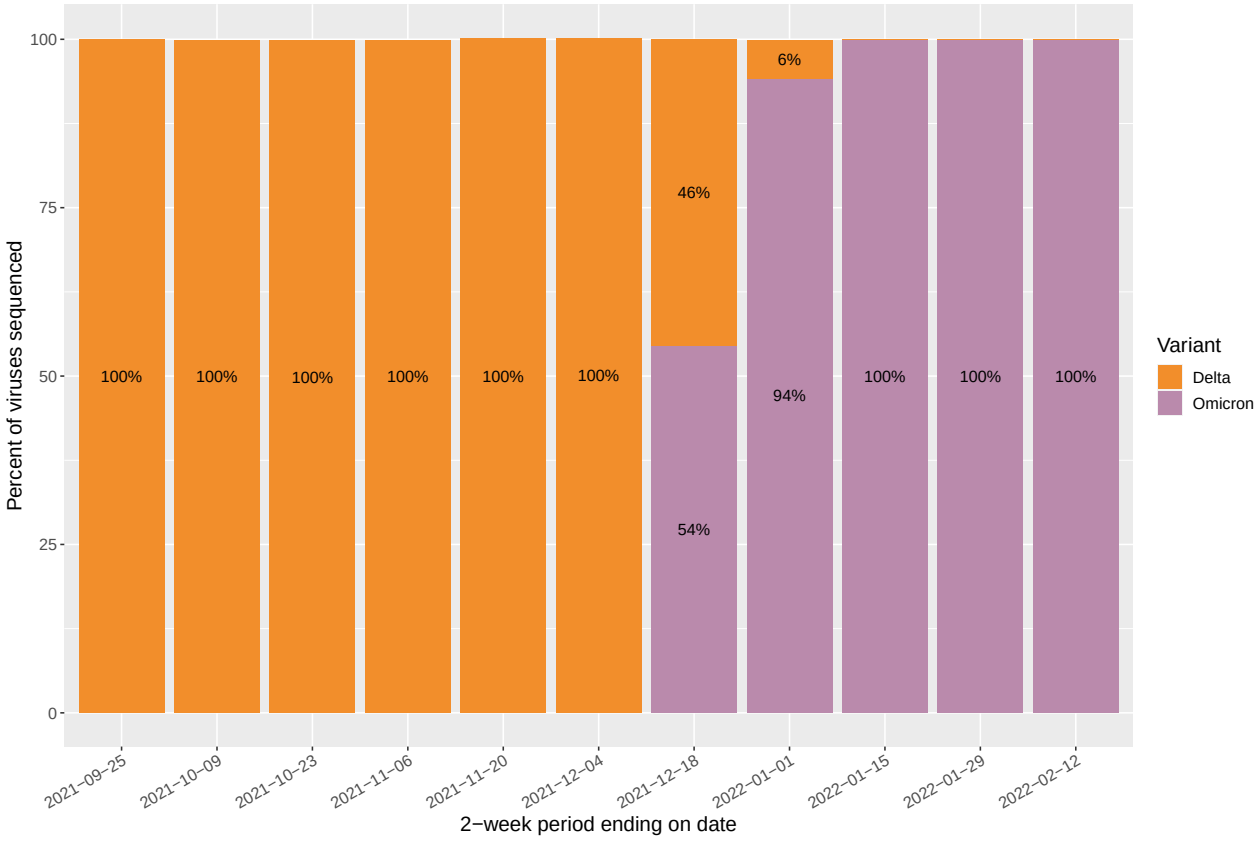

Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Maui County, grouped in two-week intervals (based on the date of sample collection).
- Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases in Maui County. This graph 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. Therefore, 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			370		
	AY.103	United States	80	13 Jul 2021	23 Dec 2021
	AY.44	United States	59	27 Jun 2021	27 Dec 2021
	AY.3	United States	47	19 Jul 2021	01 Dec 2021
	Other AY.*	Various	37	09 Jul 2021	Sep 2021
	AY.47	United States	31	19 Aug 2021	07 Dec 2021
	AY.100	South Africa/Botswana	19	22 Jul 2021	18 Nov 2021
	AY.13	United States	18	21 Jul 2021	13 Sep 2021
	AY.25	United States	16	19 Aug 2021	19 Dec 2021
	AY.2	United States	14	07 Jun 2021	06 Aug 2021
	AY.26	United States/Mexico	13	03 Aug 2021	28 Oct 2021
	AY.25.1	South Africa/Botswana	12	24 Jul 2021	10 Dec 2021
	AY.122	South Africa/Botswana	11	19 Jul 2021	01 Oct 2021
	AY.39	United States	11	25 Sep 2021	31 Oct 2021
	B.1.617.2	India	2	Dec 2021	Dec 2021
Omicron			337		
	BA.1.1	South Africa/Botswana	221	13 Dec 2021	17 Feb 2022
	BA.1	South Africa/Botswana	106	14 Dec 2021	18 Feb 2022
	BA.2	South Africa/Botswana	10	28 Jan 2022	17 Feb 2022

Table Notes:

- Lineage "Other AY.*" represents an aggregate of different AY.* sub-lineages, each with less than 5 sequenced genomes, from Maui County.

