

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

Hawaii Department of Health

2024-12-04

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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. For Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)—the virus that causes Coronavirus Disease 2019 (COVID-19), the genome is approximately 30,000 letters long, 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).

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.

Acknowledgements

This report integrates genomes sequenced since 1 Jan 2021 by:

Institution	Program/partner	Count	Percent
State Laboratories Division		28196	79.8098%
Centers for Disease Control and Prevention	National SARS-CoV-2 Strain Surveillance (NS3)	412	1.1662%
	Quest Diagnostics Incorporated	1671	4.7298%
	Laboratory Corporation of America	1645	4.6562%
	Aegis Sciences Corporation	379	1.0728%
	Helix/Illumina	185	0.5236%
	Infinity Biologix	16	0.0453%
	Mako Medical	20	0.0566%
	Fulgent Genetics	8	0.0226%
	UW Virology Lab	6	0.0170%
Tripler Army Medical Center		1698	4.8062%
University of Hawaii at Manoa		861	2.4371%
Aegis Sciences Corporation*		232	0.6567%
Total		35329	100.0000%

County distribution of genomes sequenced by institution:

	Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
State Laboratories Division (since 1 Jan 2021)	18986	4059	3879	896	376	28196
University of Hawaii at Manoa (22 Jan 2022 – 23 Aug 2022)	508	67	221	17	48	861
Aegis Sciences Corporation* (14 Sep 2022 – 16 Mar 2023)	54	11	3	0	164	232

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 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 SLD.
- Aegis Sciences Corporation* reported SARS-CoV-2 genome sequences independently of the Centers for Disease Control and Prevention (CDC) from 14 Sep 2022 to 16 Mar 2023.
- County information is not provided for specimens sequenced by CDC programs/partners and by Tripler Army Medical Center.

Highlights 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.
- 114 additional SARS-CoV-2 genome sequences were reported since the previous variant report was generated (4 Nov 2024); includes 94 from State Laboratories Division and 20 from Tripler Army Medical Center.
- 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., JN.1*) signifies inclusion of the respective lineage (e.g., JN.1) and its sub-lineages (or descendants, e.g., JN.1.*) unless otherwise specified.
- Due to the decreasing trend in COVID-19 case counts statewide, the availability of PCR-positive specimens for sequencing has steadily decreased since June 2024. Estimated variant proportions are less likely to be representative as sequencing numbers diminish.
- Due to its small population size and low case counts, very few PCR-positive specimens have been received for sequencing from Kauai County since Dec 2023.
- MC.1* is a newly tracked variant under estimated variant proportions; was previously aggregated to KP.3.1.1*.

Summary of Variants Detected in the State of Hawaii

Omicron (B.1.1.529 and descendant lineages)

First identified in Botswana on 11 Nov 2021, labeled “Omicron” by the World Health Organization (WHO) on 26 Nov 2021, and first detected in the State of Hawaii on 27 Nov 2021. BA.1 and BA.2 were the dominant primary descendants of B.1.1.529. BA.2 outcompeted BA.1 and gave rise to BA.2.12.1, BA.2.75, BA.4, BA.5, and BA.2.86, all of which later gave rise to their own descendants. The co-circulation of different Omicron lineages over time has also given rise to numerous recombinant variants. 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. Recombinants that expand and later receive a PANGO nomenclature have an X* lineage designation (e.g., XBB). The major Omicron parental lineages correspond to Nextstrain clades 21M (B.1.1.529), 21K (BA.1), 21L (BA.2), 22A (BA.4), 22B (BA.5), 22C (BA.2.12.1), 22D (BA.2.75), 22E (BQ.1), 22F (XBB), 23A (XBB.1.5), 23B (XBB.1.16), 23C (CH.1.1), 23D (XBB.1.9), 23E (XBB.2.3), 23F (EG.5.1), 23G (XBB.1.5.70), 23H (HK.3), 23I (BA.2.86), 24A (JN.1), 24B (JN.1.11.1), 24C (KP.3), 24D (XDV.1), 24E (KP.3.1.1), 24F (XEC), and 24G (KP.2.3); their evolutionary relationship can be viewed at <https://nextstrain.org/nextclade/sars-cov-2>. Other detailed information about Nextstrain clades and their relationship to various lineages can be found at <https://covariants.org/variants>.

