

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 a nucleotide code denoted as 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) that 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 a Variant of Concern (VOC) and others as Variants Being Monitored (VBM), 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 specimens that contain SARS-CoV-2 RNA, which means only specimens 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.

In February 2021, State Laboratories Division, Hawaii Department of Health increased sequencing efforts done on PCR-positive specimens to improve the State's ability to detect new variants and conduct genomic surveillance of SARS-CoV-2. According to the CDC, approximately 6% of PCR-positive cases in the State of Hawaii have been sequenced since testing began (<https://covid.cdc.gov/covid-data-tracker/#published-sars-cov-2-sequences>).

Acknowledgements

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

Institution	Program/partner	Count	Percent
Laboratory Preparedness and Response Branch, State Laboratories Division		13307	75.867%
Centers for Disease Control and Prevention	National SARS-CoV-2 Strain Surveillance (NS3)	412	2.349%
	Quest Diagnostics Incorporated	1099	6.266%
	Laboratory Corporation of America	1449	8.261%
	Aegis Sciences Corporation	379	2.161%
	Helix/Illumina	169	0.964%
	Infinity Biologix	16	0.091%
	Mako Medical	20	0.114%
	Fulgent Genetics	8	0.046%
Tripler Army Medical Center		681	3.883%
Total		17540	100.000%

Table Notes:

- In support of the State’s SARS-CoV-2 genomic surveillance program, PCR-positive specimens are regularly provided to the Laboratory Preparedness and Response Branch (LPRB), State Laboratories Division by the various commercial laboratories that operate throughout the State of Hawaii, to include Clinical Labs of Hawaii (CLH), Diagnostic Laboratory Services, Inc. (DLS), Kaiser Permanente Hawaii, and S&G Labs Hawaii. The collected specimens are then quality controlled and sequenced by the LPRB.
- The specimens sequenced by the Centers for Disease Control and Prevention (CDC) for the National SARS-CoV-2 Strain Surveillance (NS3) program are collected, quality controlled, and shipped to the CDC by the LPRB.

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

Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
7494	2617	2158	693	345	13307

Table Notes:

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

Summary and key notes

- This report reflects sequenced PCR-positive specimens only, and not all PCR-positive cases in the State of Hawaii are sequenced.
- Each successfully sequenced specimen produces one consensus SARS-CoV-2 genome sequence that is further analyzed to determine the variant.
- State Laboratories Division has reported 568 additional SARS-CoV-2 genome sequences since the previous report was generated (8/16/2022).
- The CDC and its commercial partners have reported 41 additional SARS-CoV-2 genome sequences from the State of Hawaii since the previous report was generated (8/16/2022).
- 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.), Phylogenetic Assignment of Named Global Outbreak (PANGO) lineage (alphabetical prefix and a numerical suffix), and/or Nextstrain clade (year of emergence followed by the next available letter in the alphabet, i.e., 20A, 20B, etc.). In this report, variant counts are reported using the WHO label and PANGO lineage nomenclatures only.
- For PANGO lineage nomenclature, ‘the numerical suffix has three hierarchical levels (primary, secondary and tertiary). Each full stop (period or dot) within the numerical suffix represents “descendant of”. Descendants of lineages with tertiary suffixes are assigned to the next available alphabetical prefix, in alphabetical order.’ More details can be found at <https://www.pango.network/the-pango-nomenclature-system/statement-of-nomenclature-rules/>.
- Omicron has represented 100% of the variants circulating in the State of Hawaii since 1/28/2022.
- Classifications of Omicron lineages are in flux. The parent lineage of Omicron is B.1.1.529; primary sub-lineages of the Omicron parent lineage have BA.* designations (i.e., BA.1, BA.2, BA.5 etc.). Primary sub-lineages of BA.2.12.1, BA.5.3.1, and BA.5.2.1 have BG.*, BE.*, and BF.* designations, respectively. Omicron XE, XZ, XAC, and XAP are recombinant lineages containing genetic material from BA.1* and BA.2*.
- Due to periodic updates in PANGO lineage classifications, some lineage designations may have changed since the previous report.
- The BA.5* lineage family (BA.5 and its sub-lineages) represents the vast majority (~91%) of sequenced specimens collected in the State of Hawaii from 7/31/2022 to 8/13/2022.

Variants of Concern (VOC) and Variants Being Monitored (VBM)

Evidence to date shows that vaccination generally 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 (VOHC)*”, 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 detected in the State of Hawaii

Omicron variant (B.1.1.529, BA.*, BE.*, BF.*, BG.*, XE, XZ, XAC, and XAP 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 labeled 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. 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 previous variants. More information can be found at <https://www.cdc.gov/coronavirus/2019-ncov/variants/omicron-variant.html>.

B.1.1.529 is the parent lineage of Omicron; primary sub-lineages of the Omicron parent lineage have BA.* designations (i.e., BA.1, BA.2, BA.5, etc.). Primary sub-lineages of BA.2.12.1, BA.5.3.1, and BA.5.2.1 have BG.*, BE.*, and BF.* designations, respectively. XE, XZ, XAC, and XAP are recombinant lineages in which portions of their genomes are derived from BA.1* and BA.2*. SARS-CoV-2 recombinants that receive a PANGO classification have an X* lineage designation. Omicron lineage families correspond to Nextstrain clades 21M, 21K, 21L, 22A, 22B, 22C, and 22D (<https://ncov-clades-schema.vercel.app/>).

Due to acquired mutations, particularly within the spike protein, each successively dominant Omicron lineage family (BA.1*, BA.2*, BA.2.12.1*, and now BA.5*) has been more transmissible and/or more immune evasive than the one previous. Notable information regarding each of their defining mutations can be found at <https://covariants.org/variants> (21K, 21L, 22C, and 22B, respectively).

Variants Being Monitored detected in the State of Hawaii

Alpha variant (B.1.1.7 and Q.* 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. Upon its emergence, the Alpha variant was shown to be significantly more transmissible (~50%) than the original SARS-CoV-2 virus. The Alpha variant corresponds to Nextstrain clade 20I.

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

B.1.351 was first identified in South Africa and the WHO labeled it “Beta” on May 31, 2021. This variant has the E484K spike mutation, which is associated with increased evasion of antibodies elicited by vaccination or previous infection by earlier variants. The Beta variant corresponds to Nextstrain clade 20H.

Gamma variant (P.1 and P.1.* 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. The Gamma variant corresponds to Nextstrain clade 20J.

Delta variant (B.1.617.2 and AY.* 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).

B.1.617.2 is the parent lineage of Delta; sub-lineages of Delta have the AY.* designation (i.e., AY.1, AY.2, AY.3, etc.). Delta lineage families correspond to Nextstrain clades 21A, 21I, and 21J.

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. This variant is associated with increased viral shedding compared to the original SARS-CoV-2 virus, and contains the L452R mutation in the spike protein, which has been shown to escape neutralization by monoclonal antibodies and some convalescent sera. The Epsilon variant corresponds to Nextstrain clade 21C.

Zeta variant (P.2)

P.2 was first identified in Brazil and contains a spike mutation (E484K), which is also present in B.1.351, that can potentially make it less responsive to antibodies. The Zeta variant corresponds to Nextstrain clade 20B/S.484K.

Iota variant (B.1.526)

B.1.526 was first identified in New York and was classified by the CDC as a VBM due to indications of increased transmissibility. The WHO labeled it “Iota” on May 31, 2021. Some of the genomes (but not all) of this variant contain the E484K mutation. The Iota variant corresponds to Nextstrain clade 21F.

Mu variant (B.1.621 and B.1.621.1)

