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Total variants identified for the time period shown 16

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Total variants identified for the time period shown 20

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Introduction

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

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

Collecting the genome sequences of virus specimens can reveal information about the relatedness of viruses and the similarities shared among groups of viruses. Groups of same-species viruses that share a set of genome mutations are referred to as a lineage.

Scientists compare viral genomes to better understand virus transmission, how viruses can spread from person to person. Sequencing also allows Public Health Officials to monitor viruses involved in outbreaks, characterize outbreaks, detect clusters of cases, and monitor new lineages. Novel mutations can emerge with new lineages and scientists refer to these new lineages as emerging variants.

Some of these variants are classified by the Centers for Disease Control and Prevention (CDC) as 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.

The State of Hawaii has conducted sequencing on approximately 6% of SARS-CoV-2-positive cases since testing began, according to the CDC (https://covid.cdc.gov/covid-data-tracker/#published-sars-cov-2-sequences).

In February 2021, State Laboratories Division, Hawaii Department of Health increased sequencing efforts done on positive specimens to improve the State’s ability to detect new variants.
Acknowledgements

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

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<thead>
<tr>
<th>Institution</th>
<th>Program/partner</th>
<th>Count</th>
<th>Percent</th>
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<td><strong>Total</strong></td>
<td></td>
<td><strong>13392</strong></td>
<td><strong>100.000%</strong></td>
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Table Notes:

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

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

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<tr>
<th>Honolulu County</th>
<th>Maui County</th>
<th>Hawaii County</th>
<th>Kauai County</th>
<th>unknown</th>
<th>Total</th>
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<td>1580</td>
<td>499</td>
<td>342</td>
<td>9940</td>
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</table>

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

- The data in this report are based on sequenced PCR-positive specimens only and not all PCR-positive specimens are sequenced.
- Each successfully sequenced specimen produces one consensus sequence of a SARS-CoV-2 genome that is further analyzed to determine the variant.
- State Laboratories Division has reported 542 additional sequenced SARS-CoV-2 genomes since the previous report was generated (5/25/2022).
- The CDC and its commercial partners have reported 156 additional sequenced SARS-CoV-2 genomes from the State of Hawaii since the previous report was generated (5/25/2022).
- TAMC has not reported any additional sequenced SARS-CoV-2 genomes from the State of Hawaii since the previous report was generated (5/25/2022).
- SARS-CoV-2 variant nomenclature is defined by a World Health Organization (WHO) label (letters of the Greek Alphabet, i.e., Alpha, Beta, Gamma, Delta, etc.), Pango lineage (alphabetical prefix and a numerical suffix), and/or Nextstrain clade (year of emergence followed by 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.
- Omicron has accounted for 100% of variants circulating in the State of Hawaii since mid-February 2022.
- Classifications of Omicron lineages are in flux. The parent lineage of Omicron is B.1.1.529; sub-lineages of Omicron have the BA.* designation (i.e., BA.1, BA.2, etc.). Omicron XE, which has been detected in the State of Hawaii, is a recombinant lineage containing genetic material from BA.1 and BA.2.
- BA.2 and its sub-lineages have together accounted for more than 98% of the Omicron lineages circulating in the State of Hawaii since mid-May 2022.
- The percentage of BA.2.12.1 (a sub-lineage of BA.2) has steadily increased at the state level since its detection. BA.2.12.1 contains 2 additional amino acid mutations (L452Q and S704L) in the spike protein compared to BA.2. Relative growth modeling based on sequences submitted to GISAID for surveillance purposes in the U.S. over the past 3 months (3/7/2022 to 6/7/2022) estimates BA.2.12.1 to be approximately 1.3x more transmissible than BA.2; increase in transmissibility determined using the estimated logistic growth rate and default parameters generated at https://cov-spectrum.org/explore/United%20States/Surveillance/Past3M/variants?pangoLineage=BA.2&pangoLineage1=BA.2.12.1&analysisMode=CompareToBaseline&.
- BA.4 and BA.5, which are on the rise nationally, have recently been detected in the State of Hawaii. Within the spike protein alone, both lineages contain 4 additional amino acid mutations (H69-, V70-, L452R, and F486V) and one reversion (R493Q) compared to BA.2. Relative growth modeling based on sequences submitted to GISAID for surveillance purposes in the U.S. over the past 3 months (3/7/2022 to 6/7/2022) estimates BA.4 and BA.5 to be approximately 1.6x and 1.8x more transmissible, respectively, than BA.2; increase in transmissibility determined using the estimated logistic growth rate and default parameters generated at https://cov-spectrum.org/explore/United%20States/Surveillance/Past3M/variants?pangoLineage=BA.2&pangoLineage1=BA.4&analysisMode=CompareToBaseline& and https://cov-spectrum.org/explore/United%20States/Surveillance/Past3M/variants?pangoLineage=BA.2&pangoLineage1=BA.5&analysisMode=CompareToBaseline&.
- Preliminary studies suggest that, compared to BA.2, BA.2.12.1 and BA.4/5 exhibit an increased ability to evade therapeutic antibodies and antibodies elicited by vaccination and/or prior infection (https://www.biorxiv.org/content/10.1101/2022.04.30.489997v1.full, https://www.biorxiv.org/content/10.1101/2022.05.21.492554v1.full, https://www.biorxiv.org/content/10.1101/2022.05.26.493517v1.full).
Variants of Concern (VOC) and Variants Being Monitored (VBM)