Alpha (B.1.1.7 and Q.* lineages)

First identified in the United Kingdom in Sep 2020, first detected in the State of Hawaii on 21 Jan 2021, and labeled “Alpha” by the WHO on 31 May 2021. Alpha variant corresponds to Nextstrain clade 20I. Last detected in the State of Hawaii on 2 Sep 2021.

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

First identified in South Africa in May 2020, first detected in the State of Hawaii on 16 Feb 2021, and labeled “Beta” by the WHO on 31 May 2021. Beta variant corresponds to Nextstrain clade 20H. Last detected in the State of Hawaii on 22 Sep 2021.

Gamma (P.1 and P.1.* lineages)

First identified in Brazil in Nov 2020, first detected in the State of Hawaii on 21 Mar 2021, and labeled “Gamma” by the WHO on 31 May 2021. Gamma variant corresponds to Nextstrain clade 20J. Last detected in the State of Hawaii on 21 Jul 2021.

Delta (B.1.617.2 and AY.* lineages)

First identified in India in Oct 2020, first detected in the State of Hawaii on 21 May 2021, and labeled “Delta” by the WHO on 31 May 2021. Delta parent lineages correspond to Nextstrain clades 21A, 21I, and 21J. Last detected in the State of Hawaii on 27 Jan 2022.

Epsilon (B.1.429 and B.1.427 lineages)

First identified in California in Mar 2020, first detected in the State of Hawaii on 7 Dec 2020, and labeled “Epsilon” by the WHO on 31 May 2021. Epsilon variant corresponds to Nextstrain clade 21C. Last detected in the State of Hawaii on 5 Jun 2021.

Zeta (P.2 lineage)

First identified in Brazil in Apr 2020, first detected in the State of Hawaii on 6 Feb 2021, and labeled “Zeta” by the WHO on 31 May 2021. Zeta variant corresponds to Nextstrain clade 20B/S.484K. Last detected in the State of Hawaii on 8 Feb 2021.

Iota (B.1.526 lineage)

First identified in New York in Nov 2020, first detected in the State of Hawaii on 6 Feb 2021, and labeled “Iota” by the WHO on 31 May 2021. Iota variant corresponds to Nextstrain clade 21F. Last detected in the State of Hawaii on 23 Jul 2021.

Mu (B.1.621 and B.1.621.1 lineages)

First identified in Columbia in Jan 2021, first detected in the State of Hawaii on 27 May 2021, and labeled “MU” by the WHO on 30 Aug 2021. MU variant corresponds to Nextstrain clade 21H. Last detected in the State of Hawaii on 17 Sep 2021.