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

State of Hawaii

Total variants identified

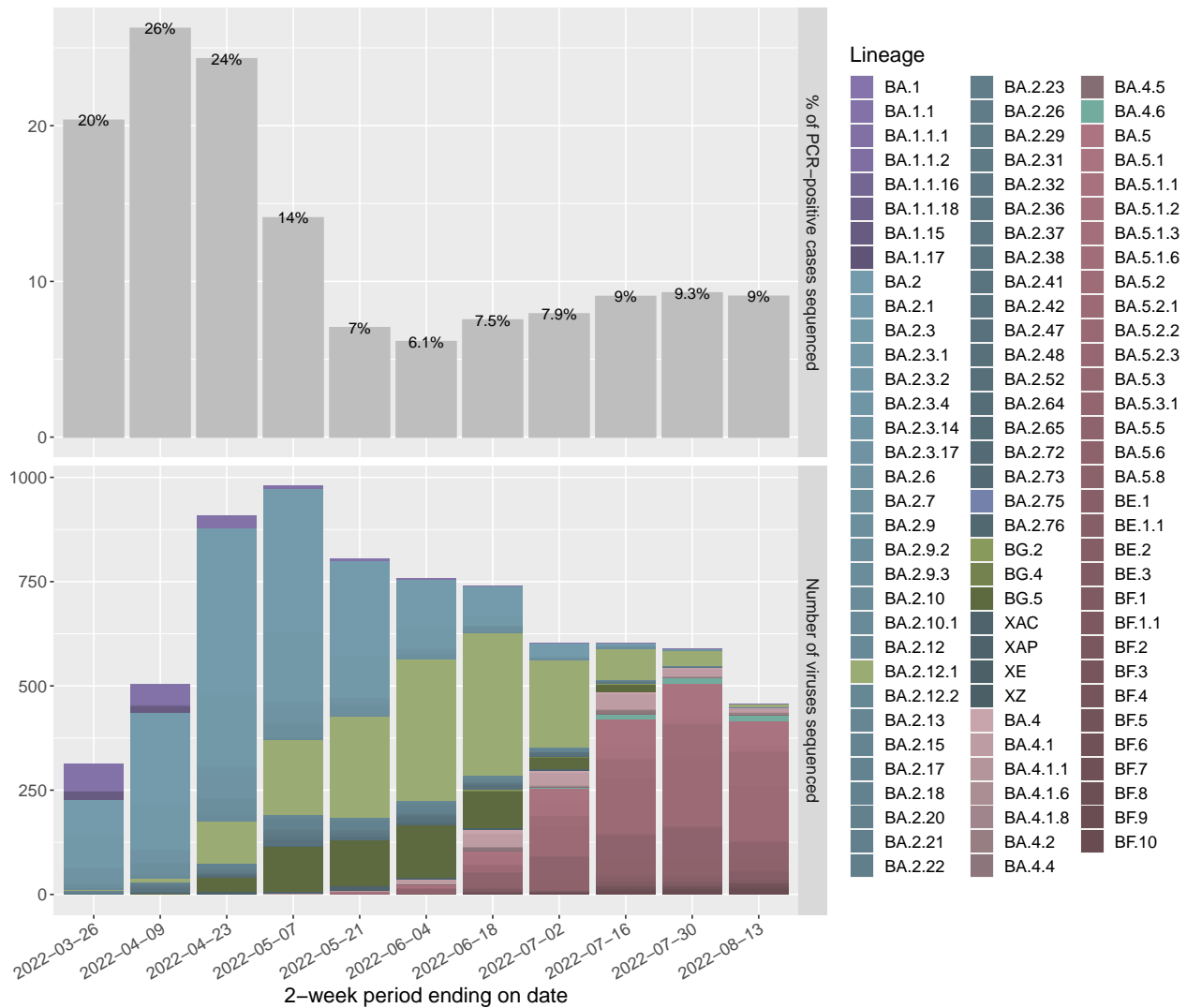


Figure Notes:

- 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).
- Omicron (BA.* + BE.* + BF.* + BG.* + XE + XZ + XAC + XAP) is a *Variant of Concern*.
- The gray bar graph (top) shows the percentage of PCR-positive cases from each 2-week time interval that were sequenced.
- The color bar graph (bottom) shows the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week time interval.
- 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

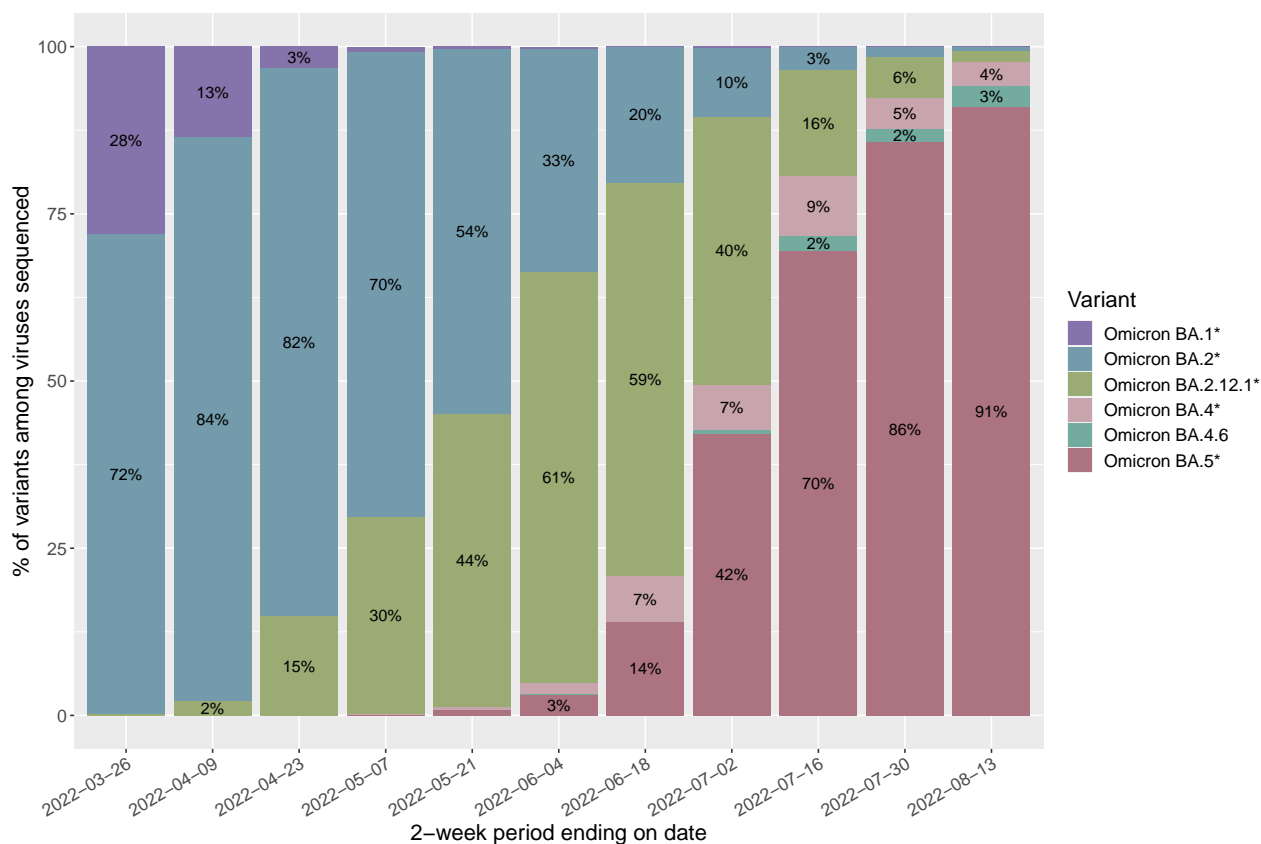


Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in the State of Hawaii, grouped in 2-week intervals (based on the date of specimen collection); percentage estimates are rounded to the nearest whole number.
- 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 specimens that were selected randomly for the purpose of surveillance, to avoid over-representing the specimens that were selected for investigations of clusters.
- The last 2-week interval numbers will most likely change, as a number of specimens 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.
- Omicron BA.1* includes BA.1 and its sub-lineages (BA.1.*).
- Omicron BA.2* includes BA.2, its sub-lineages (BA.2.*), XE, XZ, XAC, and XAP; excludes BA.2.12.1*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*).
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, and BF.*).

Variants of Concern in the State of Hawaii

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			10448		
	BA.1.1	South Africa/Botswana	1739	27 Nov 2021	19 Jun 2022
	BA.2	South Africa/Botswana	1557	06 Jan 2022	20 Jul 2022
	BA.2.12.1	USA/Canada	1545	21 Mar 2022	11 Aug 2022
	BA.2.3	Philippines	807	13 Jan 2022	22 Jul 2022
	BA.1.1.2	Japan	569	06 Dec 2021	01 Apr 2022
	BA.5.2.1	South Africa/UK/USA	523	31 May 2022	12 Aug 2022
	BG.5	USA	518	09 Apr 2022	16 Jul 2022
	Other	Various	447	02 Apr 2022	May 2022
	BA.1.15	USA	426	30 Nov 2021	09 Apr 2022
	BA.5.5	USA	255	03 May 2022	13 Aug 2022
	BA.5.1	Portugal	223	07 Jun 2022	12 Aug 2022
	BA.5.2	South Africa/UK/USA	223	13 Jun 2022	12 Aug 2022
	BA.2.3.17	USA	207	25 Jan 2022	15 Jun 2022
	BA.1	South Africa/Botswana	187	07 Dec 2021	11 Apr 2022
	BA.2.9	Europe	160	25 Jan 2022	25 Jul 2022
	BA.4.1	South Africa	138	04 May 2022	09 Aug 2022
	BA.5.6	USA	137	21 May 2022	13 Aug 2022
	BA.5.1.1	USA	132	14 May 2022	08 Aug 2022
	BA.1.1.18	USA	95	10 Dec 2021	30 Mar 2022
	BA.2.18	UK	92	21 Mar 2022	01 Jul 2022
	BA.2.3.14	South Korea	47	04 Apr 2022	30 May 2022
	BA.1.20	USA	44	14 Dec 2021	28 Feb 2022
	BA.4.6	USA/UK/Denmark	42	21 Jun 2022	13 Aug 2022
	BA.2.42	Australia	40	15 Apr 2022	02 Jul 2022
	BA.2.13	Europe	36	24 Apr 2022	22 Jul 2022
	BF.10	USA	35	05 Jun 2022	11 Aug 2022
	BA.2.10.1	Singapore	27	01 Feb 2022	15 May 2022
	BE.3	USA	27	03 Jun 2022	10 Aug 2022
	BA.1.17.2	Europe	26	14 Dec 2021	25 Feb 2022
	BA.2.29	Japan	26	27 Mar 2022	08 Jul 2022
	BE.1.1	Germany	26	18 Jun 2022	11 Aug 2022
	BA.4	South Africa	25	20 May 2022	10 Aug 2022
	BA.4.4	USA	23	04 Jun 2022	09 Aug 2022
	BF.5	Israel	23	16 Jun 2022	10 Aug 2022
	BA.2.38	India	21	21 Mar 2022	09 Aug 2022

Table Notes:

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.2% of the cumulative Omicron sequences from the State of Hawaii.

