

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

Hawaii Department of Health

2022-12-06

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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. A viral genome that contains one or more mutations is referred to as a variant.

Collecting the genome sequences of virus specimens can reveal information about the relatedness of viruses and the similarities shared among groups of viruses. A closely related group of viruses derived from a common ancestor is referred to as a lineage.

Sequencing of viral genomes allows scientists to better understand virus transmission and evolution, and how each may impact public health. Sequencing also allows public health officials to monitor and characterize outbreaks and clusters, detect new variants, and conduct genomic surveillance (analysis of trends, similarities, and differences in circulating variants).

Some SARS-CoV-2 variants are classified by the Centers for Disease Control and Prevention (CDC) as Variants 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 that is updated as new evidence becomes available (<https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html>).

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-positive 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. 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, thus 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, more than 6.5% 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 |
|--------------------------------------------|-----------------------------------------------|--------------|-----------------|
| State Laboratories Division | | 15987 | 73.785% |
| Centers for Disease Control and Prevention | National SARS-CoV-2 Strain Surveillance (NS3) | 412 | 1.902% |
| | Quest Diagnostics Incorporated | 1345 | 6.208% |
| | Laboratory Corporation of America | 1554 | 7.172% |
| | Aegis Sciences Corporation | 379 | 1.749% |
| | Helix/Illumina | 181 | 0.835% |
| | Infinity Biologix | 16 | 0.074% |
| | Mako Medical | 20 | 0.092% |
| | Fulgent Genetics | 8 | 0.037% |
| Tripler Army Medical Center | | 683 | 3.152% |
| University of Hawaii | | 861 | 3.974% |
| Aegis Sciences Corporation* | | 221 | 1.020% |
| Total | | 21667 | 100.000% |

County distribution of genomes sequenced by:

State Laboratories Division (since Jan 1, 2021)

| Honolulu County | Maui County | Hawaii County | Kauai County | unknown | Total |
|-----------------|-------------|---------------|--------------|---------|-------|
| 9037 | 3287 | 2551 | 761 | 351 | 15987 |

University of Hawaii (Jan 22, 2022 – Aug 23, 2022)

| Honolulu County | Maui County | Hawaii County | Kauai County | unknown | Total |
|-----------------|-------------|---------------|--------------|---------|-------|
| 508 | 67 | 221 | 17 | 48 | 861 |

Aegis Sciences Corporation* (since Sep 14, 2022)

| Honolulu County | Maui County | Hawaii County | Kauai County | unknown | Total |
|-----------------|-------------|---------------|--------------|---------|-------|
| 54 | 11 | 3 | 0 | 153 | 221 |

Notes:

- In support of genomic surveillance efforts, PCR-positive specimens are routinely provided to State Laboratories Division (SLD) by commercial/clinical laboratories that operate throughout the State of Hawaii, including Clinical Labs of Hawaii (CLH), Diagnostic Laboratory Services, Inc. (DLS), Kaiser Permanente Hawaii, and S&G Labs Hawaii. The specimens are then processed, sequenced, and analyzed by the Laboratory Preparedness and Response Branch (LPRB) within SLD.
- In coordination with SLD, the School of Life Sciences, University of Hawaii at Manoa provided sequencing and analysis services for 861 PCR-positive specimens processed by the LPRB.
- As of September 14, 2022, Aegis Sciences Corporation* reports SARS-CoV-2 genome sequences independently of the Centers for Disease Control and Prevention (CDC).
- County information is not provided for specimens sequenced by CDC programs/partners and by Tripler Army Medical Center.

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 reported 357 additional SARS-CoV-2 genome sequences since the previous report was generated (11/22/2022).
- CDC programs/partners reported 32 additional SARS-CoV-2 genome sequences from the State of Hawaii since the previous report was generated.
- Aegis Sciences Corporation reported 5 additional SARS-CoV-2 genome sequences from the State of Hawaii since the previous report was generated.
- SARS-CoV-2 variant nomenclature is defined by a World Health Organization (WHO) label (letters of the Greek Alphabet, e.g., 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, e.g., 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/>.
- In this report, an asterisk (*) following a lineage designation (e.g., BA.5*) signifies inclusion of the respective lineage (e.g., BA.5) and its sub-lineages (or descendants, e.g., BA.5.*) unless otherwise specified. An asterisk following the dot of a lineage designation (e.g., BA.*, BA.5.*, BA.5.1.*) signifies only inclusion of lineages with an additional numerical suffix that follows the respective dot.
- Lineages called using pangolin v4.1.3, pangolin-data v1.16, and usher v0.5.4.
- 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 B.1.1.529 have BA.* designations (e.g., BA.1, BA.2, BA.5). Primary sub-lineages of BA.2.12.1, BA.2.3.20, BA.2.75.1, BA.2.75.3, BA.2.75.4, BA.2.75.5, BA.2.75.6, BA.2.75.9, BA.5.1.10, BA.5.1.21, BA.5.2.1, BA.5.2.6, BA.5.2.24, and BA.5.3.1 have BG.*, CM.*, BL.*, BM.*, BR.*, BN.*, BY.*, CB.*, BK.*, BT.*, BF.*, CP.*, CK.*, and BE.* designations, respectively. Primary sub-lineages of BE.1.1.1 and BM.4.1.1 have BQ.* and CH.* designations, respectively. XAP, XAS, and XBB are Omicron recombinants; a recombinant forms when the genomes of two lineages (infecting a person simultaneously) undergo recombination during the viral replication process, producing a variant that is distinct from both parent lineages.
- BA.5* (BA.5 and its sub-lineages, except BA.5.2.6 and BF.7) represents ~34% of the estimated variant proportions in the State of Hawaii for the latest 2-week collection period (11/6/2022 – 11/19/2022).
- BQ.1* and BQ.1.1* combined represents ~42% of the estimated variant proportions in the State of Hawaii for the latest 2-week collection period.
- Estimated variant proportions may not be truly representative in counties with low sequencing numbers (e.g., Kauai County).
- Estimated variant proportions at the national level can be found at <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>.

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 VOC and VBM 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 in the State of Hawaii

Omicron (B.1.1.529, BA.*, BE.*, BF.*, BG.*, BK.*, BL.*, BM.*, BN.*, BQ.*, BR.*, BT.*, BY.*, CB.*, CH.*, CK.*, CM.*, CP.*, XAP, XAS, and XBB* 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 have been associated with increased infectivity and decreased neutralizing activity of monoclonal antibodies and convalescent sera. 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 (e.g., BA.1, BA.2, BA.5). Primary sub-lineages of BA.2.12.1, BA.2.3.20, BA.2.75.1, BA.2.75.3, BA.2.75.4, BA.2.75.5, BA.2.75.6, BA.2.75.9, BA.5.1.10, BA.5.1.21, BA.5.2.1, BA.5.2.6, BA.5.2.24, and BA.5.3.1 have BG.*, CM.*, BL.*, BM.*, BR.*, BN.*, BY.*, CB.*, BK.*, BT.*, BF.*, CP.*, CK.*, and BE.* designations, respectively. Primary sub-lineages of BE.1.1.1 and BM.4.1.1 have BQ.* and CH.* designations, respectively. SARS-CoV-2 recombinants that receive a PANGO classification have an X* lineage designation. A recombinant forms when the genomes of two lineages (infecting a person simultaneously) undergo recombination during the viral replication process, producing a variant that is distinct from both parent lineages. XAP is derived from BA.1* and BA.2*, XAS is derived from BA.2* and BA.5*, and XBB is derived from BJ.1 (a primary sub-lineage of BA.2.10.1) and BM.1.1.1. Omicron variants correspond to Nextstrain clades 21M, 21K, 21L, 22A, 22B, 22C, 22D, 22E, and 22F (<https://ncov-clades-schema.vercel.app/>).

Due to acquired mutations within the spike protein, each successively dominant Omicron variant/sub-variant (BA.1*, BA.2*, BA.2.12.1*, BA.5*, and BQ.1*/BQ.1.1*) has been increasingly better at evading antibodies elicited by vaccinations and/or prior infections; notable information regarding each of their defining mutations can be found at <https://covariants.org/variants> (21K, 21L, 22C, 22B, and 22E, respectively). Furthermore, **the majority of circulating Omicron sub-variants (e.g., BQ.1, BQ.1.1, BA.4.6, BA.5.2.6, BF.7, BA.2.75.2) contain spike mutations shown to confer resistance to currently used anti-SARS-CoV-2 monoclonal antibodies** (<https://www.covid19treatmentguidelines.nih.gov/therapies/statement-on-omicron-subvariants/>).

Variants Being Monitored in the State of Hawaii

Alpha (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 virus. The Alpha variant corresponds to Nextstrain clade 20I.

Beta (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 (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 (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 spike mutation shown to escape neutralization by monoclonal antibodies and some convalescent sera, as well as a few additional spike mutations predicted to have functional consequences. B.1.617.2 is the parent lineage of Delta; sub-lineages of Delta have the AY.* designation. Delta variants correspond to Nextstrain clades 21A, 21I, and 21J.

Epsilon (B.1.429 and B.1.427 lineages)

The closely related lineages, B.1.429 and B.1.427, were first identified in California. The WHO labeled them “Epsilon” on May 31, 2021. This variant is associated with increased viral shedding compared to the original virus, and contains the L452R spike mutation shown to escape neutralization by monoclonal antibodies and some convalescent sera. The Epsilon variant corresponds to Nextstrain clade 21C.

Zeta (P.2 lineage)

P.2 was first identified in Brazil and contains the E484K spike mutation, 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 (B.1.526 lineage)

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 genomes (but not all) of this variant contain the E484K spike mutation. The Iota variant corresponds to Nextstrain clade 21F.

Mu (B.1.621 and B.1.621.1 lineages)

Lineage B.1.621 was first identified in Columbia in Jan 2021 and contains some spike mutations in common with the Beta (B.1.351) and Gamma (P.1) variants that have been associated with increased transmissibility (N501Y) and partial antibody escape (E484K). The MU variant corresponds to Nextstrain clade 21H.