State of Hawaii

Total Variants Identified

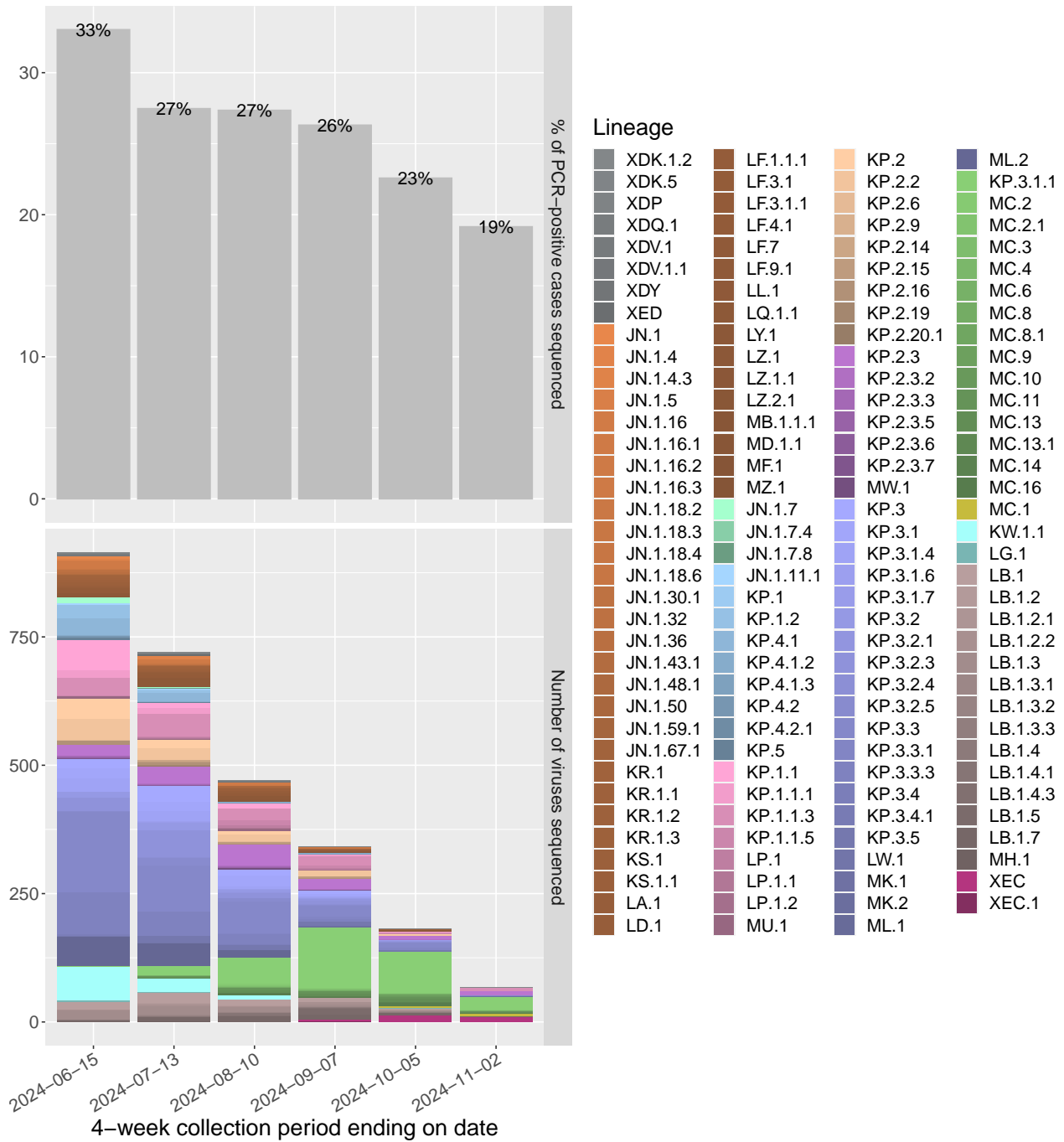


Figure Notes: Graph depicts SARS-CoV-2 variants by lineage identified in the State of Hawaii in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