Variants Being Monitored in the State of Hawaii

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			754		
	B.1.1.7	UK	703	21 Jan 2021	14 Aug 2021
	Q.3	USA	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	USA	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	USA/Mexico	18	29 Mar 2021	21 Jul 2021
	P.1.13	USA	14	03 May 2021	07 Jun 2021
Delta			4831		
	AY.103	USA	1028	21 May 2021	12 Jan 2022
	AY.44	USA	950	07 Jun 2021	19 Jan 2022
	Other AY.*	Various	709	01 Aug 2021	Sep 2021
	AY.3	USA	496	28 Jun 2021	02 Jan 2022
	AY.25	USA	432	21 Jun 2021	20 Jan 2022
	AY.54	USA	312	23 Jun 2021	21 Nov 2021
	AY.100	South Africa/Botswana	172	17 Jul 2021	12 Dec 2021
	AY.25.1	South Africa/Botswana	160	08 Jul 2021	27 Jan 2022
	AY.1	Europe	134	30 Jun 2021	30 Nov 2021
	AY.119	USA	134	06 Jul 2021	21 Dec 2021
	AY.26	USA/Mexico	117	07 Jun 2021	28 Dec 2021
	AY.117	USA	97	15 Jul 2021	17 Dec 2021
	B.1.617.2	India	90	28 May 2021	16 Dec 2021
Epsilon			774		
	B.1.429	USA	715	31 Dec 2020	03 Jun 2021
	B.1.427	USA	59	07 Dec 2020	05 Jun 2021
Zeta	P.2	Brazil	2	Feb 2021	Feb 2021
Iota	B.1.526	USA	128	06 Feb 2021	23 Jul 2021
Mu			53		
	B.1.621	Columbia	43	03 Jun 2021	17 Sep 2021
	B.1.621.1	USA	10	27 May 2021	11 Aug 2021

Table Notes:

- Lineage “Other AY.*” represents an aggregation of different AY.* lineages in which each alone accounts for <2% of the cumulative Delta sequences from the State of Hawaii.

Honolulu County

Total variants identified

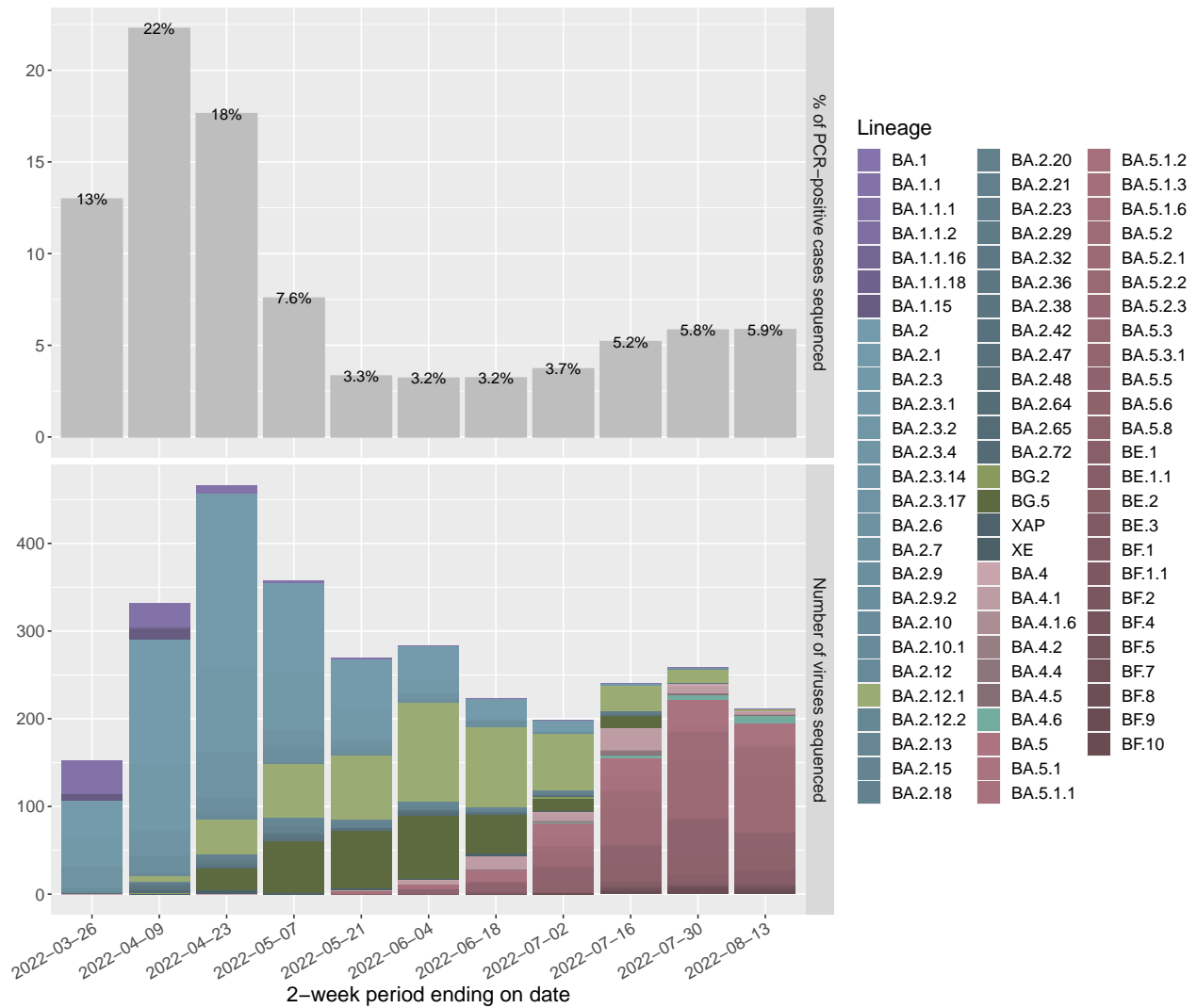


Figure Notes:

- 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).
- Omicron (BA.* + BE.* + BF.* + BG.* + XE + XAP) is a *Variant of Concern*.
- The gray bar graph (top) shows the percentage of PCR-positive cases from each 2-week time interval that were sequenced.
- The color bar graph (bottom) shows the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week time interval.
- 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