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

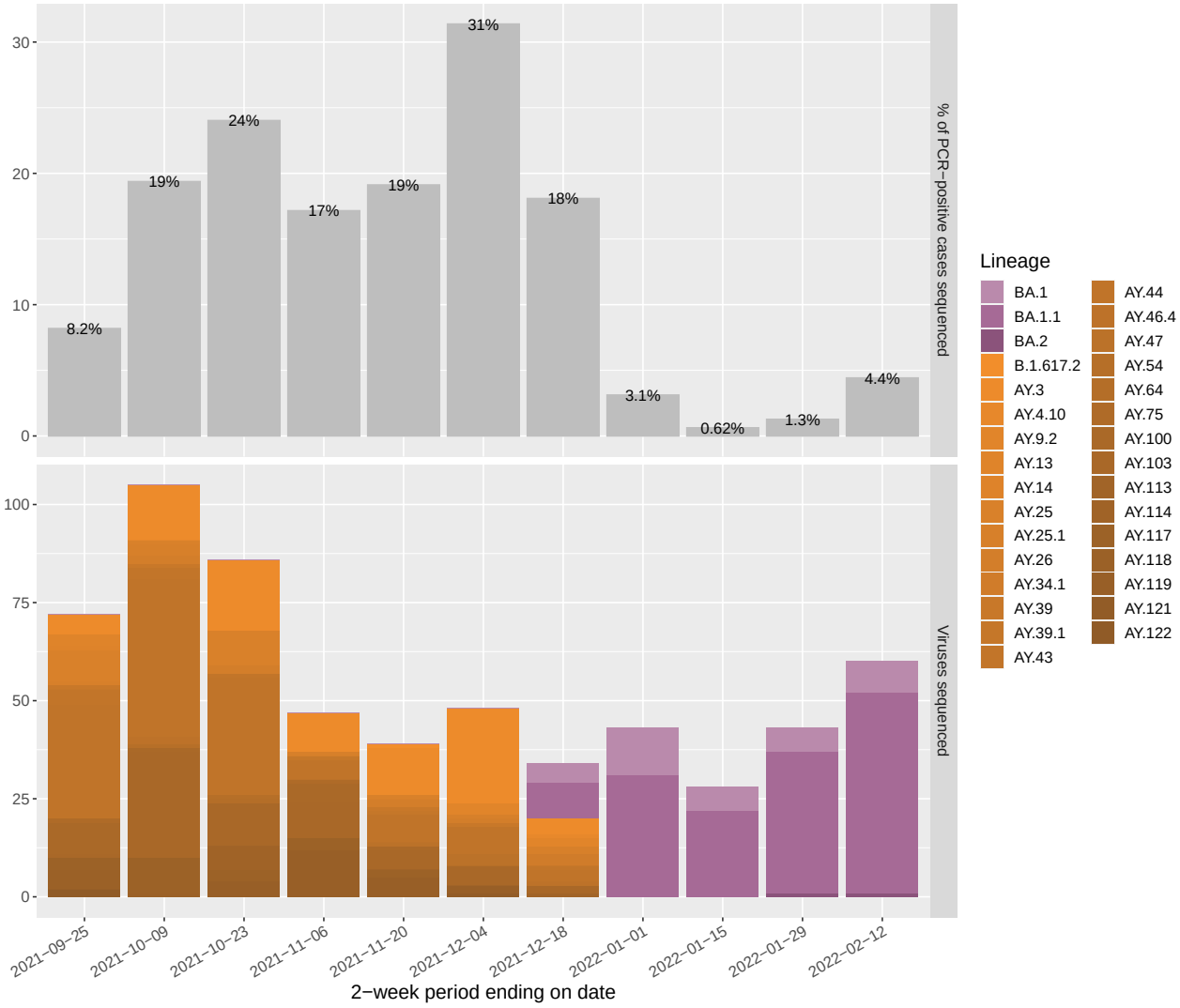

Figure Notes:

- The 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 shown are Delta (lineages B.1.617.2 + AY.*) and Omicron (lineages B.1.1.529 + BA.*).
- None of the variants being monitored were detected during the time periods shown.
- The gray bar graph (top) shows the percentage of PCR-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 graph does not estimate prevalence in the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.