Estimated Variant Proportions for the State of Hawaii

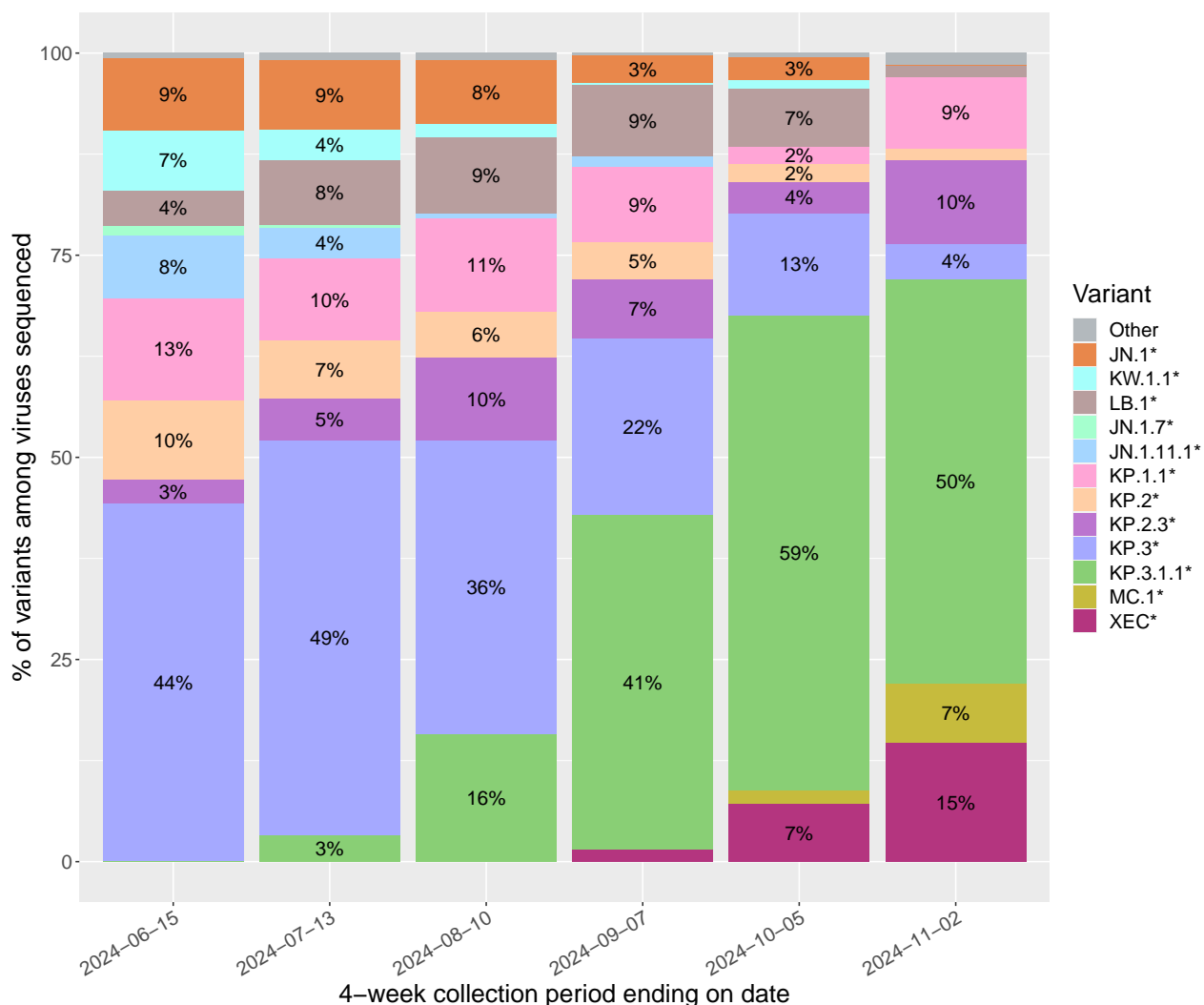


Figure Notes: Graph depicts an estimation of aggregated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for the State of Hawaii, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant depicted is an aggregation of the parental lineage shown and its respective sub-lineages; an asterisk (*) indicates inclusion of sub-lineages. “Other”, when depicted, represents an aggregation of all other lineages not aggregated to the variants shown. The lineages aggregated to each variant can be deduced by the color gradient scheme in the previous figure.