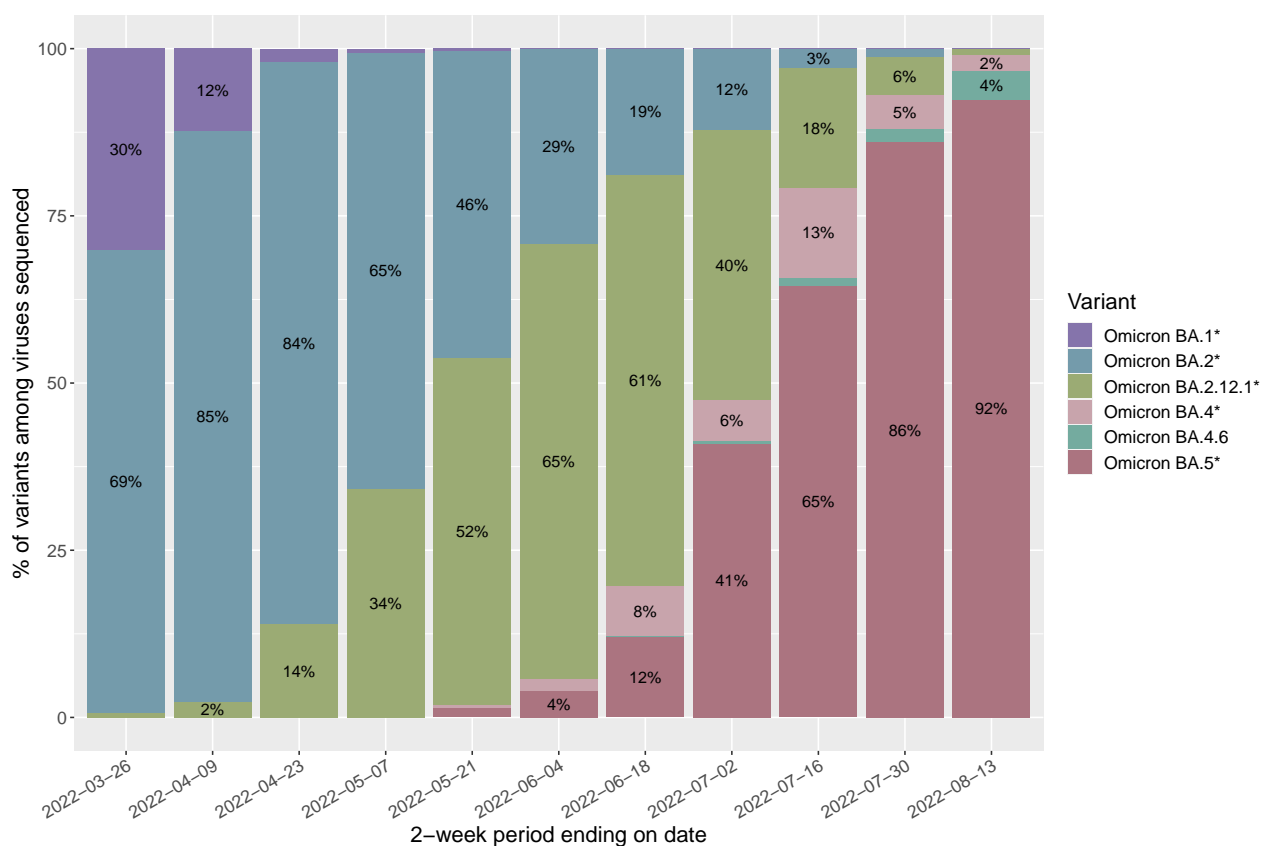


Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Honolulu County, grouped in 2-week intervals (based on the date of specimen collection); percentage estimates are rounded to the nearest whole number.
- 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 specimens that were selected randomly for the purpose of surveillance of community variants, to avoid over-representing the specimens 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.
- Omicron BA.1* includes BA.1 and its sub-lineages (BA.1.*).
- Omicron BA.2* includes BA.2, its sub-lineages (BA.2.*), XE, and XAP; excludes BA.2.12.1*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*)
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, and BF.*).

Variants of Concern in Honolulu County

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			4229		
	BA.1.1	South Africa/Botswana	683	27 Nov 2021	11 May 2022
	BA.2	South Africa/Botswana	625	27 Jan 2022	20 Jul 2022
	BA.2.12.1	USA/Canada	499	21 Mar 2022	08 Aug 2022
	BA.2.3	Philippines	370	30 Jan 2022	24 Jun 2022
	BA.1.1.2	Japan	300	06 Dec 2021	31 Mar 2022
	BG.5	USA	298	09 Apr 2022	16 Jul 2022
	BA.5.2.1	South Africa/UK/USA	183	05 Jun 2022	12 Aug 2022
	BA.1.15	USA	164	30 Nov 2021	07 Apr 2022
	Other	Various	159	02 Apr 2022	May 2022
	BA.2.3.17	USA	121	05 Feb 2022	02 Jun 2022
	BA.5.5	USA	109	29 May 2022	13 Aug 2022
	BA.5.2	South Africa/UK/USA	94	20 Jun 2022	12 Aug 2022
	BA.5.1	Portugal	86	11 Jun 2022	12 Aug 2022
	BA.5.6	USA	73	18 Jun 2022	13 Aug 2022
	BA.2.9	Europe	70	14 Mar 2022	29 Jun 2022
	BA.4.1	South Africa	62	22 May 2022	09 Aug 2022
	BA.5.1.1	USA	54	14 May 2022	08 Aug 2022
	BA.1	South Africa/Botswana	43	07 Dec 2021	14 Mar 2022
	BA.1.1.18	USA	35	10 Dec 2021	30 Mar 2022
	BA.2.3.14	South Korea	30	04 Apr 2022	30 May 2022
	BA.2.18	UK	29	12 Apr 2022	01 Jul 2022
	BA.2.13	Europe	20	25 Apr 2022	21 Jun 2022
	BA.4.6	USA/UK/Denmark	18	26 Jun 2022	13 Aug 2022
	BE.1.1	Germany	18	18 Jun 2022	11 Aug 2022
	BA.2.38	India	13	21 Mar 2022	28 Jul 2022
	BA.1.20	USA	12	14 Dec 2021	05 Feb 2022
	BE.1	South Africa/UK/Austria	12	13 Jul 2022	12 Aug 2022
	BA.2.10.1	Singapore	11	03 Mar 2022	25 Apr 2022
	BF.10	USA	11	09 Jul 2022	10 Aug 2022
	BA.4	South Africa	9	20 May 2022	10 Aug 2022
	BA.4.4	USA	9	10 Jun 2022	03 Aug 2022
	XE	UK	9	26 Mar 2022	31 May 2022

Table Notes:

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.2% of the cumulative Omicron sequences from Honolulu County.

Variants Being Monitored in Honolulu County

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			477		
	B.1.1.7	UK	444	21 Jan 2021	14 Aug 2021
	Q.3	USA	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	USA	50	24 Apr 2021	13 Jul 2021
	P.1	Brazil	15	24 Mar 2021	11 Jul 2021
	P.1.13	USA	14	03 May 2021	07 Jun 2021
	P.1.17	USA/Mexico	14	29 Mar 2021	20 Jul 2021
	P.1.12	Peru	1	Apr 2021	Apr 2021
Delta			2182		
	AY.103	USA	582	20 Jun 2021	18 Dec 2021
	AY.44	USA	363	07 Jun 2021	22 Dec 2021
	Other AY.*	Various	244	01 Aug 2021	Sep 2021
	AY.54	USA	212	23 Jun 2021	21 Nov 2021
	AY.3	USA	202	28 Jun 2021	17 Dec 2021
	AY.25	USA	162	21 Jun 2021	04 Jan 2022
	AY.100	South Africa/Botswana	81	23 Jul 2021	12 Dec 2021
	AY.1	Europe	74	30 Jun 2021	30 Nov 2021
	AY.26	USA/Mexico	60	07 Jun 2021	21 Nov 2021
	AY.25.1	South Africa/Botswana	57	18 Jul 2021	11 Dec 2021
	AY.117	USA	50	15 Jul 2021	11 Nov 2021
	AY.119	USA	48	06 Jul 2021	13 Dec 2021
	B.1.617.2	India	47	28 May 2021	25 Oct 2021
Epsilon			346		
	B.1.429	USA	315	05 Jan 2021	29 May 2021
	B.1.427	USA	31	07 Jan 2021	05 Jun 2021
Zeta	P.2	Brazil	2	Feb 2021	Feb 2021
Iota	B.1.526	USA	26	08 Feb 2021	23 Jul 2021
Mu			21		
	B.1.621	Columbia	18	03 Jun 2021	28 Jul 2021
	B.1.621.1	USA	3	May 2021	Aug 2021

Table Notes:

- Lineage “Other AY.*” represents an aggregation of different AY.* lineages in which each alone accounts for <2% of the cumulative Delta sequences from Honolulu County.