Estimated proportions of variants circulating in Hawaii County

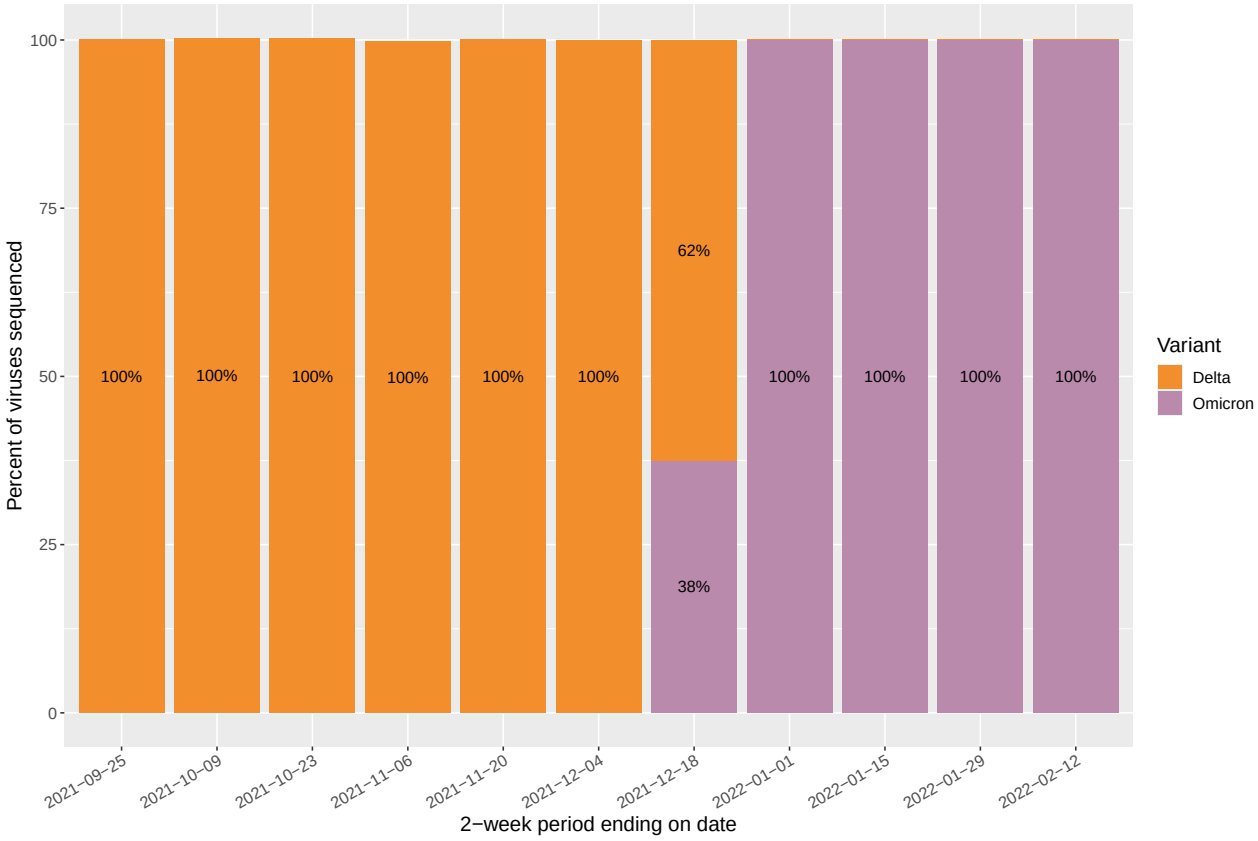

Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Hawaii County, grouped in two-week intervals (based on the date of sample collection).
- Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases in Hawaii County. This graph 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. Therefore, 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			737		
	AY.44	United States	209	11 Jun 2021	16 Dec 2021
	AY.3	United States	109	31 Jul 2021	16 Dec 2021
	AY.103	United States	91	21 May 2021	16 Dec 2021
	AY.25	United States	52	19 Jul 2021	09 Nov 2021
	AY.100	South Africa/Botswana	41	17 Jul 2021	12 Nov 2021
	AY.46.4	United States	27	21 Jun 2021	06 Dec 2021
	Other AY.*	Various	27	12 Jul 2021	Oct 2021
	AY.118	United States	26	08 Jul 2021	27 Sep 2021
	AY.25.1	South Africa/Botswana	26	11 Aug 2021	17 Dec 2021
	AY.117	United States	24	15 Aug 2021	17 Nov 2021
	AY.119	United States	24	03 Aug 2021	24 Nov 2021
	AY.26	United States/Mexico	16	24 Jun 2021	03 Dec 2021