It is important to note that evidence to date shows that vaccination leads to milder cases, not requiring hospitalization, for all Variants of Concern and Variants Being Monitored that are described here, even if the efficacy of antibodies is diminished against some of these variants compared to the original version of the virus.

Also, none of these variants are classified as a “Variant of High Consequence (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 that have been detected in the State of Hawaii

Omicron variant (B.1.1.529, BA.* lineages, and XE)

B.1.1.529 is the parent lineage of Omicron; sub-lineages of Omicron have the BA.* designation (i.e., BA.1, BA.2, BA.4, etc.). XE is a recombinant lineage of BA.1 and BA.2, with the majority of its genome, including the gene encoding for the spike protein, coming from BA.2. SARS-CoV-2 recombinants that receive a Pango classification have an X* lineage designation (i.e., XE, XG, XH, etc.). Technical information regarding the lineage designation of XE can be found at https://github.com/cov-lineages/pango-designation/issues/454.

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, including at least 30 amino acid substitutions. Several of these mutations, including S477N, N501Y, and E484K, have been associated with increased infectivity and decreased neutralizing activity of monoclonal antibodies and convalescent sera. Evidence indicates that Omicron spreads more easily than the original SARS-CoV-2 virus and the Delta variant, but generally causes less severe disease than infection with previous variants. Lineages of Omicron also correspond to Nextstrain clades 21M, 21K, 21L, 22A, 22B, and 22C. For more information about Omicron, go to https://www.cdc.gov/coronavirus/2019-ncov/variants/omicron-variant.html.

Variants Being Monitored that have been 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. This variant is concerning because it has been shown to be significantly more transmissible (~50%) than the original SARS-CoV-2 lineages and reports from the United Kingdom suggest that B.1.1.7 cases are more likely to require hospitalization. B.1.1.7 does not appear to evade vaccine-induced neutralizing antibody responses. The Alpha variant also 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 is highly infectious and can quickly spread from person to person. Preliminary studies suggest that antibodies from previous infection or from vaccination may be less effective at preventing infection against this variant.
due to presence of the E484K mutation in the spike protein. The Beta variant also 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. Preliminary studies suggest that antibodies from previous infection or from vaccination may be less effective at preventing infection against this variant. The Gamma variant also corresponds to Nextstrain clade 20J.

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

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.).

B.1.617.2 was first identified in India and the WHO labeled it “Delta” on May 31, 2021. This variant contains the L452R mutation in the spike protein, which has been shown to escape neutralization by monoclonal antibodies and some convalescent sera, as well as a few additional spike mutations predicted to have functional consequences (e.g. T478K). The Delta variant is highly contagious, more than 2x as contagious as previous variants. Lineages of Delta also 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. They can quickly spread from person-to-person, with an estimated ~20% higher efficiency than the original virus. The Epsilon variant also 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 also corresponds to Nextstrain clade 20B/S.484K.

**Iota variant (B.1.526)**

B.1.526 was first identified in New York and is classified by CDC as a VBM because of indications that it has increased transmissibility. The WHO labeled it “Iota” on May 31, 2021. Some of the genomes (but not all) of this variant contain the E484K mutation. The Iota variant also 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 it has a couple of mutations in common with the Beta (B.1.351) and Gamma (P.1) variants, which have been associated with high transmissibility (N501Y) and a level of decreased vaccine efficiency (E484K). The MU variant also corresponds to Nextstrain clade 21H.
State of Hawaii

Total variants identified for the time period shown

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 (B.1.1.529 + BA.* + XE) is a Variant of Concern.
- Delta (B.1.617.2 + AY.*) is a Variant Being Monitored.
- The gray bar graph (top) shows the percentage of PCR-positive cases from each 2-week time interval that were sequenced.
- SARS-CoV-2 genome sequencing may not be a random sample of all cases. This graph does not estimate prevalence in the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.
Estimated proportions of variants circulating in the State of Hawaii