Maui County

Total variants identified

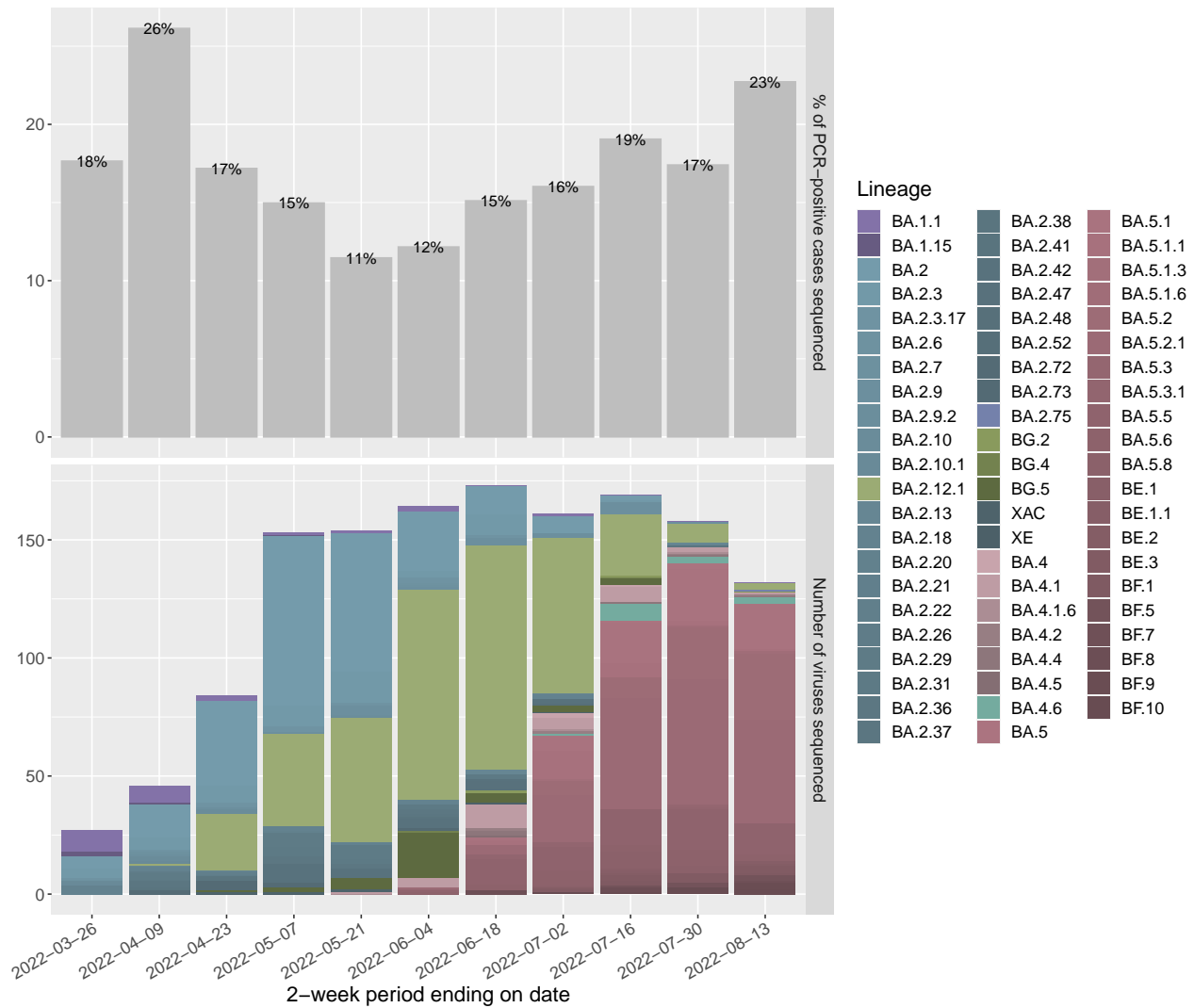


Figure Notes:

- 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).
- Omicron (BA.* + BE.* + BF.* + BG.* + XE + XAC) is a *Variant of Concern*.
- The gray bar graph (top) shows the percentage of PCR-positive cases from each 2-week time interval that were sequenced.
- The color bar graph (bottom) shows the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week time interval.
- 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

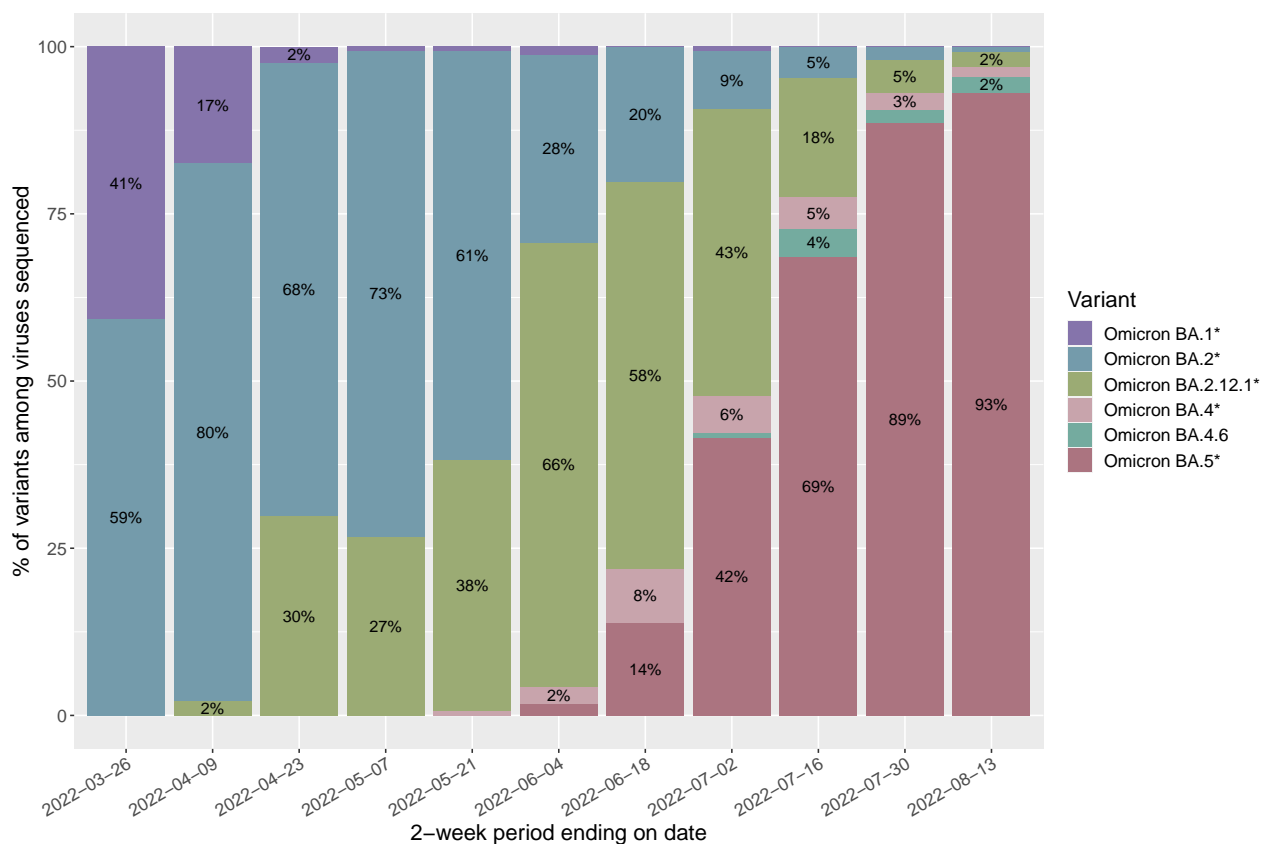


Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Maui County, grouped in 2-week intervals (based on the date of specimen collection); percentage estimates are rounded to the nearest whole number.
- 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 specimens that were selected randomly for the purpose of surveillance of community variants, to avoid over-representing the specimens 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.
- Omicron BA.1* includes BA.1 and its sub-lineages (BA.1.*).
- Omicron BA.2* includes BA.2, its sub-lineages (BA.2.*), XE, and XAC; excludes BA.2.12.1*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*)
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, and BF.*).

Variants of Concern in Maui County

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			1870		
	BA.2.12.1	USA/Canada	404	09 Apr 2022	11 Aug 2022
	BA.2	South Africa/Botswana	262	28 Jan 2022	12 Jul 2022
	BA.1.1	South Africa/Botswana	257	16 Dec 2021	19 Jun 2022
	BA.5.2.1	South Africa/UK/USA	169	31 May 2022	12 Aug 2022
	BA.1.15	USA	86	14 Dec 2021	09 Apr 2022
	Other	Various	86	07 Apr 2022	May 2022
	BA.5.5	USA	67	02 Jun 2022	12 Aug 2022
	BA.5.1	Portugal	65	17 Jun 2022	12 Aug 2022
	BA.5.2	South Africa/UK/USA	65	19 Jun 2022	12 Aug 2022
	BA.2.3	Philippines	62	05 Feb 2022	14 Jul 2022
	BG.5	USA	37	19 Apr 2022	16 Jul 2022
	BA.4.1	South Africa	29	09 May 2022	05 Aug 2022
	BA.1	South Africa/Botswana	26	17 Dec 2021	25 Feb 2022
	BA.1.1.2	Japan	23	13 Dec 2021	15 Feb 2022
	BA.5.1.1	USA	23	17 Jun 2022	04 Aug 2022
	BA.5.6	USA	22	27 May 2022	04 Aug 2022
	BA.2.9	Europe	20	08 Mar 2022	25 Jul 2022
	BA.2.42	Australia	19	24 Apr 2022	23 Jun 2022
	BA.1.1.18	USA	17	30 Dec 2021	22 Feb 2022
	BA.2.29	Japan	15	08 Apr 2022	16 May 2022
	BA.4.6	USA/UK/Denmark	14	29 Jun 2022	10 Aug 2022
	BA.2.18	UK	13	21 Mar 2022	20 Jun 2022
	BA.5.8	USA/UK/Denmark	11	30 Jun 2022	23 Jul 2022
	BA.2.3.17	USA	10	21 Mar 2022	15 Jun 2022
	BA.2.31	Israel	10	02 May 2022	06 Jun 2022
	BE.3	USA	10	28 Jun 2022	07 Aug 2022
	BA.1.20	USA	9	19 Dec 2021	28 Feb 2022
	BA.2.72	USA/Germany/Swit	8	08 Apr 2022	04 May 2022
	BA.2.10	Asia	7	22 Feb 2022	14 Apr 2022
	BA.2.36	Europe	7	27 Apr 2022	30 May 2022
	BF.10	USA	7	23 Jun 2022	11 Aug 2022
	BA.5.3.1	South Africa/UK/Austria	5	10 Jun 2022	25 Jul 2022
	BF.5	Israel	5	16 Jul 2022	08 Aug 2022

Table Notes:

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for $\leq 0.2\%$ of the cumulative Omicron sequences from Maui County.