Omicron Variants Detected in the State of Hawaii

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				27360
	Other	01 Apr 2023	31 Oct 2023	10610
	BA.1.1	27 Nov 2021	19 Jun 2022	1682
	BA.2.12.1	21 Mar 2022	29 Sep 2022	1613
	BA.2	18 Jan 2022	12 Jul 2022	1580
	XBB.1.5	13 Dec 2022	26 Aug 2023	1567
	BA.5.2.1	31 May 2022	03 Jan 2023	1051
	BA.2.3	06 Jan 2022	22 Jul 2022	837
	BA.1.1.2	06 Dec 2021	01 Apr 2022	588
	BG.5	09 Apr 2022	21 Aug 2022	533
	BA.5.2	17 Jun 2022	11 Jan 2023	462
	JN.1	04 Nov 2023	03 Jul 2024	460
	BA.1.15	30 Nov 2021	09 Apr 2022	426
	BQ.1.1	27 Sep 2022	27 Mar 2023	418
	HV.1	27 Jul 2023	06 Feb 2024	415
	BA.5.1	07 Jun 2022	29 Jan 2023	407
	JN.1.4	06 Nov 2023	20 Jun 2024	381
	KP.3.3	18 Apr 2024	16 Oct 2024	363
	BA.5.5	03 May 2022	28 Oct 2022	362
	BQ.1	16 Sep 2022	13 Feb 2023	313
	KP.3.1.1	29 May 2024	13 Nov 2024	295
	BA.5.6	21 May 2022	03 Dec 2022	253
	BA.2.3.17	25 Jan 2022	15 Jun 2022	208
	XBB.1.16	20 Mar 2023	04 Nov 2023	208
	GJ.1.2	03 May 2023	14 Nov 2023	197
	EG.5.1.1	31 May 2023	05 Jan 2024	194
	KP.3.3.3	17 Apr 2024	30 Sep 2024	177
	BA.4.1	04 May 2022	29 Nov 2022	168
	BA.1	07 Dec 2021	11 Apr 2022	162
	BA.5.1.1	14 May 2022	02 Dec 2022	162
	BF.5	17 Jun 2022	19 Dec 2022	162
	BA.2.9	25 Jan 2022	25 Jul 2022	161
	BA.4.6	21 Jun 2022	20 Jan 2023	156
	KW.1.1	05 Mar 2024	14 Sep 2024	150
	KP.2.3	03 Apr 2024	31 Oct 2024	135
	KP.1.1.3	10 May 2024	01 Nov 2024	134
	ML.2	30 Apr 2024	24 Aug 2024	127
	XBB.1.16.6	02 May 2023	19 Nov 2023	122
	KP.1.1	20 Feb 2024	03 Aug 2024	121

Note: Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.4% of the cumulative Omicron sequences from the State of Hawaii.

Pre-Omicron Variants Detected in the State of Hawaii

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha				797
	B.1.1.7	21 Jan 2021	14 Aug 2021	745
	Q.3	21 Mar 2021	02 Sep 2021	52
Beta	B.1.351	16 Feb 2021	22 Sep 2021	20
Gamma				191
	P.1.10	24 Apr 2021	14 Jul 2021	84
	P.1	24 Mar 2021	21 Jul 2021	55
	P.1.12	21 Mar 2021	28 Apr 2021	20
	P.1.17	29 Mar 2021	21 Jul 2021	18
	P.1.13	03 May 2021	07 Jun 2021	14
Delta				5623
	AY.103	21 May 2021	12 Jan 2022	1228
	AY.44	07 Jun 2021	19 Jan 2022	1038
	Other AY.*	01 Aug 2021	30 Jul 2021	622
	AY.3	24 Jun 2021	02 Jan 2022	562
	AY.25	21 Jun 2021	20 Jan 2022	539
	AY.54	28 May 2021	21 Nov 2021	395
	AY.100	17 Jul 2021	12 Dec 2021	196
	AY.25.1	08 Jul 2021	27 Jan 2022	192
	AY.1	30 Jun 2021	30 Nov 2021	185
	AY.119	06 Jul 2021	21 Dec 2021	136
	AY.26	07 Jun 2021	28 Dec 2021	131
	AY.117	15 Jul 2021	17 Dec 2021	127
	AY.122	09 Jul 2021	26 Nov 2021	107
	AY.47	21 Jul 2021	07 Dec 2021	98
	B.1.617.2	04 Jun 2021	16 Dec 2021	67
Epsilon				781
	B.1.429	31 Dec 2020	03 Jun 2021	723
	B.1.427	07 Dec 2020	05 Jun 2021	58
Zeta	P.2	06 Feb 2021	08 Feb 2021	2
Iota	B.1.526	06 Feb 2021	23 Jul 2021	128
Mu				58
	B.1.621	03 Jun 2021	17 Sep 2021	45
	B.1.621.1	27 May 2021	24 Aug 2021	13