![Graph showing estimated proportions of variants]

**Figure Notes:**

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in the State of Hawaii, grouped in two-week intervals (based on the date of specimen collection).
- Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases in the State of Hawaii. This graph has been generated only counting 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*) is an aggregation of BA.1 and its sub-lineages (i.e., BA.1.1, BA.1.15, etc.).
- Omicron (BA.2*) is an aggregation of BA.2 and its sub-lineages (i.e., BA.2.3, BA.2.9, etc.) except BA.2.12.1.
## Variants of Concern in the State of Hawaii

<table>
<thead>
<tr>
<th>Variant</th>
<th>Lineage</th>
<th>Area of emergence</th>
<th>Cumulative cases detected</th>
<th>Earliest specimen collection date</th>
<th>Most recent specimen collection date</th>
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<td>Omicron</td>
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<td></td>
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<td>BA.4</td>
<td>South Africa</td>
<td>3</td>
<td>May 2022</td>
<td>May 2022</td>
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*Table Notes:*

- Lineage “Other BA.*” represents an aggregation of different BA.* lineages, except BA.4 and BA.5, in which each alone accounts for <0.2% of the cumulative Omicron cases detected in the State of Hawaii.
### Variants Being Monitored in the State of Hawaii

<table>
<thead>
<tr>
<th>Variant</th>
<th>Lineage</th>
<th>Area of emergence</th>
<th>Cumulative cases detected</th>
<th>Earliest specimen collection date</th>
<th>Most recent specimen collection date</th>
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<td>49</td>
<td>21 Mar 2021</td>
<td>02 Sep 2021</td>
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<td>Beta</td>
<td>B.1.351</td>
<td>South Africa</td>
<td>19</td>
<td>16 Feb 2021</td>
<td>22 Sep 2021</td>
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<tr>
<td>Gamma</td>
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<td>Peru</td>
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<td>AY.100</td>
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**Table Notes:**

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

Total variants identified for the time period shown

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 (B.1.1.529 + BA.* + XE) is a Variant of Concern.
- Delta (B.1.617.2 + AY.*) is a Variant Being Monitored.
- The gray bar graph (top) shows the percentage of PCR-positive cases from each 2-week time interval that were sequenced.
- SARS-CoV-2 genome sequencing may not be a random sample of all cases. This graph does not estimate prevalence in the population.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.
Estimated proportions of variants circulating in Honolulu County

Figure Notes:
- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Honolulu County, grouped in two-week intervals (based on the date of specimen collection).
- Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases in Honolulu County. This graph has been generated only counting 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.
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- Omicron (BA.2*) is an aggregation of BA.2 and its sub-lineages (i.e., BA.2.3, BA.2.9, etc.) except BA.2.12.1.
## Variants of Concern in Honolulu County

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**Table Notes:**

- Lineage “Other BA.*” represents an aggregation of different BA.* lineages, except BA.4 and BA.5, in which each alone accounts for <0.2% of the cumulative Omicron cases detected in Honolulu County.
## Variants Being Monitored in Honolulu County

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**Table Notes:**
- Lineage “Other AY.*” represents an aggregation of different AY.* lineages in which each alone accounts for <2% of the cumulative Delta cases detected in Honolulu County.
Maui County

Total variants identified for the time period shown

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Estimated proportions of variants circulating in Maui County

Figure Notes:

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## Variants Being Monitored in Maui County

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**Table Notes:**
- Lineage “Other AY.*” represents an aggregation of different AY.* lineages in which each alone accounts for <2% of the cumulative Delta cases detected in Maui County.
Figure Notes:

- The graph shows the total number of variants detected in Hawaii County in each 2-week interval ending on the date shown (date represents when the specimen was collected from a patient).
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Estimated proportions of variants circulating in Hawaii County

Figure Notes:

- The graph shows biweekly percentage estimates of SARS-CoV-2 variants circulating in Hawaii County, grouped in two-week intervals (based on the date of specimen collection).
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## Variants of Concern in Hawaii County

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### Variants Being Monitored in Hawaii County

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**Table Notes:**
- Lineage “Other AY.*” represents an aggregation of different AY.* lineages in which each alone accounts for <2% of the cumulative Delta cases detected in Hawaii County.
**Kauai County**

**Total variants identified for the time period shown**

![Graph showing total variants identified in Kauai County](image)

**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).
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## Variants Being Monitored in Kauai County

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