State of Hawaii

Total variants identified

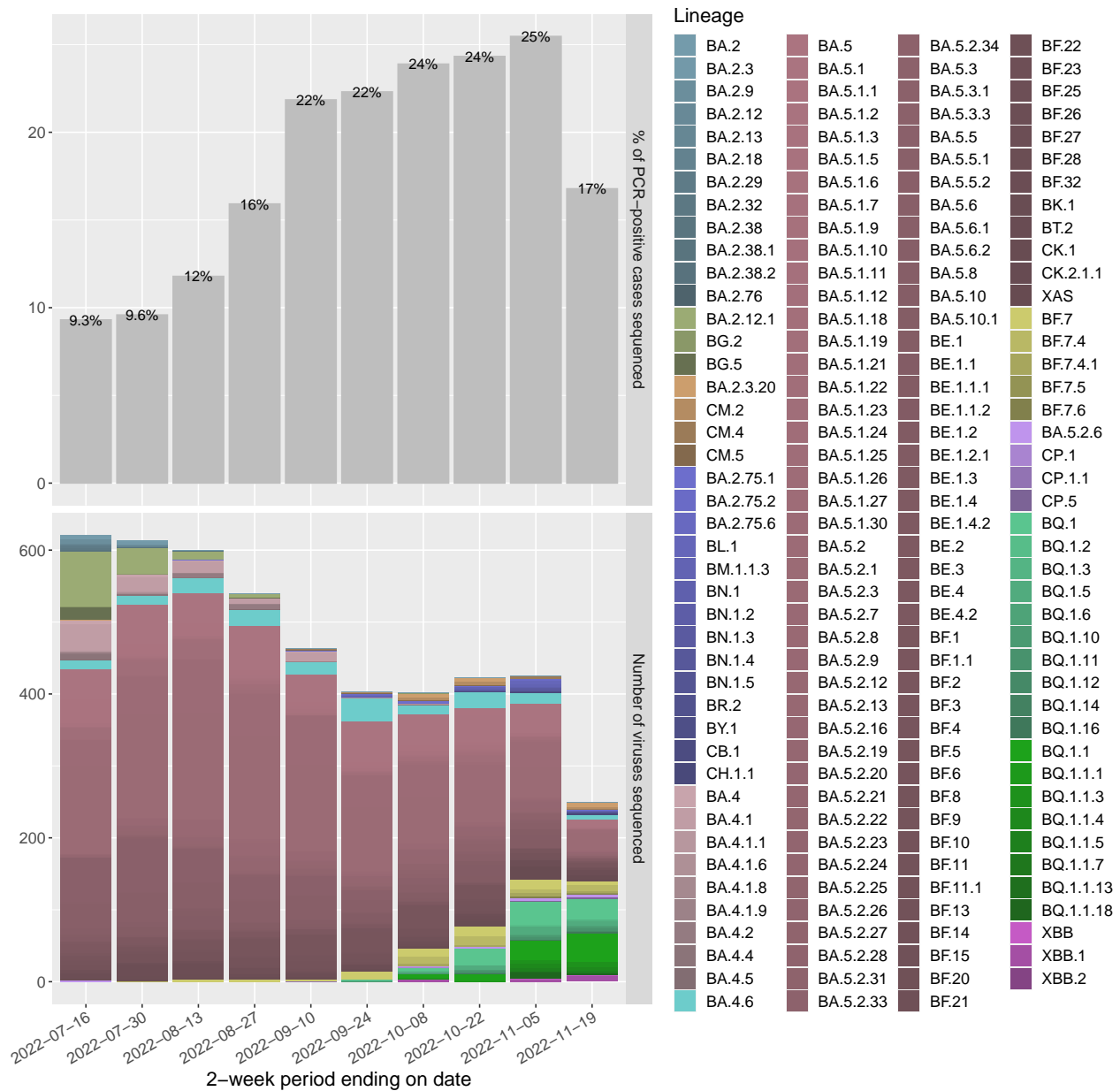


Figure Notes:

- Graph depicts the total number of variants by lineage identified in the State of Hawaii in each 2-week period ending on the date shown (date represents when the specimen was collected from a patient).
- Upper (gray) bars represent the percentage of PCR-positive cases from each 2-week period that were sequenced.
- Lower (color) bars represent the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week period.
- 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 variant proportions in the State of Hawaii

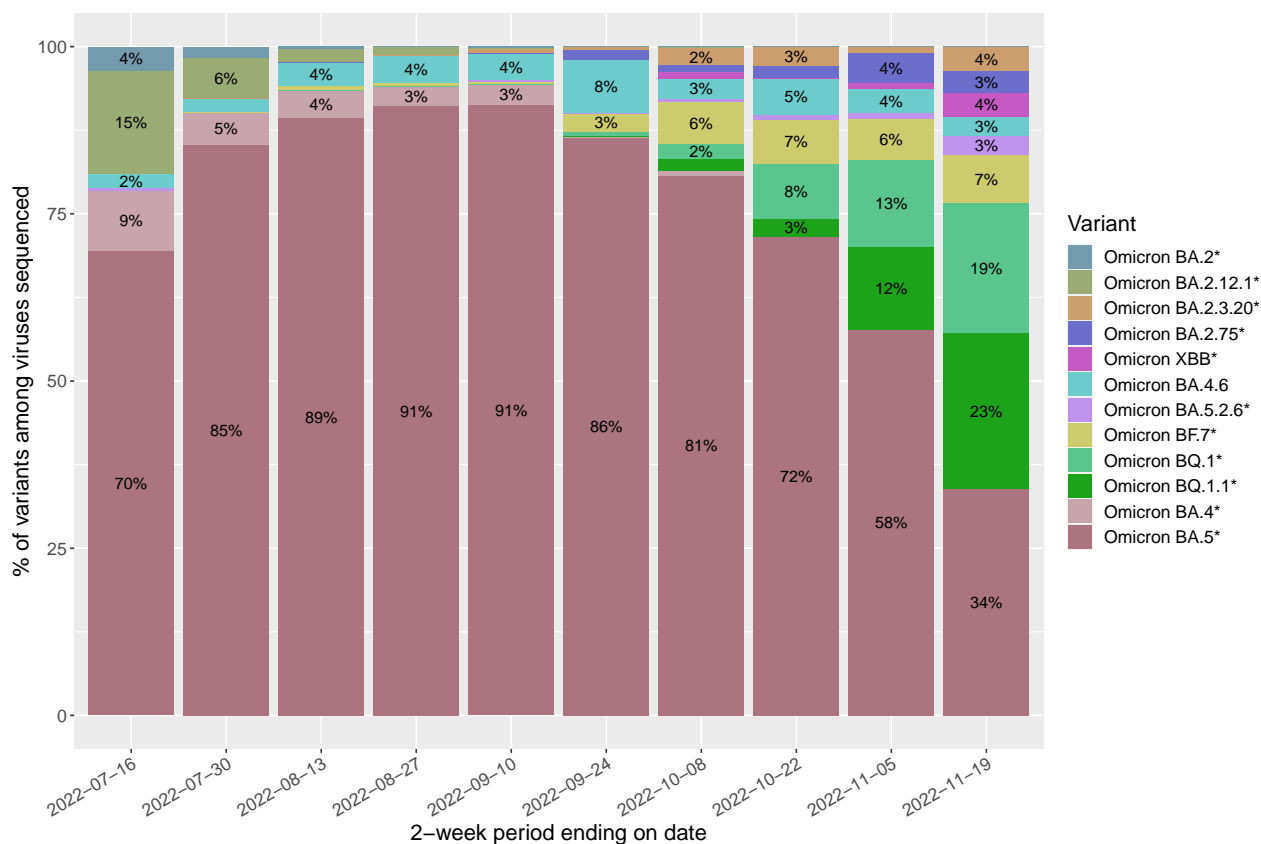


Figure Notes:

- Graph depicts percentage estimates of SARS-CoV-2 variants circulating in the State of Hawaii, grouped in 2-week periods (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. This graph was generated only counting specimens that were selected randomly for the purpose of surveillance.
- 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, thus trends based on historical data can change over time.
- Omicron BA.2* includes BA.2 and its sub-lineages (BA.2.*); excludes BA.2.3.20*, BA.2.12.1*, and BA.2.75*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*).
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.2.75* includes BA.2.75 and its sub-lineages (BA.2.75.*, BL.*, BM.*, BN.*, BR.*, BY.*, CB.*, CH.*).
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.5* includes BA.5, its sub-lineages (BA.5.*, BE.*, BF.*, BK.*, BT.*, CK.*), and XAS; excludes BA.5.2.6* and BF.7*.
- Omicron BA.5.2.6* includes BA.5.2.6 and its sub-lineages (CP.*).
- Omicron BF.7* includes BF.7 and its sub-lineages (BF.7.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*).
- Omicron XBB* includes XBB and its sub-lineages (XBB.*).