	AY.122	South Africa/Botswana	15	19 Jul 2021	22 Sep 2021
	AY.1	Europe	9	20 Jul 2021	03 Sep 2021
	AY.43	Europe	9	13 Sep 2021	17 Dec 2021
	AY.47	United States	8	05 Aug 2021	26 Nov 2021
	AY.114	South Africa/Botswana	6	10 Oct 2021	22 Oct 2021
	AY.54	United States	6	01 Jul 2021	22 Oct 2021
	AY.39	United States	5	30 Aug 2021	29 Nov 2021
	AY.9.2	South Africa/Botswana	5	22 Nov 2021	09 Dec 2021
	B.1.617.2	India	2	Jul 2021	Nov 2021
Omicron			199		
	BA.1.1	South Africa/Botswana	157	10 Dec 2021	17 Feb 2022
	BA.1	South Africa/Botswana	40	10 Dec 2021	18 Feb 2022
	BA.2	South Africa/Botswana	2	Jan 2022	Jan 2022

Table Notes:

- Lineage "Other AY.*" represents an aggregate of different AY.* sub-lineages, each with less than 5 sequenced genomes, from Hawaii County.

Variants being monitored in Hawaii County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Alpha			66		
	B.1.1.7	United Kingdom	55	22 Feb 2021	16 Jul 2021
	Q.3	United States	11	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			44		
	B.1.429	California	38	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