Variants Being Monitored in Maui County

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			41		
	B.1.1.7	UK	39	01 Mar 2021	11 Jul 2021
	Q.3	USA	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	USA	1	May 2021	May 2021
Delta			370		
	AY.103	USA	80	13 Jul 2021	23 Dec 2021
	AY.44	USA	59	27 Jun 2021	27 Dec 2021
	AY.3	USA	47	19 Jul 2021	01 Dec 2021
	Other AY.*	Various	37	09 Jul 2021	Sep 2021
	AY.47	USA	31	19 Aug 2021	07 Dec 2021
	AY.100	South Africa/Botswana	19	22 Jul 2021	18 Nov 2021
	AY.13	USA	18	21 Jul 2021	13 Sep 2021
	AY.25	USA	16	19 Aug 2021	19 Dec 2021
	AY.2	USA	14	07 Jun 2021	06 Aug 2021
	AY.26	USA/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	USA	11	25 Sep 2021	31 Oct 2021
	B.1.617.2	India	2	Dec 2021	Dec 2021
Epsilon			272		
	B.1.429	USA	265	08 Jan 2021	18 May 2021
	B.1.427	USA	7	27 Apr 2021	10 May 2021
Iota	B.1.526	USA	16	12 Mar 2021	25 Jun 2021

Table Notes:

- Lineage “Other AY.*” represents an aggregation of different AY.* lineages in which each alone accounts for <2% of the cumulative Delta sequences from Maui County.

Hawaii County

Total variants identified

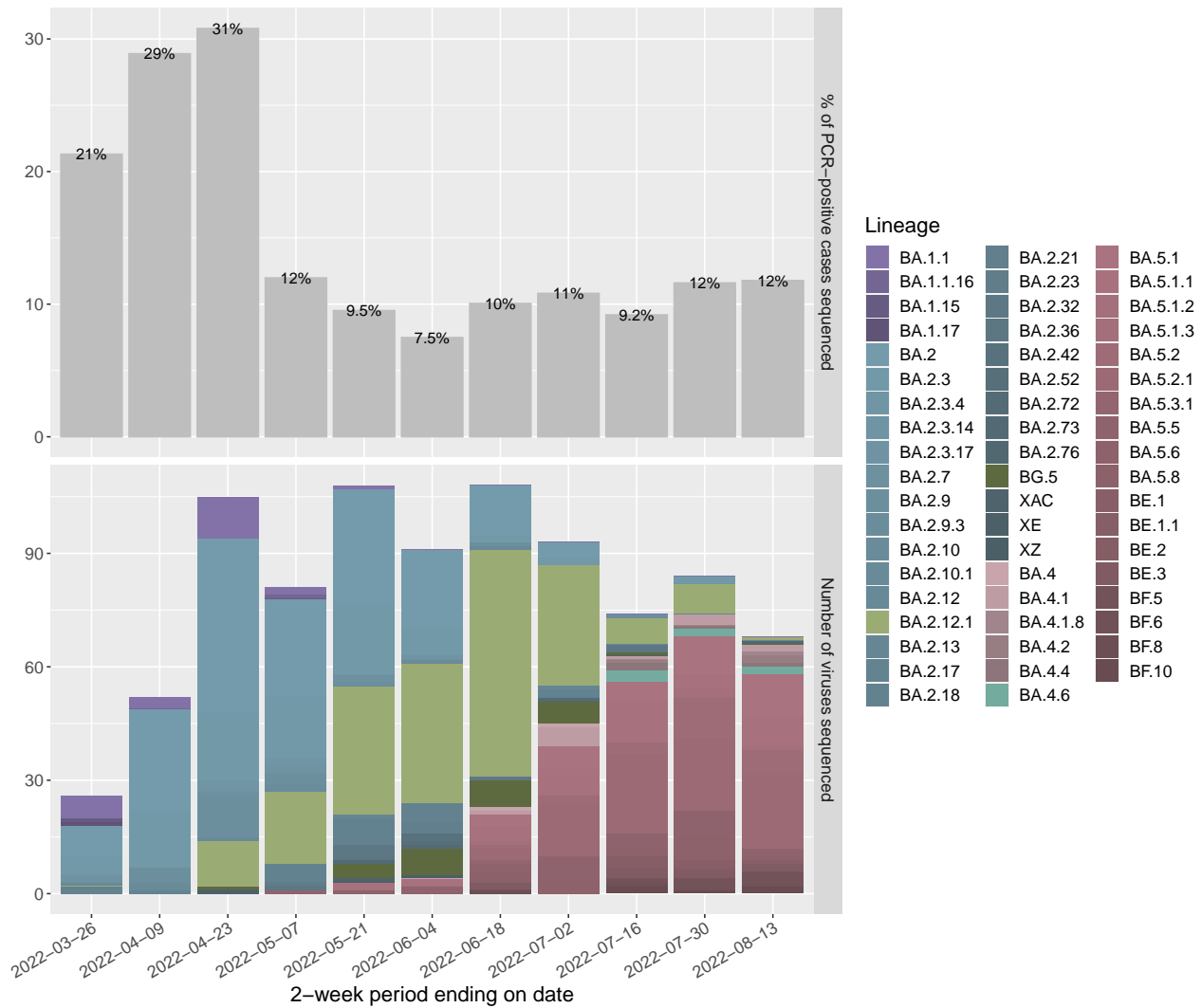


Figure Notes:

- 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).
- Omicron (BA.* + BE.* + BF.* + BG.* + XE + XZ + XAC) is a *Variant of Concern*.
- The gray bar graph (top) shows the percentage of PCR-positive cases from each 2-week time interval that were sequenced.
- The color bar graph (bottom) shows the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week time interval.
- 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

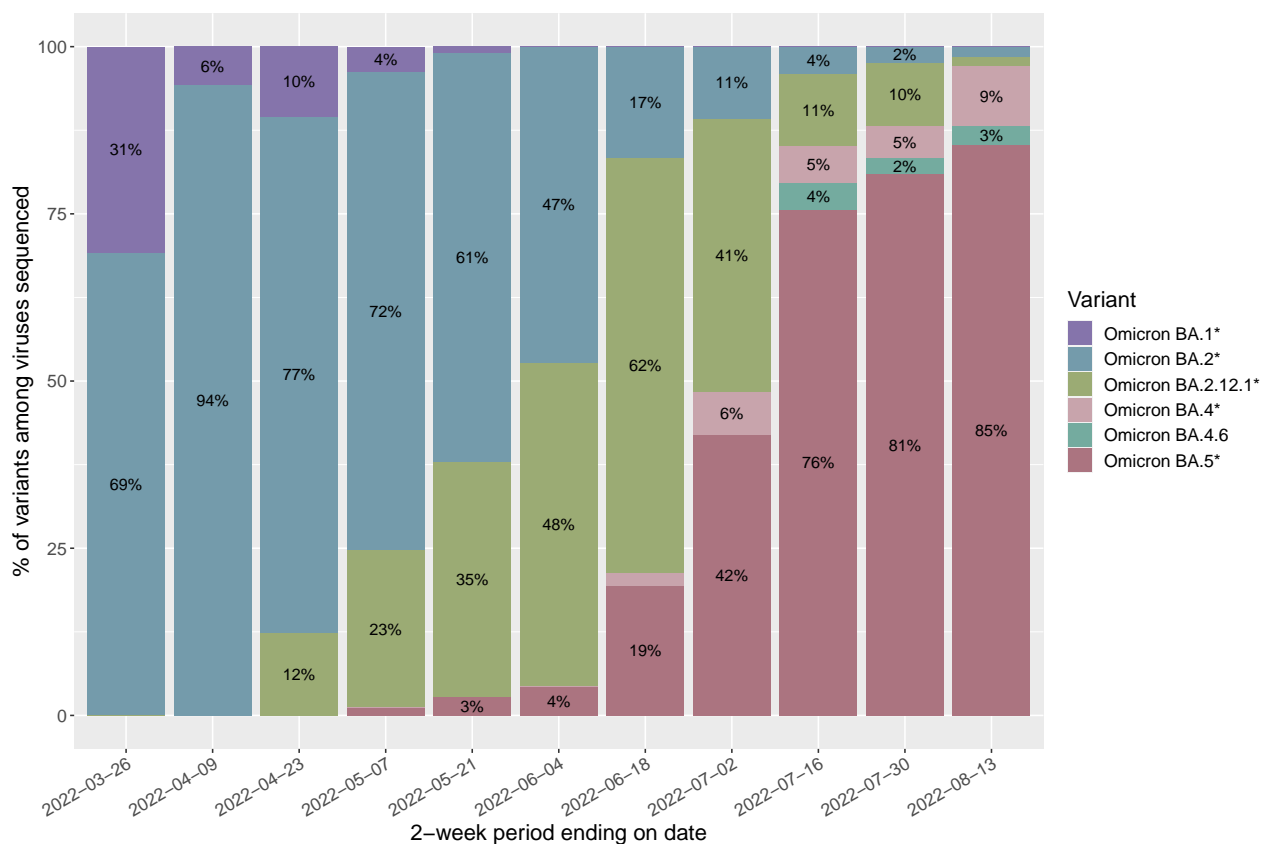


Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Hawaii County, grouped in 2-week intervals (based on the date of specimen collection); percentage estimates are rounded to the nearest whole number.
- 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 specimens that were selected randomly for the purpose of surveillance of community variants, to avoid over-representing the specimens 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.
- Omicron BA.1* includes BA.1 and its sub-lineages (BA.1.*).
- Omicron BA.2* includes BA.2, its sub-lineages (BA.2.*), XE, XZ, and XAC; excludes BA.2.12.1*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*).
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, and BF.*).