Variants of Concern in the State of Hawaii

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|-----------|-------------------------|----------------------|-----------------------------------|--------------------------------------|
| Omicron | | | 13715 | | |
| | BA.1.1 | South Africa/Botswana | 1740 | 27 Nov 2021 | 19 Jun 2022 |
| | Other | Various | 1627 | 01 Feb 2022 | 31 Oct 2022 |
| | BA.2.12.1 | USA/Canada | 1614 | 21 Mar 2022 | 29 Sep 2022 |
| | BA.2 | South Africa/Botswana | 1573 | 18 Jan 2022 | 06 Sep 2022 |
| | BA.5.2.1 | South Africa/UK/USA | 1015 | 31 May 2022 | 19 Nov 2022 |
| | BA.2.3 | Philippines | 839 | 06 Jan 2022 | 22 Jul 2022 |
| | BA.1.1.2 | Japan | 569 | 06 Dec 2021 | 01 Apr 2022 |
| | BG.5 | USA | 533 | 09 Apr 2022 | 21 Aug 2022 |
| | BA.5.2 | South Africa/UK/USA | 468 | 17 Jun 2022 | 17 Nov 2022 |
| | BA.1.15 | USA | 426 | 30 Nov 2021 | 09 Apr 2022 |
| | BA.5.1 | Portugal | 422 | 07 Jun 2022 | 18 Nov 2022 |
| | BA.5.5 | USA | 360 | 03 May 2022 | 28 Oct 2022 |
| | BA.5.6 | USA | 252 | 21 May 2022 | 09 Nov 2022 |
| | BA.2.3.17 | USA | 208 | 25 Jan 2022 | 15 Jun 2022 |
| | BA.1 | South Africa/Botswana | 187 | 07 Dec 2021 | 11 Apr 2022 |
| | BA.4.6 | USA/UK/Denmark | 178 | 21 Jun 2022 | 15 Nov 2022 |
| | BF.5 | Israel | 170 | 16 Jun 2022 | 15 Nov 2022 |
| | BA.4.1 | South Africa | 167 | 04 May 2022 | 30 Sep 2022 |
| | BA.2.9 | Europe | 164 | 25 Jan 2022 | 25 Jul 2022 |
| | BA.5.1.1 | USA | 161 | 14 May 2022 | 13 Oct 2022 |
| | BA.1.1.18 | USA | 95 | 10 Dec 2021 | 30 Mar 2022 |
| | BA.2.18 | UK | 93 | 21 Mar 2022 | 11 Jul 2022 |
| | BF.10 | USA | 90 | 05 Jun 2022 | 31 Oct 2022 |
| | BQ.1 | Nigeria | 88 | 16 Sep 2022 | 18 Nov 2022 |
| | BA.5.1.23 | Spain | 83 | 23 Jun 2022 | 27 Oct 2022 |
| | BQ.1.1 | Global | 80 | 27 Sep 2022 | 19 Nov 2022 |
| | BA.5.2.9 | USA | 79 | 20 Jun 2022 | 15 Nov 2022 |
| | BE.1.1 | Germany | 67 | 18 Jun 2022 | 10 Nov 2022 |
| | BF.7 | UK/Belgium/Denmark | 66 | 19 Jul 2022 | 16 Nov 2022 |
| | BA.5.2.21 | Indonesia | 63 | 07 Jul 2022 | 14 Nov 2022 |
| | BE.1 | South Africa/UK/Austria | 51 | 30 May 2022 | 02 Nov 2022 |
| | BA.2.3.14 | South Korea | 49 | 04 Apr 2022 | 30 May 2022 |
| | BE.3 | USA | 48 | 03 Jun 2022 | 17 Oct 2022 |
| | BF.26 | North America | 46 | 13 Jun 2022 | 18 Nov 2022 |
| | BA.1.20 | USA | 44 | 14 Dec 2021 | 28 Feb 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 the State of Hawaii.

Variants Being Monitored in the State of Hawaii

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|------------|-----------------------|----------------------|-----------------------------------|--------------------------------------|
| Alpha | | | 797 | | |
| | B.1.1.7 | UK | 743 | 21 Jan 2021 | 14 Aug 2021 |
| | Q.3 | USA | 52 | 21 Mar 2021 | 02 Sep 2021 |
| | Q.4 | South Africa/Botswana | 2 | 28 Apr 2021 | 29 Apr 2021 |
| Beta | B.1.351 | South Africa | 20 | 16 Feb 2021 | 22 Sep 2021 |
| Gamma | | | 191 | | |
| | P.1.10 | USA | 84 | 24 Apr 2021 | 14 Jul 2021 |
| | P.1 | Brazil | 54 | 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 | 15 | 03 May 2021 | 28 Jun 2021 |
| Delta | | | 5622 | | |
| | AY.103 | USA | 1228 | 21 May 2021 | 12 Jan 2022 |
| | AY.44 | USA | 1039 | 07 Jun 2021 | 19 Jan 2022 |
| | Other AY.* | Various | 612 | 01 Aug 2021 | 30 Jul 2021 |
| | AY.3 | USA | 562 | 24 Jun 2021 | 02 Jan 2022 |
| | AY.25 | USA | 532 | 21 Jun 2021 | 20 Jan 2022 |
| | AY.54 | USA | 367 | 23 Jun 2021 | 21 Nov 2021 |
| | AY.100 | South Africa/Botswana | 197 | 17 Jul 2021 | 12 Dec 2021 |
| | AY.25.1 | South Africa/Botswana | 196 | 08 Jul 2021 | 27 Jan 2022 |
| | AY.1 | Europe | 186 | 30 Jun 2021 | 30 Nov 2021 |
| | AY.119 | USA | 136 | 06 Jul 2021 | 21 Dec 2021 |
| | AY.26 | USA/Mexico | 132 | 07 Jun 2021 | 28 Dec 2021 |
| | AY.117 | USA | 128 | 15 Jul 2021 | 17 Dec 2021 |
| | AY.122 | South Africa/Botswana | 107 | 09 Jul 2021 | 26 Nov 2021 |
| | B.1.617.2 | India | 102 | 28 May 2021 | 16 Dec 2021 |
| | AY.47 | USA | 98 | 21 Jul 2021 | 07 Dec 2021 |
| Epsilon | | | 781 | | |
| | B.1.429 | USA | 722 | 31 Dec 2020 | 03 Jun 2021 |
| | B.1.427 | USA | 59 | 07 Dec 2020 | 05 Jun 2021 |
| Zeta | P.2 | Brazil | 2 | 06 Feb 2021 | 08 Feb 2021 |
| Iota | B.1.526 | USA | 128 | 06 Feb 2021 | 23 Jul 2021 |
| Mu | | | 58 | | |
| | B.1.621 | Columbia | 45 | 03 Jun 2021 | 17 Sep 2021 |
| | B.1.621.1 | USA | 13 | 27 May 2021 | 24 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

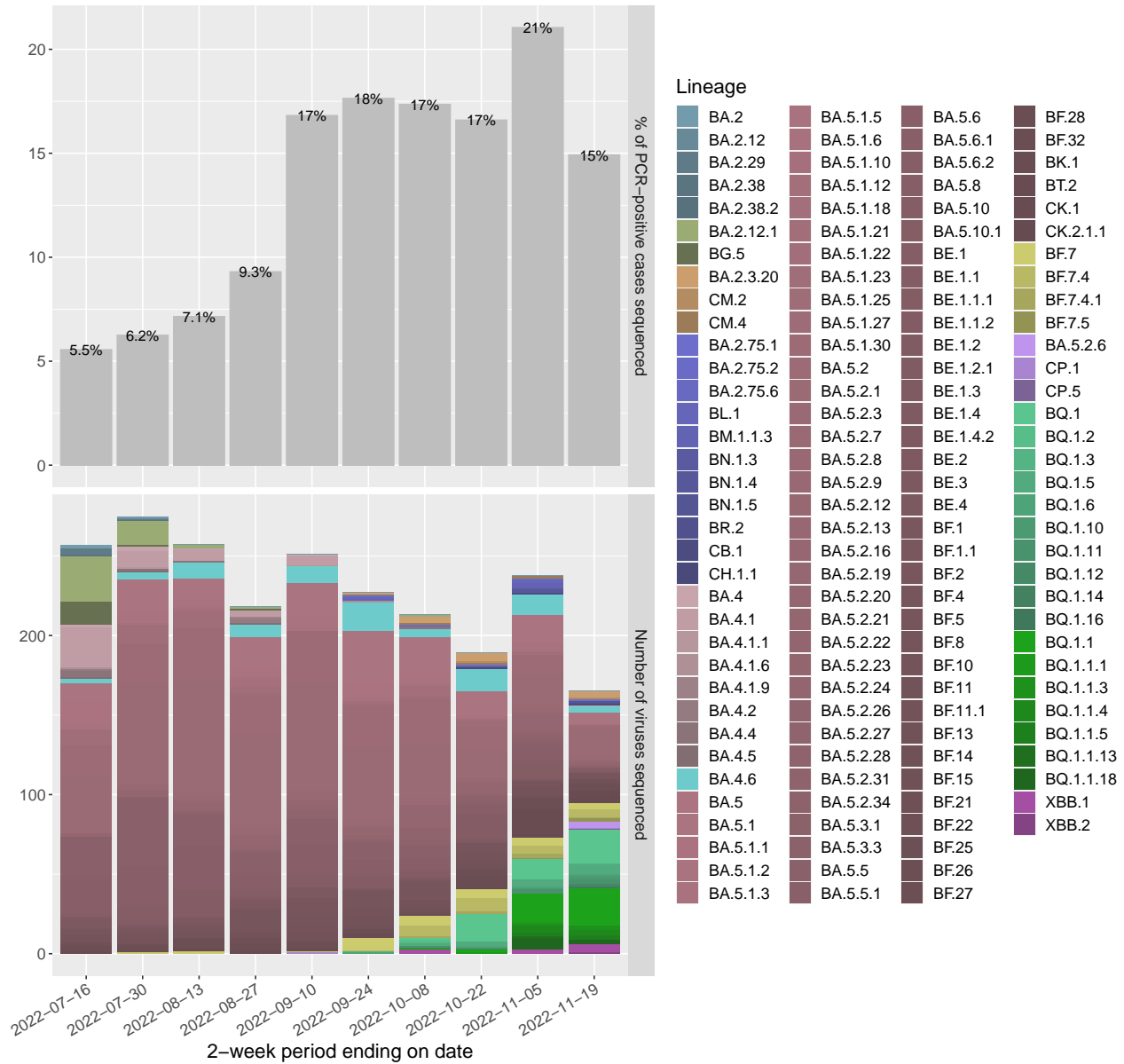


Figure Notes:

- Graph depicts the total number of variants by lineage identified in Honolulu County in each 2-week period ending on the date shown (date represents when the specimen was collected from a patient).
- Upper (gray) bars represent the percentage of PCR-positive cases from each 2-week period that were sequenced.
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- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.