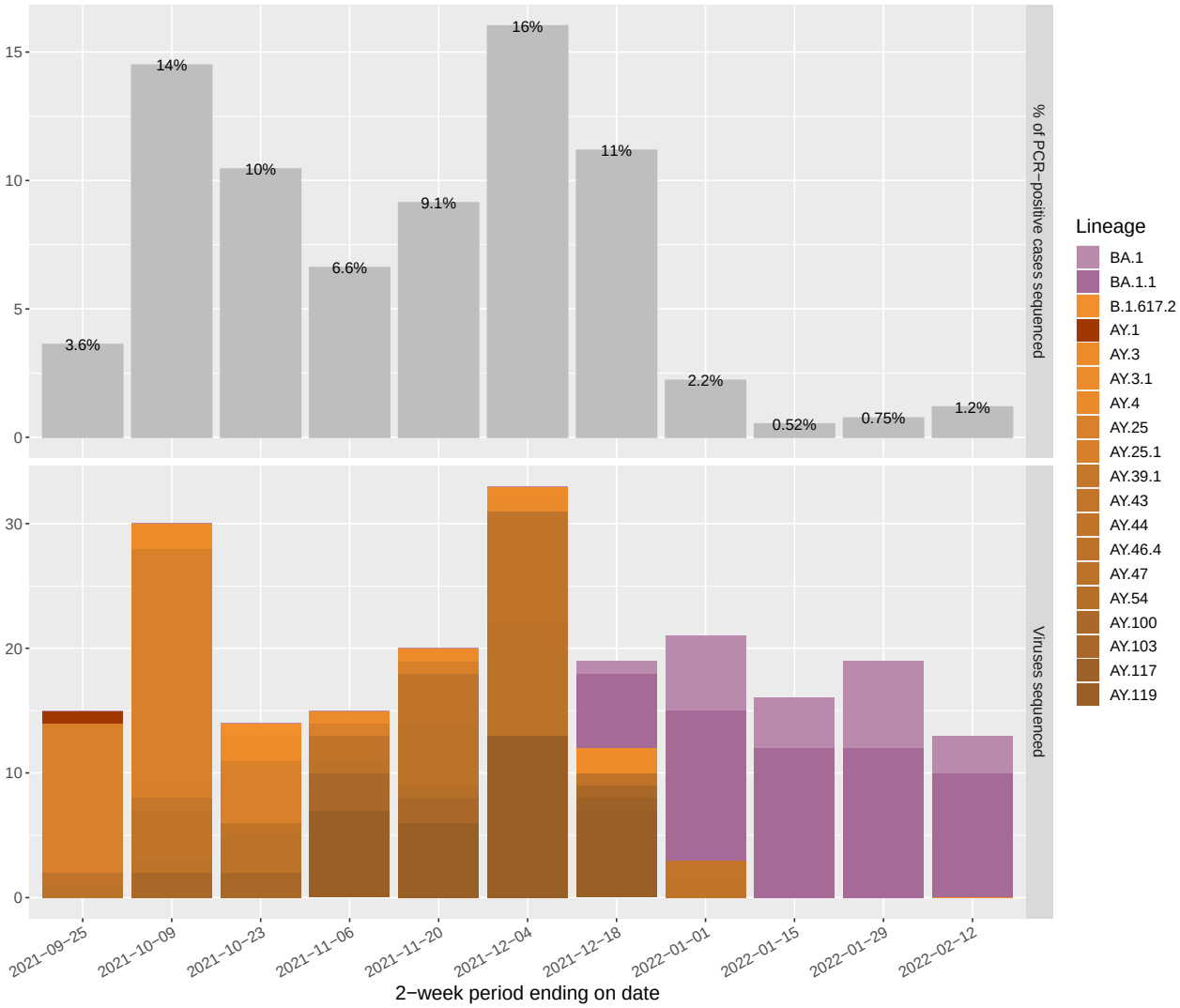

Figure Notes:

- The 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 shown are Delta (lineages B.1.617.2 + AY.*) and Omicron (lineages B.1.1.529 + BA.*).
- None of the variants being monitored were detected during the time periods shown.
- The gray bar graph (top) shows the percentage of PCR-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 graph does not estimate prevalence in the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.