Variants of Concern in Hawaii County

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			1185		
	BA.2.12.1	USA/Canada	210	13 Apr 2022	04 Aug 2022
	BA.2	South Africa/Botswana	179	19 Jan 2022	27 Jun 2022
	BA.1.1	South Africa/Botswana	159	13 Dec 2021	09 May 2022
	BA.2.3	Philippines	89	30 Jan 2022	22 Jul 2022
	BA.5.2.1	South Africa/UK/USA	77	12 Jun 2022	11 Aug 2022
	BA.1.1.2	Japan	64	10 Dec 2021	01 Mar 2022
	Other	Various	57	Apr 2022	May 2022
	BA.5.1.1	USA	38	14 May 2022	07 Aug 2022
	BA.5.1	Portugal	35	07 Jun 2022	10 Aug 2022
	BG.5	USA	26	13 Apr 2022	12 Jul 2022
	BA.1	South Africa/Botswana	25	17 Dec 2021	02 Mar 2022
	BA.5.5	USA	25	03 May 2022	02 Aug 2022
	BA.1.15	USA	24	10 Dec 2021	22 Mar 2022
	BA.5.2	South Africa/UK/USA	23	17 Jun 2022	12 Aug 2022
	BA.2.9	Europe	21	28 Mar 2022	03 Jul 2022
	BA.2.18	UK	19	24 Apr 2022	24 Jun 2022
	BA.5.6	USA	14	21 May 2022	09 Aug 2022
	BA.2.3.17	USA	12	24 Feb 2022	05 May 2022
	BA.4.1	South Africa	12	16 Jun 2022	08 Aug 2022
	BA.1.1.16	Canada/USA	9	28 Jan 2022	27 Apr 2022
	BE.3	USA	9	08 Jun 2022	01 Aug 2022
	BF.5	Israel	8	07 Jul 2022	10 Aug 2022
	BA.1.1.18	USA	7	15 Dec 2021	02 Mar 2022
	BA.1.17.2	Europe	7	30 Dec 2021	25 Feb 2022
	BA.2.32	Indonesia	7	06 May 2022	16 Jul 2022
	BA.4.6	USA/UK/Denmark	7	11 Jul 2022	08 Aug 2022
	BA.1.20	USA	5	21 Dec 2021	03 Jan 2022
	BF.10	USA	5	06 Jul 2022	09 Aug 2022
	BA.2.10.1	Singapore	4	23 Feb 2022	13 Apr 2022
	BA.2.3.4	Canada	4	19 Apr 2022	03 May 2022
	BA.4.4	USA	4	12 Jul 2022	09 Aug 2022

Table Notes:

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.3% of the cumulative Omicron sequences from Hawaii County.

Variants Being Monitored in Hawaii County

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			66		
	B.1.1.7	UK	55	22 Feb 2021	16 Jul 2021
	Q.3	USA	11	21 Mar 2021	20 Aug 2021
Gamma			16		
	P.1.10	USA	12	27 May 2021	13 Jun 2021
	P.1	Brazil	3	May 2021	Jun 2021
	P.1.17	USA/Mexico	1	Jun 2021	Jun 2021
Delta			737		
	AY.44	USA	209	11 Jun 2021	16 Dec 2021
	AY.3	USA	109	31 Jul 2021	16 Dec 2021
	AY.103	USA	91	21 May 2021	16 Dec 2021
	Other AY.*	Various	74	01 Jul 2021	Oct 2021
	AY.25	USA	52	19 Jul 2021	09 Nov 2021
	AY.100	South Africa/Botswana	41	17 Jul 2021	12 Nov 2021
	AY.46.4	USA	27	21 Jun 2021	06 Dec 2021
	AY.118	USA	26	08 Jul 2021	27 Sep 2021
	AY.25.1	South Africa/Botswana	26	11 Aug 2021	17 Dec 2021
	AY.117	USA	24	15 Aug 2021	17 Nov 2021
	AY.119	USA	24	03 Aug 2021	24 Nov 2021
	AY.26	USA/Mexico	16	24 Jun 2021	03 Dec 2021
	AY.122	South Africa/Botswana	15	19 Jul 2021	22 Sep 2021
	B.1.617.2	India	3	Jul 2021	Nov 2021
Epsilon			44		
	B.1.429	USA	38	25 Jan 2021	26 May 2021
	B.1.427	USA	6	04 Feb 2021	17 May 2021
Iota	B.1.526	USA	73	06 Feb 2021	07 Jul 2021
Mu	B.1.621	Columbia	1	Jun 2021	Jun 2021

Table Notes:

- Lineage “Other AY.*” represents an aggregation of different AY.* lineages in which each alone accounts for <2% of the cumulative Delta sequences from Hawaii County.

Kauai County

Total variants identified

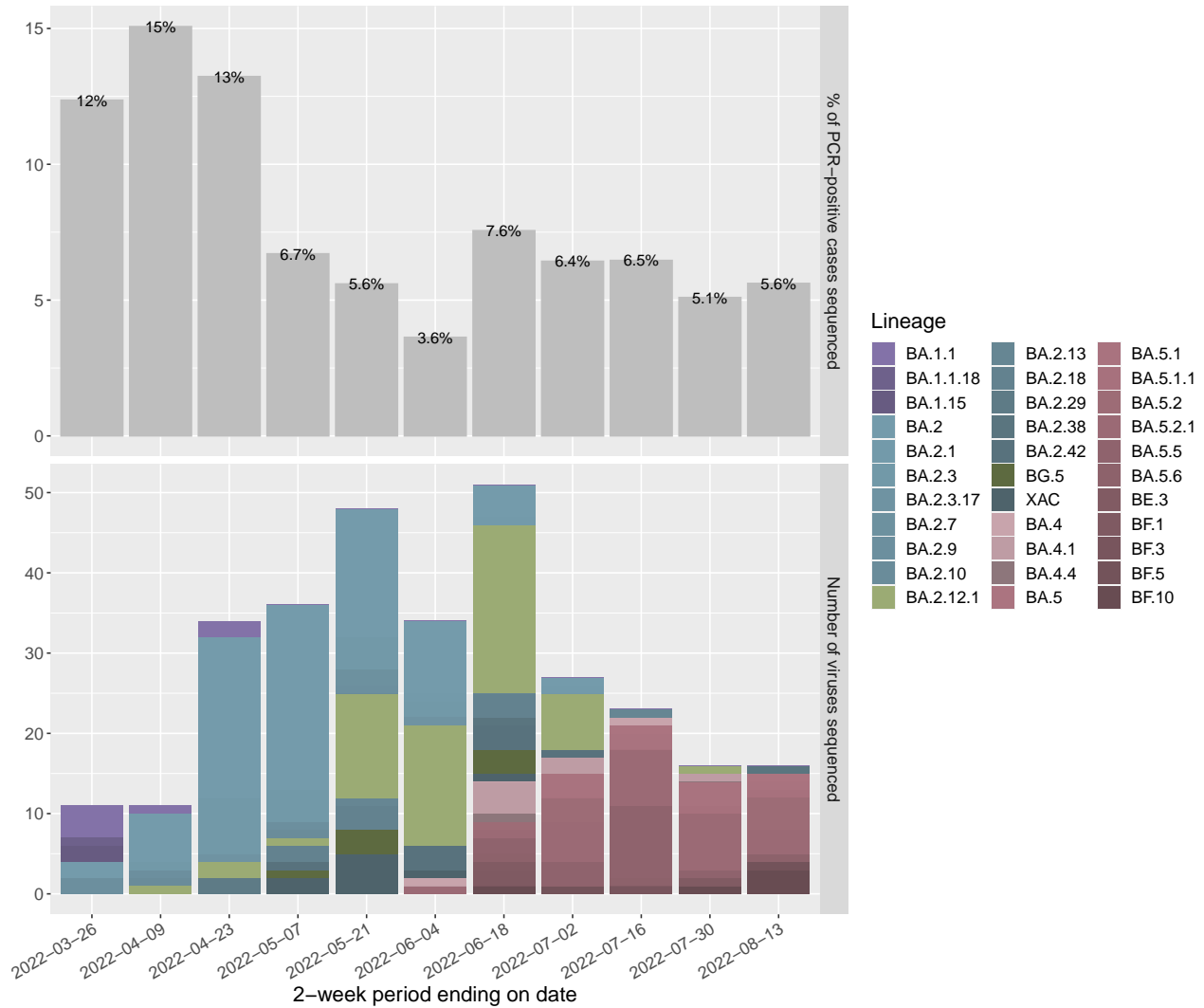


Figure Notes:

- 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).
- Omicron (BA.* + BE.* + BF.* + BG.* + XAC) is a *Variant of Concern*.
- The gray bar graph (top) shows the percentage of PCR-positive cases from each 2-week time interval that were sequenced.
- The color bar graph (bottom) shows the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week time interval.
- 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

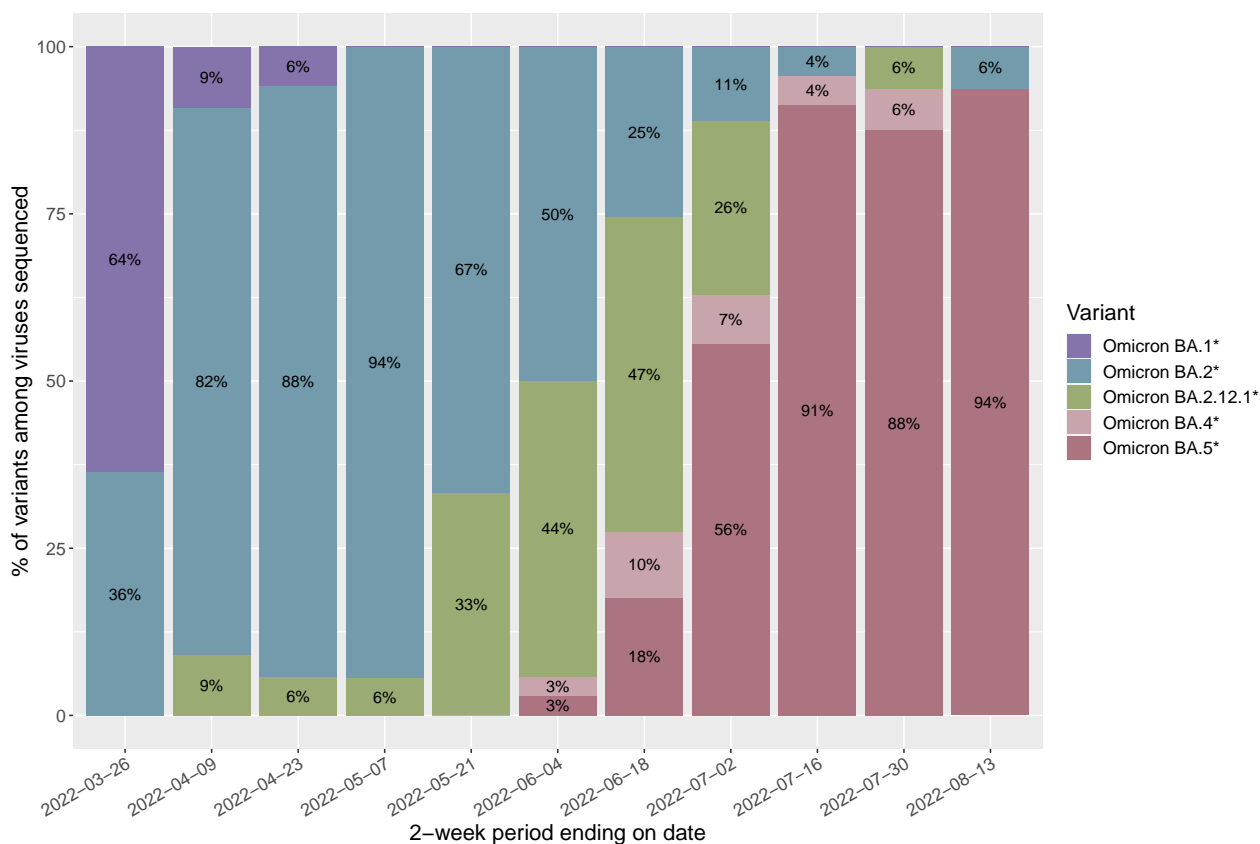


Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Kauai County, grouped in 2-week intervals (based on the date of specimen collection); percentage estimates are rounded to the nearest whole number.
- 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 specimens that were selected randomly for the purpose of surveillance of community variants, to avoid over-representing the specimens 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.
- Omicron BA.1* includes BA.1 and its sub-lineages (BA.1.*).
- Omicron BA.2* includes BA.2, its sub-lineages (BA.2.*), and XAC; excludes BA.2.12.1*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*).
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, and BF.*).

Variants of Concern in Kauai County

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			407		
	BA.2	South Africa/Botswana	81	17 Mar 2022	28 Jun 2022
	BA.1.1	South Africa/Botswana	63	15 Dec 2021	19 Apr 2022
	BA.2.12.1	USA/Canada	61	30 Mar 2022	27 Jul 2022
	BA.5.2.1	South Africa/UK/USA	24	03 Jun 2022	09 Aug 2022
	BA.2.3	Philippines	19	09 Mar 2022	24 May 2022
	BA.5.5	USA	15	13 Jun 2022	27 Jul 2022
	BA.1.15	USA	13	28 Dec 2021	23 Mar 2022
	BA.1	South Africa/Botswana	12	16 Dec 2021	07 Feb 2022
	BA.5.1	Portugal	9	23 Jun 2022	01 Aug 2022
	XAC	USA/Canada	9	28 Apr 2022	14 Jun 2022
	BA.2.42	Australia	8	07 May 2022	02 Jul 2022
	BA.2.18	UK	8	24 Apr 2022	16 Jun 2022
	BA.1.1.18	USA	8	28 Dec 2021	21 Mar 2022
	BA.5.2	South Africa/UK/USA	8	13 Jun 2022	10 Aug 2022
	BA.1.1.2	Japan	8	15 Dec 2021	09 Feb 2022
	BG.5	USA	7	03 May 2022	13 Jun 2022
	BA.4.1	South Africa	7	08 Jun 2022	26 Jul 2022
	BA.2.9	Europe	5	17 Mar 2022	09 May 2022
	BF.10	USA	5	13 Jun 2022	11 Aug 2022
	BA.5.6	USA	3	Jun 2022	Aug 2022
	BA.2.1	UK	3	May 2022	Jun 2022
	BA.2.7	USA	2	May 2022	May 2022
	BF.5	Israel	2	Jun 2022	Aug 2022
	BA.2.10	Asia	2	Apr 2022	May 2022
	BA.5	South Africa	2	Jul 2022	Aug 2022
	BA.2.38	India	2	Jun 2022	Aug 2022
	BA.5.1.1	USA	2	Jul 2022	Aug 2022
	BA.2.3.17	USA	2	Apr 2022	May 2022
	BA.1.18	Europe/North America	2	Dec 2021	Jan 2022
	BA.4	South Africa	2	Jun 2022	Jul 2022
	BA.2.29	Japan	2	Apr 2022	Apr 2022
	BE.3	USA	2	Jun 2022	Jul 2022
	BF.1	Denmark/Spain/UK	2	Jun 2022	Jun 2022
	BA.2.13	Europe	2	May 2022	Jul 2022
	BA.1.20	USA	1	Jan 2022	Jan 2022
	BA.1.1.14	Europe	1	Feb 2022	Feb 2022
	BF.3	India	1	Jul 2022	Jul 2022
	BA.1.17.2	Europe	1	Feb 2022	Feb 2022
	BA.4.4	USA	1	Jun 2022	Jun 2022

Variants Being Monitored in Kauai County

Variant	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			19		
	B.1.1.7	UK	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	USA	1	May 2021	May 2021
Delta			233		
	AY.25	USA	70	16 Jul 2021	10 Nov 2021
	AY.119	USA	35	28 Aug 2021	21 Dec 2021
	AY.44	USA	34	01 Jul 2021	21 Dec 2021
	Other AY.*	Various	25	Aug 2021	Sep 2021
	AY.47	USA	19	27 Jul 2021	29 Nov 2021
	AY.103	USA	16	01 Aug 2021	15 Dec 2021
	AY.1	Europe	10	09 Aug 2021	23 Aug 2021
	AY.3	USA	8	30 Sep 2021	15 Dec 2021
	AY.54	USA	8	06 Jul 2021	09 Nov 2021
	AY.67	South Africa/Botswana	6	06 Jun 2021	29 Jun 2021
	B.1.617.2	India	2	Sep 2021	Oct 2021
Epsilon			30		
	B.1.429	USA	28	07 Jan 2021	08 May 2021
	B.1.427	USA	2	Apr 2021	Apr 2021
Iota	B.1.526	USA	1	Apr 2021	Apr 2021
Mu	B.1.621	Columbia	1	Jul 2021	Jul 2021

Table Notes:

- Lineage “Other AY.*” represents an aggregation of different AY.* lineages in which each alone accounts for <2% of the cumulative Delta sequences from Kauai County.