Estimated variant proportions in Honolulu County

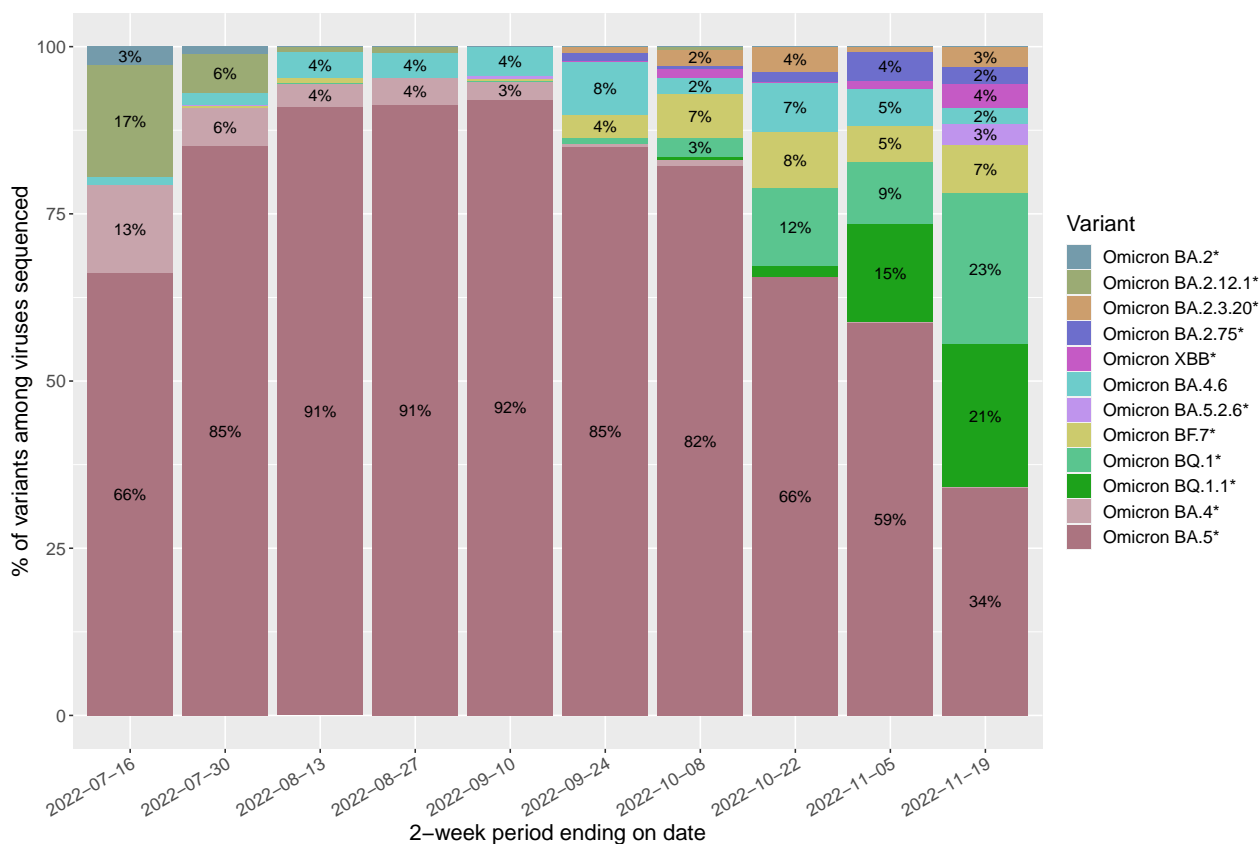


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- Sequencing of certain specimens can be delayed for technical reasons. Therefore, the dataset used for this report is dynamic and specimens that are newly sequenced will be added to the dataset as sequencing occurs, thus trends based on historical data can change over time.
- Omicron BA.2* includes BA.2 and its sub-lineages (BA.2.*); excludes BA.2.3.20*, BA.2.12.1*, and BA.2.75*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*).
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.2.75* includes BA.2.75 and its sub-lineages (BA.2.75.*, BL.*, BM.*, BN.*, BR.*, BY.*, CB.*, CH.*).
- 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.*, BF.*, BK.*, BT.*, CK.*); excludes BA.5.2.6* and BF.7*.
- Omicron BA.5.2.6* includes BA.5.2.6 and its sub-lineages (CP.*).
- Omicron BF.7* includes BF.7 and its sub-lineages (BF.7.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*).
- Omicron XBB* includes XBB and its sub-lineages (XBB.*).

Variants of Concern in Honolulu County

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|-----------|-----------------------|----------------------|-----------------------------------|--------------------------------------|
| Omicron | | | 5826 | | |
| | Other | Various | 758 | 01 Aug 2022 | 31 Oct 2022 |
| | BA.1.1 | South Africa/Botswana | 683 | 27 Nov 2021 | 11 May 2022 |
| | BA.2 | South Africa/Botswana | 623 | 27 Jan 2022 | 20 Jul 2022 |
| | BA.2.12.1 | USA/Canada | 504 | 21 Mar 2022 | 29 Sep 2022 |
| | BA.5.2.1 | South Africa/UK/USA | 441 | 05 Jun 2022 | 19 Nov 2022 |
| | BA.2.3 | Philippines | 367 | 30 Jan 2022 | 24 Jun 2022 |
| | BG.5 | USA | 303 | 09 Apr 2022 | 21 Aug 2022 |
| | BA.1.1.2 | Japan | 300 | 06 Dec 2021 | 31 Mar 2022 |
| | BA.5.2 | South Africa/UK/USA | 223 | 22 Jun 2022 | 17 Nov 2022 |
| | BA.5.1 | Portugal | 173 | 11 Jun 2022 | 18 Nov 2022 |
| | BA.5.5 | USA | 166 | 29 May 2022 | 28 Oct 2022 |
| | BA.1.15 | USA | 164 | 30 Nov 2021 | 07 Apr 2022 |
| | BA.5.6 | USA | 134 | 18 Jun 2022 | 04 Nov 2022 |
| | BA.2.3.17 | USA | 121 | 05 Feb 2022 | 02 Jun 2022 |
| | BA.4.6 | USA/UK/Denmark | 92 | 26 Jun 2022 | 15 Nov 2022 |
| | BA.4.1 | South Africa | 80 | 22 May 2022 | 04 Sep 2022 |
| | BA.5.1.1 | USA | 75 | 14 May 2022 | 13 Oct 2022 |
| | BA.2.9 | Europe | 70 | 14 Mar 2022 | 29 Jun 2022 |
| | BF.5 | Israel | 60 | 17 Jun 2022 | 15 Nov 2022 |
| | BQ.1 | Nigeria | 52 | 04 Oct 2022 | 18 Nov 2022 |
| | BQ.1.1 | Global | 44 | 07 Oct 2022 | 18 Nov 2022 |
| | BA.1 | South Africa/Botswana | 43 | 07 Dec 2021 | 14 Mar 2022 |
| | BE.1.1 | Germany | 40 | 18 Jun 2022 | 10 Nov 2022 |
| | BF.10 | USA | 38 | 09 Jul 2022 | 31 Oct 2022 |
| | BA.5.1.23 | Spain | 36 | 24 Jun 2022 | 16 Aug 2022 |
| | BA.1.1.18 | USA | 35 | 10 Dec 2021 | 30 Mar 2022 |
| | BA.5.2.21 | Indonesia | 33 | 11 Jul 2022 | 04 Nov 2022 |
| | BF.7 | UK/Belgium/Denmark | 33 | 19 Jul 2022 | 16 Nov 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 |
| | BF.26 | North America | 27 | 04 Jul 2022 | 18 Nov 2022 |
| | BF.7.4 | Europe | 25 | 28 Sep 2022 | 18 Nov 2022 |
| | BA.5.2.20 | Indonesia | 24 | 19 Jul 2022 | 07 Nov 2022 |

Table Notes:

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.4% of the cumulative Omicron sequences from Honolulu County.

Variants Being Monitored in Honolulu County

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|------------|-----------------------|----------------------|-----------------------------------|--------------------------------------|
| Alpha | | | 514 | | |
| | B.1.1.7 | UK | 481 | 21 Jan 2021 | 14 Aug 2021 |
| | Q.3 | USA | 33 | 03 Apr 2021 | 02 Sep 2021 |
| Beta | B.1.351 | South Africa | 17 | 16 Feb 2021 | 22 Sep 2021 |
| Gamma | | | 98 | | |
| | P.1.10 | USA | 53 | 24 Apr 2021 | 13 Jul 2021 |
| | P.1 | Brazil | 15 | 24 Mar 2021 | 11 Jul 2021 |
| | P.1.13 | USA | 15 | 03 May 2021 | 28 Jun 2021 |
| | P.1.17 | USA/Mexico | 14 | 29 Mar 2021 | 20 Jul 2021 |
| | P.1.12 | Peru | 1 | 03 Apr 2021 | 03 Apr 2021 |
| Delta | | | 2635 | | |
| | AY.103 | USA | 732 | 20 Jun 2021 | 18 Dec 2021 |
| | AY.44 | USA | 417 | 07 Jun 2021 | 22 Dec 2021 |
| | Other AY.* | Various | 283 | 01 Aug 2021 | 30 Nov 2021 |
| | AY.54 | USA | 259 | 23 Jun 2021 | 21 Nov 2021 |
| | AY.3 | USA | 237 | 24 Jun 2021 | 17 Dec 2021 |
| | AY.25 | USA | 200 | 21 Jun 2021 | 04 Jan 2022 |
| | AY.1 | Europe | 107 | 30 Jun 2021 | 30 Nov 2021 |
| | AY.100 | South Africa/Botswana | 88 | 23 Jul 2021 | 12 Dec 2021 |
| | AY.117 | USA | 74 | 15 Jul 2021 | 11 Nov 2021 |
| | AY.26 | USA/Mexico | 69 | 07 Jun 2021 | 21 Nov 2021 |
| | AY.25.1 | South Africa/Botswana | 64 | 18 Jul 2021 | 11 Dec 2021 |
| | B.1.617.2 | India | 55 | 28 May 2021 | 25 Oct 2021 |
| | AY.119 | USA | 50 | 06 Jul 2021 | 13 Dec 2021 |
| Epsilon | | | 351 | | |
| | B.1.429 | USA | 320 | 05 Jan 2021 | 29 May 2021 |
| | B.1.427 | USA | 31 | 07 Jan 2021 | 05 Jun 2021 |
| Zeta | P.2 | Brazil | 2 | 06 Feb 2021 | 08 Feb 2021 |
| Iota | B.1.526 | USA | 26 | 08 Feb 2021 | 23 Jul 2021 |
| Mu | | | 25 | | |
| | B.1.621 | Columbia | 19 | 03 Jun 2021 | 28 Jul 2021 |
| | B.1.621.1 | USA | 6 | 27 May 2021 | 24 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