Estimated proportions of variants circulating in Kauai County

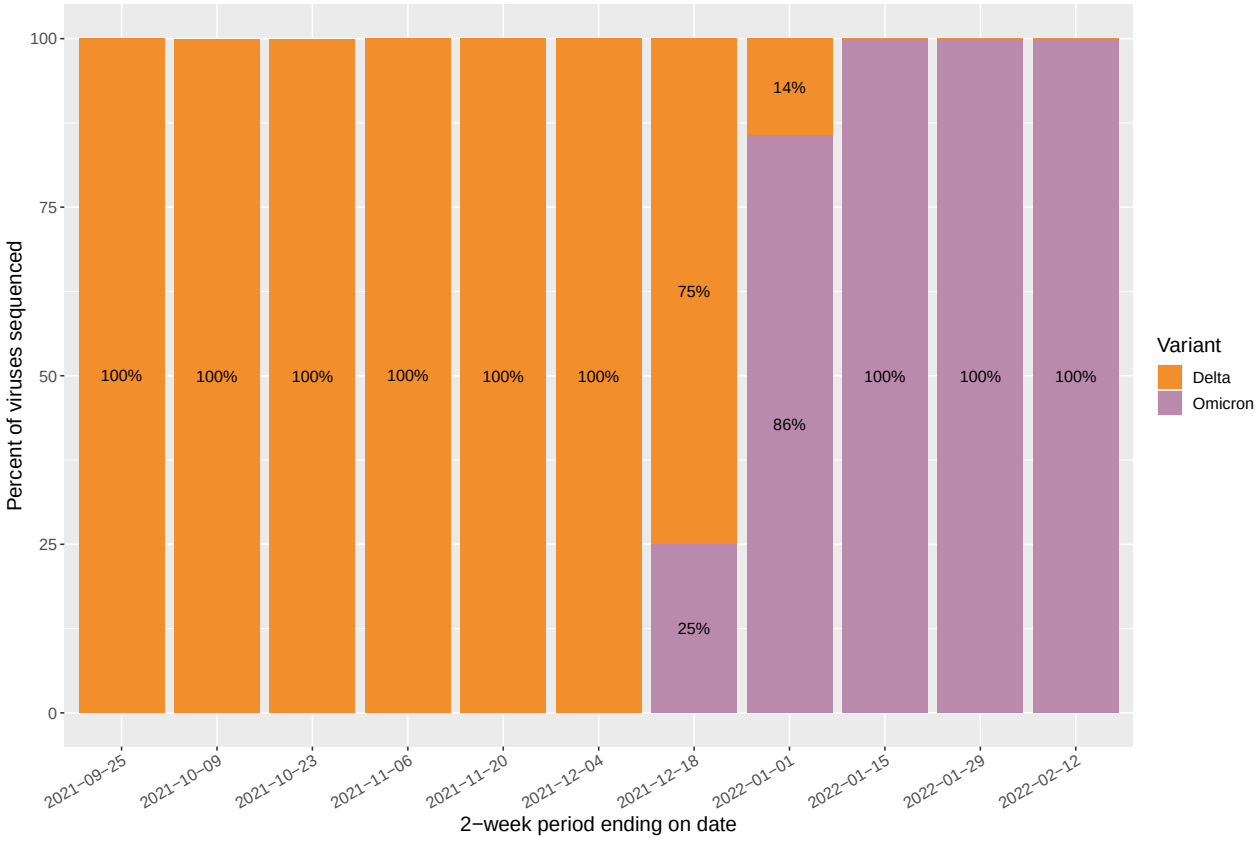

Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Kauai County, grouped in two-week intervals (based on the date of sample collection).
- Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases in Kauai County. This graph 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. Therefore, 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			232		
	AY.25	United States	70	16 Jul 2021	10 Nov 2021
	AY.119	United States	34	28 Aug 2021	18 Dec 2021
	AY.44	United States	34	01 Jul 2021	21 Dec 2021
	Other AY.*	Various	25	Aug 2021	Sep 2021
	AY.47	United States	19	27 Jul 2021	29 Nov 2021
	AY.103	United States	16	01 Aug 2021	15 Dec 2021
	AY.1	Europe	11	09 Aug 2021	21 Sep 2021
	AY.3	United States	8	30 Sep 2021	15 Dec 2021
	AY.54	United States	8	06 Jul 2021	09 Nov 2021
	AY.67	South Africa/Botswana	6	06 Jun 2021	29 Jun 2021
	B.1.617.2	India	1	Oct 2021	Oct 2021
Omicron			75		
	BA.1.1	South Africa/Botswana	54	15 Dec 2021	18 Feb 2022
	BA.1	South Africa/Botswana	21	16 Dec 2021	07 Feb 2022

Table Notes:

- Lineage "Other AY.*" represents an aggregate of different AY.* sub-lineages, each with less than 5 sequenced genomes, from Kauai County.

Variants being monitored in Kauai County

Variant	Lineage	Area of emergence	Cumulative cases detected	Earliest specimen collection date	Most recent specimen collection date
Alpha			19		
	B.1.1.7	United Kingdom	18	05 Apr 2021	13 Jul 2021
	Q.4	South Africa/Botswana	1	Apr 2021	Apr 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