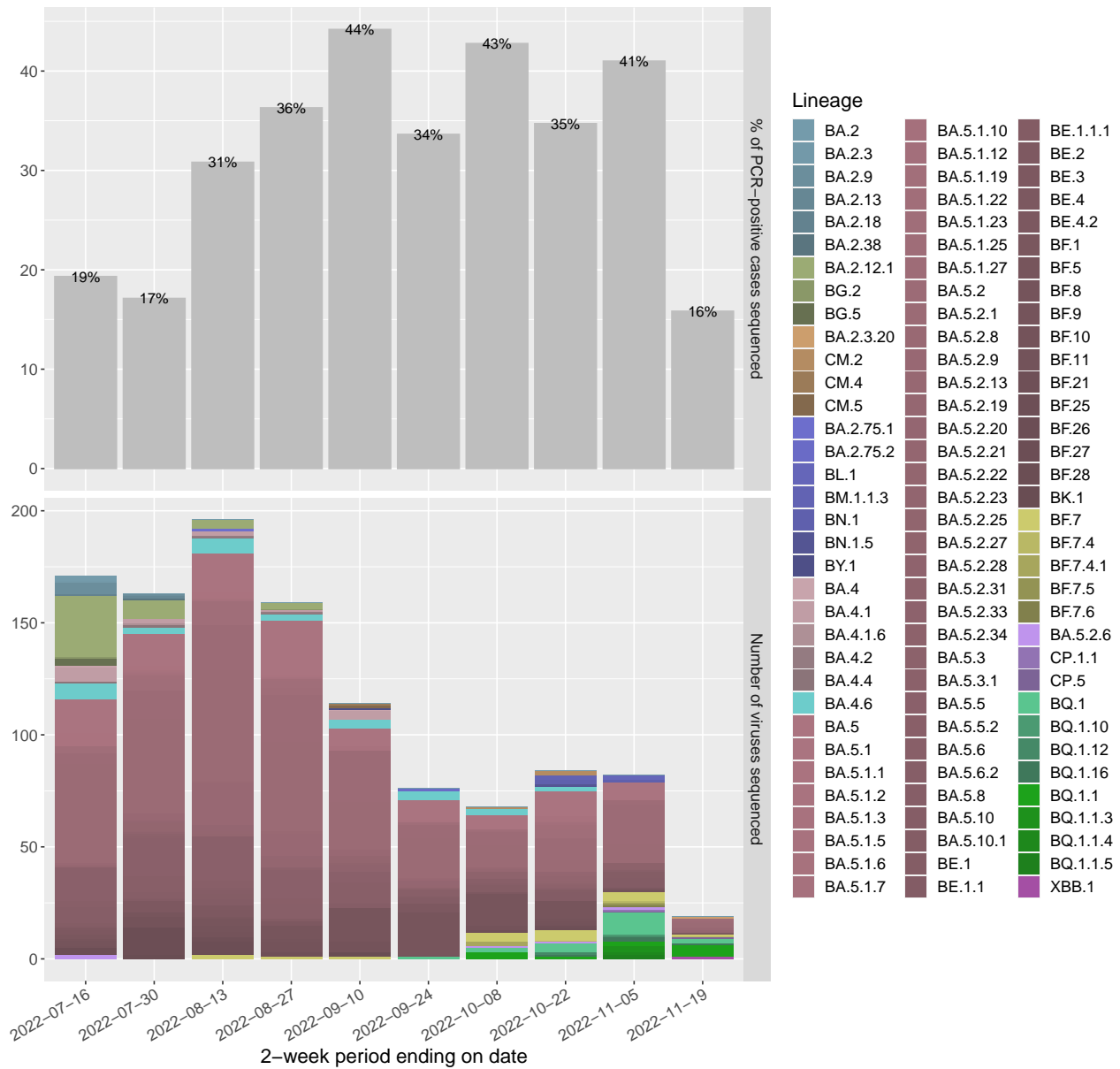


Figure Notes:

- Graph depicts the total number of variants by lineage identified in Maui County in each 2-week period ending on the date shown (date represents when the specimen was collected from a patient).
- Upper (gray) bars represent the percentage of PCR-positive cases from each 2-week period that were sequenced.
- Lower (color) bars represent the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week period.
- 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 variant proportions in Maui County

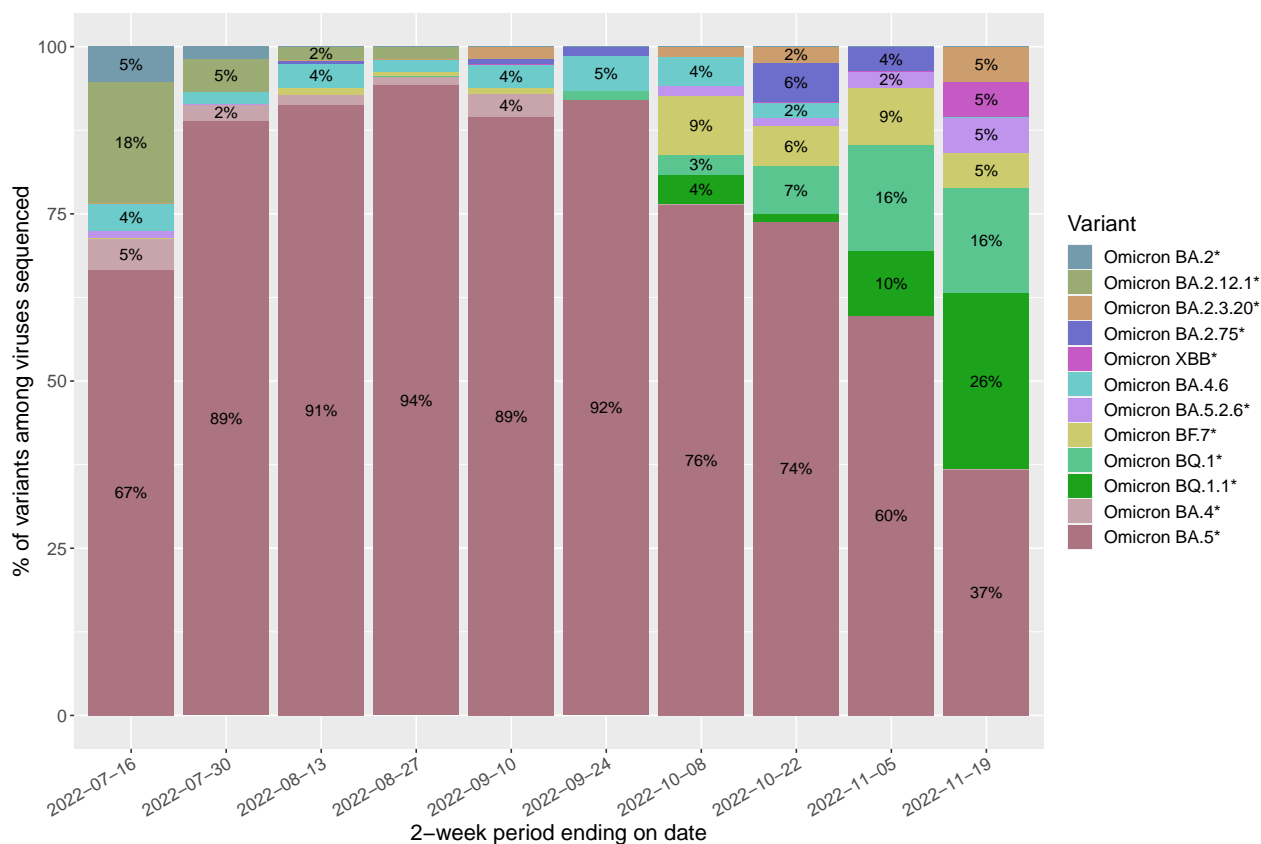


Figure Notes:

- Graph depicts percentage estimates of SARS-CoV-2 variants circulating in Maui County, grouped in 2-week periods (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. This graph was generated only counting specimens that were selected randomly for the purpose of surveillance.
- 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, thus trends based on historical data can change over time.
- Omicron BA.2* includes BA.2 and its sub-lineages (BA.2.*); excludes BA.2.3.20*, BA.2.12.1*, and BA.2.75*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*).
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.2.75* includes BA.2.75 and its sub-lineages (BA.2.75.*, BL.*, BM.*, BN.*, BR.*, BY.*, CB.*, CH.*).
- 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.*, BF.*, BK.*, BT.*, CK.*); excludes BA.5.2.6* and BF.7*.
- Omicron BA.5.2.6* includes BA.5.2.6 and its sub-lineages (CP.*).
- Omicron BF.7* includes BF.7 and its sub-lineages (BF.7.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*).
- Omicron XBB* includes XBB and its sub-lineages (XBB.*).

Variants of Concern in Maui County

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|-----------|-----------------------|----------------------|-----------------------------------|--------------------------------------|
| Omicron | | | 2551 | | |
| | BA.2.12.1 | USA/Canada | 413 | 06 Apr 2022 | 26 Aug 2022 |
| | Other | Various | 293 | 01 Nov 2022 | 31 May 2022 |
| | BA.5.2.1 | South Africa/UK/USA | 259 | 31 May 2022 | 13 Nov 2022 |
| | BA.1.1 | South Africa/Botswana | 257 | 16 Dec 2021 | 19 Jun 2022 |
| | BA.2 | South Africa/Botswana | 254 | 13 Feb 2022 | 12 Jul 2022 |
| | BA.5.2 | South Africa/UK/USA | 126 | 19 Jun 2022 | 16 Nov 2022 |
| | BA.5.1 | Portugal | 109 | 17 Jun 2022 | 04 Nov 2022 |
| | BA.5.5 | USA | 95 | 02 Jun 2022 | 12 Oct 2022 |
| | BA.1.15 | USA | 86 | 14 Dec 2021 | 09 Apr 2022 |
| | BA.2.3 | Philippines | 72 | 28 Jan 2022 | 14 Jul 2022 |
| | BF.5 | Israel | 68 | 16 Jul 2022 | 19 Oct 2022 |
| | BA.5.6 | USA | 44 | 27 May 2022 | 25 Oct 2022 |
| | BA.5.2.9 | USA | 41 | 01 Jul 2022 | 06 Nov 2022 |
| | BG.5 | USA | 37 | 19 Apr 2022 | 16 Jul 2022 |
| | BA.4.1 | South Africa | 35 | 09 May 2022 | 06 Sep 2022 |
| | BA.4.6 | USA/UK/Denmark | 34 | 29 Jun 2022 | 20 Oct 2022 |
| | BA.5.1.23 | Spain | 32 | 23 Jun 2022 | 19 Oct 2022 |
| | BA.1 | South Africa/Botswana | 26 | 17 Dec 2021 | 25 Feb 2022 |
| | BA.5.1.1 | USA | 26 | 17 Jun 2022 | 17 Aug 2022 |
| | BA.1.1.2 | Japan | 23 | 13 Dec 2021 | 15 Feb 2022 |
| | BF.10 | USA | 21 | 23 Jun 2022 | 14 Oct 2022 |
| | BA.2.9 | Europe | 20 | 08 Mar 2022 | 25 Jul 2022 |
| | BA.2.42 | Australia | 19 | 24 Apr 2022 | 23 Jun 2022 |
| | BQ.1 | Nigeria | 19 | 16 Sep 2022 | 08 Nov 2022 |
| | BF.7 | UK/Belgium/Denmark | 18 | 01 Aug 2022 | 15 Nov 2022 |
| | BA.1.1.18 | USA | 17 | 30 Dec 2021 | 22 Feb 2022 |
| | BE.3 | USA | 17 | 28 Jun 2022 | 29 Sep 2022 |
| | BA.2.29 | Japan | 15 | 08 Apr 2022 | 16 May 2022 |
| | BE.1.1 | Germany | 15 | 13 Jul 2022 | 27 Oct 2022 |
| | BA.2.18 | UK | 14 | 21 Mar 2022 | 11 Jul 2022 |
| | BA.5.8 | USA/UK/Denmark | 12 | 30 Jun 2022 | 07 Oct 2022 |
| | BF.27 | Singapore | 12 | 05 Jul 2022 | 01 Aug 2022 |
| | BA.5.2.21 | Indonesia | 11 | 07 Jul 2022 | 14 Nov 2022 |
| | BQ.1.1 | Global | 11 | 06 Oct 2022 | 14 Nov 2022 |

Table Notes:

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.4% of the cumulative Omicron sequences from Maui County.

Variants Being Monitored in Maui County

| WHO label | 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 | 03 Apr 2021 | 28 May 2021 |
| Beta | B.1.351 | South Africa | 1 | 08 Jul 2021 | 08 Jul 2021 |
| Gamma | | | 43 | | |
| | P.1 | Brazil | 23 | 18 Apr 2021 | 20 Jun 2021 |
| | P.1.12 | Peru | 19 | 21 Mar 2021 | 28 Apr 2021 |
| | P.1.10 | USA | 1 | 10 May 2021 | 10 May 2021 |
| Delta | | | 434 | | |
| | AY.103 | USA | 95 | 13 Jul 2021 | 23 Dec 2021 |
| | AY.44 | USA | 65 | 27 Jun 2021 | 27 Dec 2021 |
| | AY.3 | USA | 60 | 19 Jul 2021 | 01 Dec 2021 |
| | Other AY.* | Various | 43 | 02 Aug 2021 | 30 Sep 2021 |
| | AY.47 | USA | 31 | 19 Aug 2021 | 07 Dec 2021 |
| | AY.100 | South Africa/Botswana | 23 | 22 Jul 2021 | 18 Nov 2021 |
| | AY.13 | USA | 22 | 21 Jul 2021 | 13 Sep 2021 |
| | AY.25 | USA | 18 | 12 Aug 2021 | 19 Dec 2021 |
| | AY.25.1 | South Africa/Botswana | 18 | 24 Jul 2021 | 10 Dec 2021 |
| | AY.122 | South Africa/Botswana | 16 | 19 Jul 2021 | 01 Oct 2021 |
| | AY.26 | USA/Mexico | 16 | 03 Aug 2021 | 28 Oct 2021 |
| | AY.2 | USA | 14 | 07 Jun 2021 | 06 Aug 2021 |
| | AY.39 | USA | 11 | 25 Sep 2021 | 31 Oct 2021 |
| | B.1.617.2 | India | 2 | 02 Dec 2021 | 16 Dec 2021 |
| Epsilon | | | 273 | | |
| | B.1.429 | USA | 266 | 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

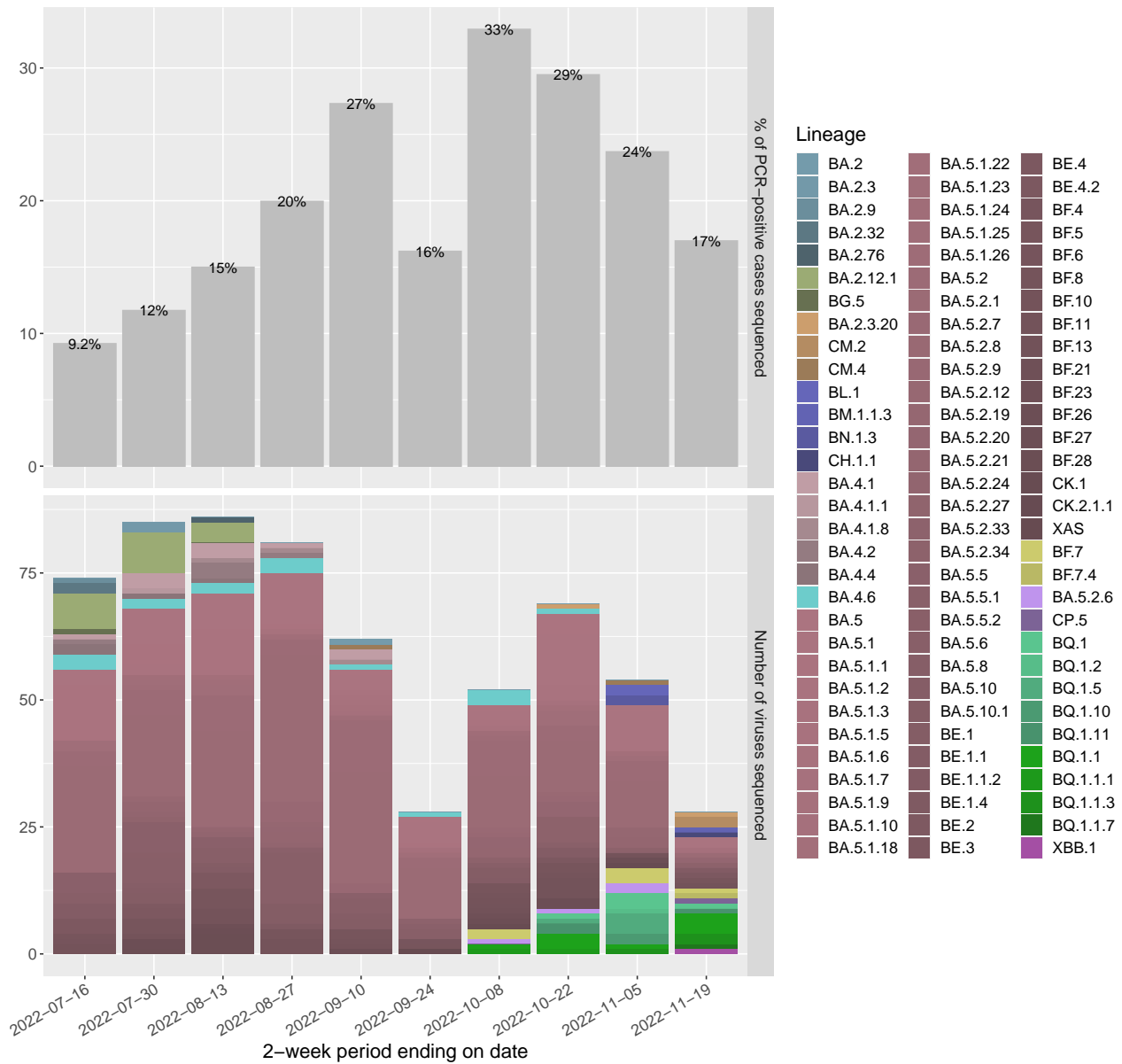


Figure Notes:

- Graph depicts the total number of variants by lineage identified in Hawaii County in each 2-week period ending on the date shown (date represents when the specimen was collected from a patient).
- Upper (gray) bars represent the percentage of PCR-positive cases from each 2-week period that were sequenced.
- Lower (color) bars represent the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week period.
- 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 variant proportions in Hawaii County

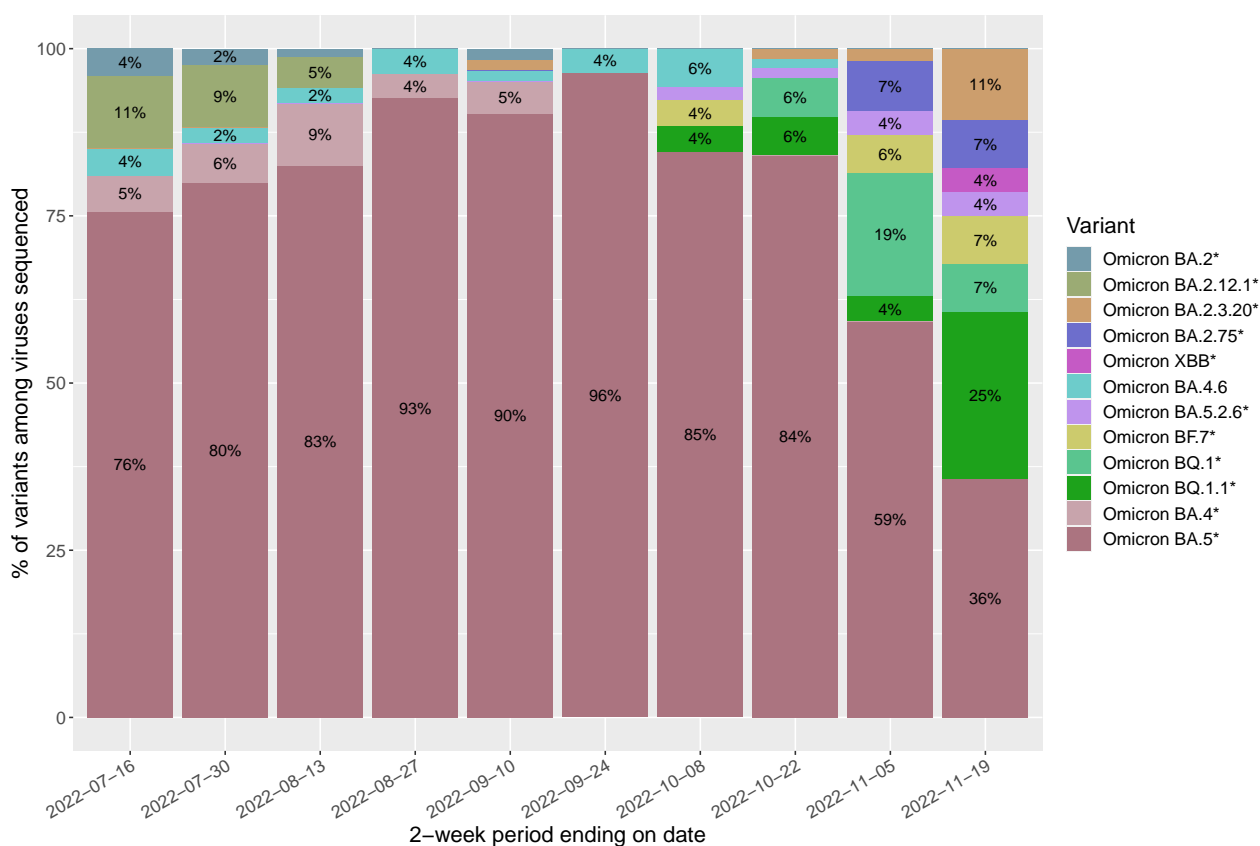


Figure Notes:

- Graph depicts percentage estimates of SARS-CoV-2 variants circulating in Hawaii County, grouped in 2-week periods (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. This graph was generated only counting specimens that were selected randomly for the purpose of surveillance.
- 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, thus trends based on historical data can change over time.
- Omicron BA.2* includes BA.2 and its sub-lineages (BA.2.*); excludes BA.2.3.20*, BA.2.12.1*, and BA.2.75*.
- Omicron BA.2.12.1* includes BA.2.12.1 and its sub-lineages (BG.*).
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.2.75* includes BA.2.75 and its sub-lineages (BA.2.75.*, BL.*, BM.*, BN.*, BR.*, BY.*, CB.*, CH.*).
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.5* includes BA.5, its sub-lineages (BA.5.*, BE.*, BF.*, BK.*, BT.*, CK.*), and XAS; excludes BA.5.2.6* and BF.7*.
- Omicron BA.5.2.6* includes BA.5.2.6 and its sub-lineages (CP.*).
- Omicron BF.7* includes BF.7 and its sub-lineages (BF.7.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*).
- Omicron XBB* includes XBB and its sub-lineages (XBB.*).

Variants of Concern in Hawaii County

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|-----------|-------------------------|----------------------|-----------------------------------|--------------------------------------|
| Omicron | | | 1581 | | |
| | Other | Various | 231 | 01 Aug 2022 | 31 Oct 2022 |
| | BA.2.12.1 | USA/Canada | 213 | 13 Apr 2022 | 12 Aug 2022 |
| | BA.2 | South Africa/Botswana | 182 | 19 Jan 2022 | 06 Sep 2022 |
| | BA.5.2.1 | South Africa/UK/USA | 163 | 12 Jun 2022 | 15 Nov 2022 |
| | BA.1.1 | South Africa/Botswana | 159 | 13 Dec 2021 | 09 May 2022 |
| | BA.2.3 | Philippines | 90 | 30 Jan 2022 | 22 Jul 2022 |
| | BA.1.1.2 | Japan | 64 | 10 Dec 2021 | 01 Mar 2022 |
| | BA.5.1 | Portugal | 62 | 07 Jun 2022 | 10 Nov 2022 |
| | BA.5.2 | South Africa/UK/USA | 47 | 17 Jun 2022 | 31 Oct 2022 |
| | BA.5.1.1 | USA | 41 | 14 May 2022 | 28 Sep 2022 |
| | BA.5.6 | USA | 32 | 21 May 2022 | 28 Sep 2022 |
| | BA.5.5 | USA | 27 | 03 May 2022 | 12 Sep 2022 |
| | BG.5 | USA | 26 | 13 Apr 2022 | 12 Jul 2022 |
| | BA.1 | South Africa/Botswana | 25 | 17 Dec 2021 | 02 Mar 2022 |
| | BA.1.15 | USA | 24 | 10 Dec 2021 | 22 Mar 2022 |
| | BA.2.9 | Europe | 21 | 28 Mar 2022 | 03 Jul 2022 |
| | BA.2.18 | UK | 19 | 24 Apr 2022 | 24 Jun 2022 |
| | BF.5 | Israel | 18 | 07 Jul 2022 | 06 Nov 2022 |
| | BA.4.1 | South Africa | 16 | 16 Jun 2022 | 01 Sep 2022 |
| | BA.4.6 | USA/UK/Denmark | 16 | 11 Jul 2022 | 21 Oct 2022 |
| | BA.2.3.17 | USA | 12 | 24 Feb 2022 | 05 May 2022 |
| | BF.10 | USA | 12 | 06 Jul 2022 | 24 Oct 2022 |
| | BA.5.1.23 | Spain | 10 | 27 Jun 2022 | 24 Oct 2022 |
| | BE.1 | South Africa/UK/Austria | 10 | 22 Jul 2022 | 06 Oct 2022 |
| | BE.3 | USA | 10 | 08 Jun 2022 | 07 Aug 2022 |
| | BA.1.1.16 | Canada/USA | 9 | 28 Jan 2022 | 27 Apr 2022 |
| | BA.5.2.21 | Indonesia | 9 | 25 Jul 2022 | 02 Nov 2022 |
| | BQ.1.1 | Global | 9 | 07 Oct 2022 | 19 Nov 2022 |
| | BA.5 | South Africa | 8 | 29 Aug 2022 | 23 Oct 2022 |
| | BA.5.2.34 | Israel/USA | 8 | 07 Oct 2022 | 14 Nov 2022 |
| | BA.5.2.9 | USA | 8 | 14 Aug 2022 | 10 Oct 2022 |

Table Notes:

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.5% of the cumulative Omicron sequences from Hawaii County.

Variants Being Monitored in Hawaii County

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|------------|-----------------------|----------------------|-----------------------------------|--------------------------------------|
| Alpha | | | 71 | | |
| | B.1.1.7 | UK | 57 | 22 Feb 2021 | 22 Jul 2021 |
| | Q.3 | USA | 14 | 21 Mar 2021 | 20 Aug 2021 |
| Gamma | | | 17 | | |
| | P.1.10 | USA | 12 | 27 May 2021 | 13 Jun 2021 |
| | P.1 | Brazil | 4 | 10 May 2021 | 02 Jun 2021 |
| | P.1.17 | USA/Mexico | 1 | 14 Jun 2021 | 14 Jun 2021 |
| Delta | | | 951 | | |
| | AY.44 | USA | 229 | 11 Jun 2021 | 16 Dec 2021 |
| | AY.3 | USA | 123 | 31 Jul 2021 | 16 Dec 2021 |
| | AY.103 | USA | 113 | 21 May 2021 | 16 Dec 2021 |
| | AY.25 | USA | 108 | 19 Jul 2021 | 09 Nov 2021 |
| | Other AY.* | Various | 84 | 01 Jul 2021 | 30 Jul 2021 |
| | AY.100 | South Africa/Botswana | 54 | 17 Jul 2021 | 12 Nov 2021 |
| | AY.25.1 | South Africa/Botswana | 45 | 28 Jul 2021 | 17 Dec 2021 |
| | AY.118 | USA | 41 | 08 Jul 2021 | 27 Sep 2021 |
| | AY.117 | USA | 30 | 11 Aug 2021 | 17 Nov 2021 |
| | AY.122 | South Africa/Botswana | 29 | 19 Jul 2021 | 22 Sep 2021 |
| | AY.46.4 | USA | 27 | 21 Jun 2021 | 06 Dec 2021 |
| | AY.119 | USA | 24 | 03 Aug 2021 | 24 Nov 2021 |
| | AY.26 | USA/Mexico | 19 | 24 Jun 2021 | 03 Dec 2021 |
| | AY.1 | Europe | 18 | 20 Jul 2021 | 03 Sep 2021 |
| | B.1.617.2 | India | 7 | 06 Jul 2021 | 08 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 | 13 Jun 2021 | 13 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

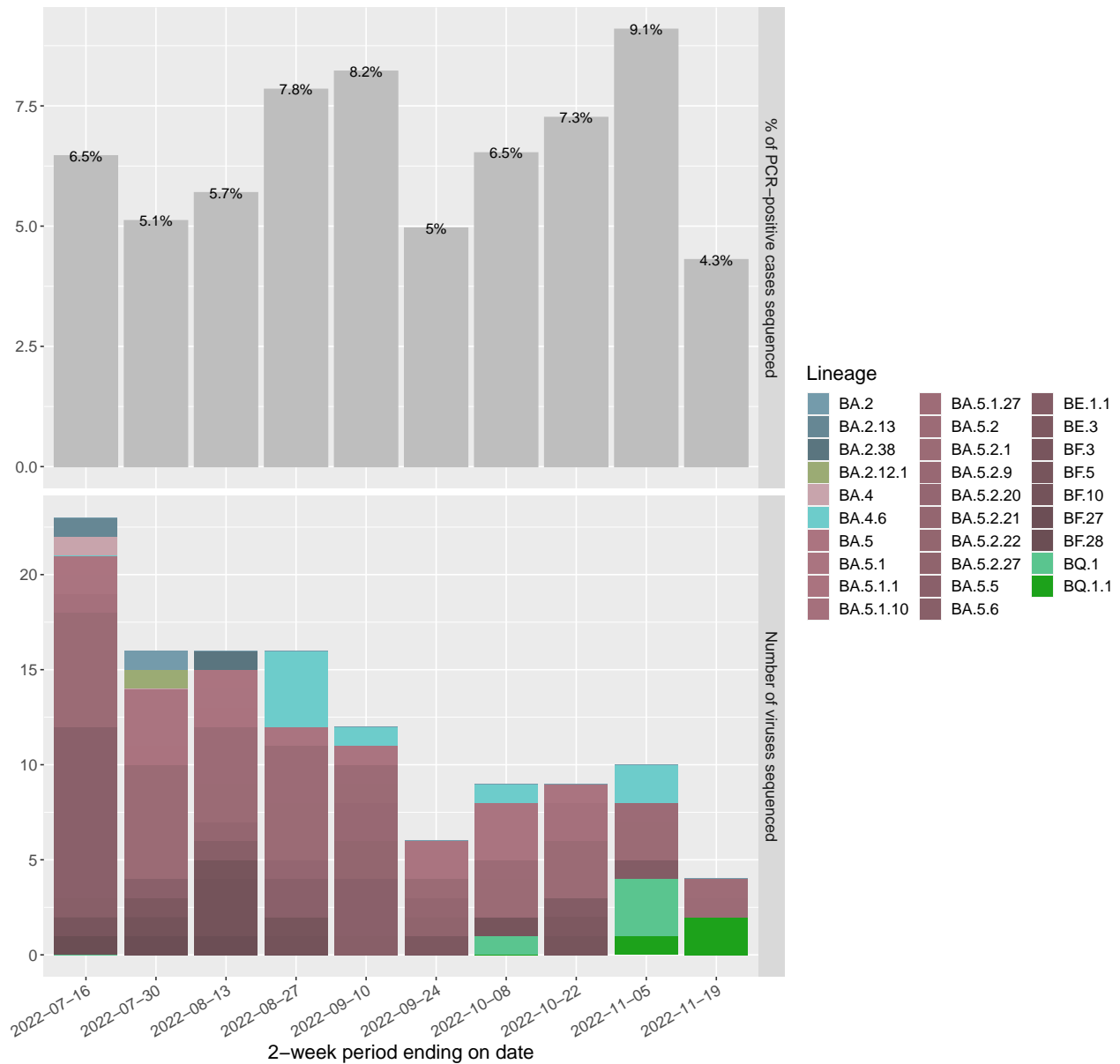


Figure Notes:

- Graph depicts the total number of variants by lineage identified in Kauai County in each 2-week period ending on the date shown (date represents when the specimen was collected from a patient).
- Upper (gray) bars represent the percentage of PCR-positive cases from each 2-week period that were sequenced.
- Lower (color) bars represent the number of viruses sequenced (one sequenced virus equates to one PCR-positive case) from each 2-week period.
- 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 variant proportions in Kauai County

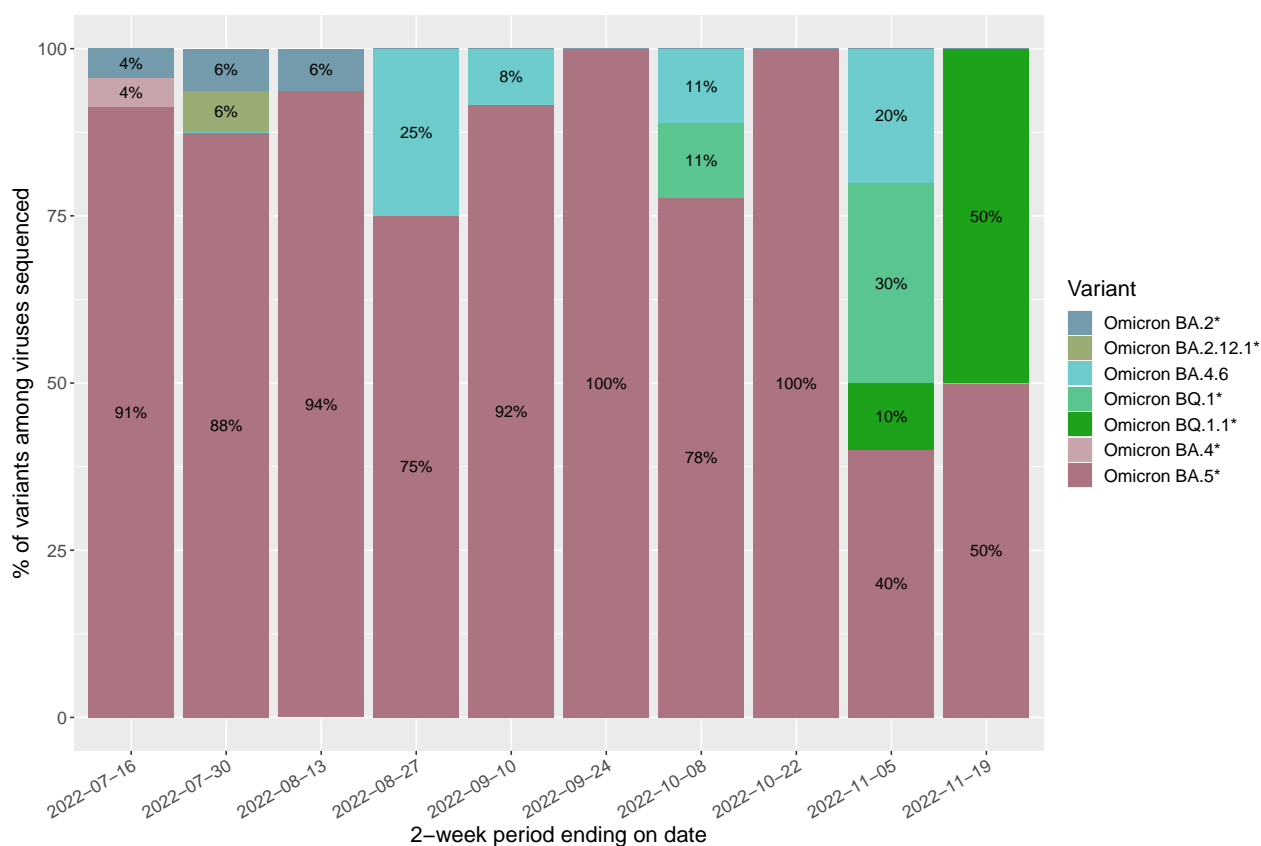


Figure Notes:

- Graph depicts percentage estimates of SARS-CoV-2 variants circulating in Kauai County, grouped in 2-week periods (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. This graph was generated only counting specimens that were selected randomly for the purpose of surveillance.
- 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, thus trends based on historical data can change over time.
- Omicron BA.2* includes BA.2 and its sub-lineages (BA.2.*); excludes BA.2.3.20*, BA.2.12.1*, and BA.2.75*.
- 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.*, BF.*, BK.*, BT.*, CK.*); excludes BA.5.2.6 and BF.7.
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*).

Variants of Concern in Kauai County

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|-----------|-----------------------|----------------------|-----------------------------------|--------------------------------------|
| Omicron | | | 475 | | |
| | BA.2 | South Africa/Botswana | 83 | 17 Mar 2022 | 26 Jul 2022 |
| | BA.1.1 | South Africa/Botswana | 63 | 15 Dec 2021 | 19 Apr 2022 |
| | BA.2.12.1 | USA/Canada | 62 | 30 Mar 2022 | 27 Jul 2022 |
| | Other | Various | 43 | 02 Jun 2022 | 27 Oct 2022 |
| | BA.5.2.1 | South Africa/UK/USA | 32 | 03 Jun 2022 | 02 Nov 2022 |
| | BA.2.3 | Philippines | 19 | 09 Mar 2022 | 24 May 2022 |
| | BA.5.5 | USA | 18 | 13 Jun 2022 | 31 Aug 2022 |
| | BA.5.1 | Portugal | 16 | 23 Jun 2022 | 19 Oct 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.5.2 | South Africa/UK/USA | 11 | 02 Jul 2022 | 17 Nov 2022 |
| | XAC | USA/Canada | 9 | 28 Apr 2022 | 14 Jun 2022 |
| | BA.1.1.18 | USA | 8 | 28 Dec 2021 | 21 Mar 2022 |
| | BA.1.1.2 | Japan | 8 | 15 Dec 2021 | 09 Feb 2022 |
| | BA.2.18 | UK | 8 | 24 Apr 2022 | 16 Jun 2022 |
| | BA.2.42 | Australia | 8 | 07 May 2022 | 02 Jul 2022 |
| | BA.4.6 | USA/UK/Denmark | 8 | 23 Aug 2022 | 04 Nov 2022 |
| | BG.5 | USA | 7 | 03 May 2022 | 13 Jun 2022 |
| | BA.4.1 | South Africa | 6 | 08 Jun 2022 | 26 Jun 2022 |
| | BF.10 | USA | 6 | 13 Jun 2022 | 19 Aug 2022 |
| | BA.2.9 | Europe | 5 | 17 Mar 2022 | 09 May 2022 |
| | BF.5 | Israel | 5 | 21 Jun 2022 | 17 Oct 2022 |
| | BA.5.2.9 | USA | 4 | 27 Jun 2022 | 30 Aug 2022 |
| | BA.5.6 | USA | 4 | 16 Jun 2022 | 29 Aug 2022 |
| | BE.3 | USA | 4 | 15 Jun 2022 | 17 Oct 2022 |
| | BQ.1 | Nigeria | 4 | 30 Sep 2022 | 02 Nov 2022 |
| | BA.2.1 | UK | 3 | 25 May 2022 | 20 Jun 2022 |
| | BA.5.1.10 | USA/Italy/UK | 3 | 06 Jul 2022 | 14 Oct 2022 |
| | BQ.1.1 | Global | 3 | 04 Nov 2022 | 10 Nov 2022 |

Table Notes:

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.5% of the cumulative Omicron sequences from Kauai County.

Variants Being Monitored in Kauai County

| WHO label | Lineage | Area of emergence | Cumulative sequences | Earliest specimen collection date | Most recent specimen collection date |
|-----------|------------|-----------------------|----------------------|-----------------------------------|--------------------------------------|
| Alpha | | | 20 | | |
| | B.1.1.7 | UK | 19 | 05 Apr 2021 | 13 Jul 2021 |
| | Q.4 | South Africa/Botswana | 1 | 28 Apr 2021 | 28 Apr 2021 |
| Gamma | | | 2 | | |
| | P.1 | Brazil | 1 | 31 May 2021 | 31 May 2021 |
| | P.1.10 | USA | 1 | 14 May 2021 | 14 May 2021 |
| Delta | | | 246 | | |
| | AY.25 | USA | 70 | 16 Jul 2021 | 10 Nov 2021 |
| | AY.44 | USA | 37 | 29 Jun 2021 | 21 Dec 2021 |
| | AY.119 | USA | 35 | 28 Aug 2021 | 21 Dec 2021 |
| | Other AY.* | Various | 25 | 03 Nov 2021 | 29 Nov 2021 |
| | AY.47 | USA | 19 | 27 Jul 2021 | 29 Nov 2021 |
| | AY.1 | Europe | 18 | 09 Aug 2021 | 30 Aug 2021 |
| | AY.103 | USA | 17 | 01 Aug 2021 | 15 Dec 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 | 7 | 06 Jun 2021 | 30 Jun 2021 |
| | B.1.617.2 | India | 2 | 21 Sep 2021 | 18 Oct 2021 |
| Epsilon | | | 31 | | |
| | B.1.429 | USA | 29 | 07 Jan 2021 | 08 May 2021 |
| | B.1.427 | USA | 2 | 27 Apr 2021 | 27 Apr 2021 |
| Iota | B.1.526 | USA | 1 | 14 Apr 2021 | 14 Apr 2021 |
| Mu | B.1.621 | Columbia | 2 | 29 Jun 2021 | 06 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.