Note: 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

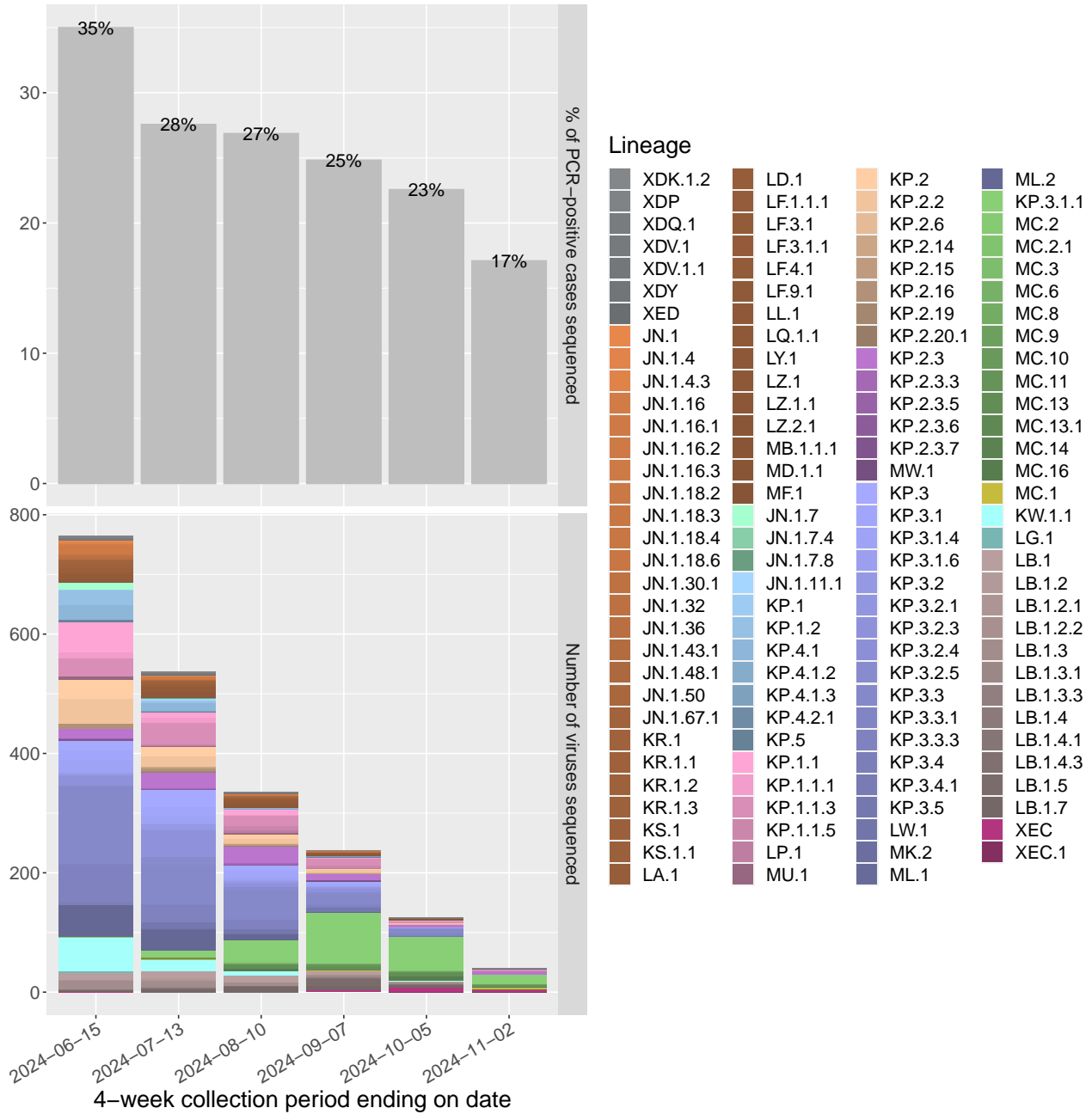


Figure Notes: Graph depicts SARS-CoV-2 variants by lineage identified in Honolulu County in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

Estimated Variant Proportions for Honolulu County

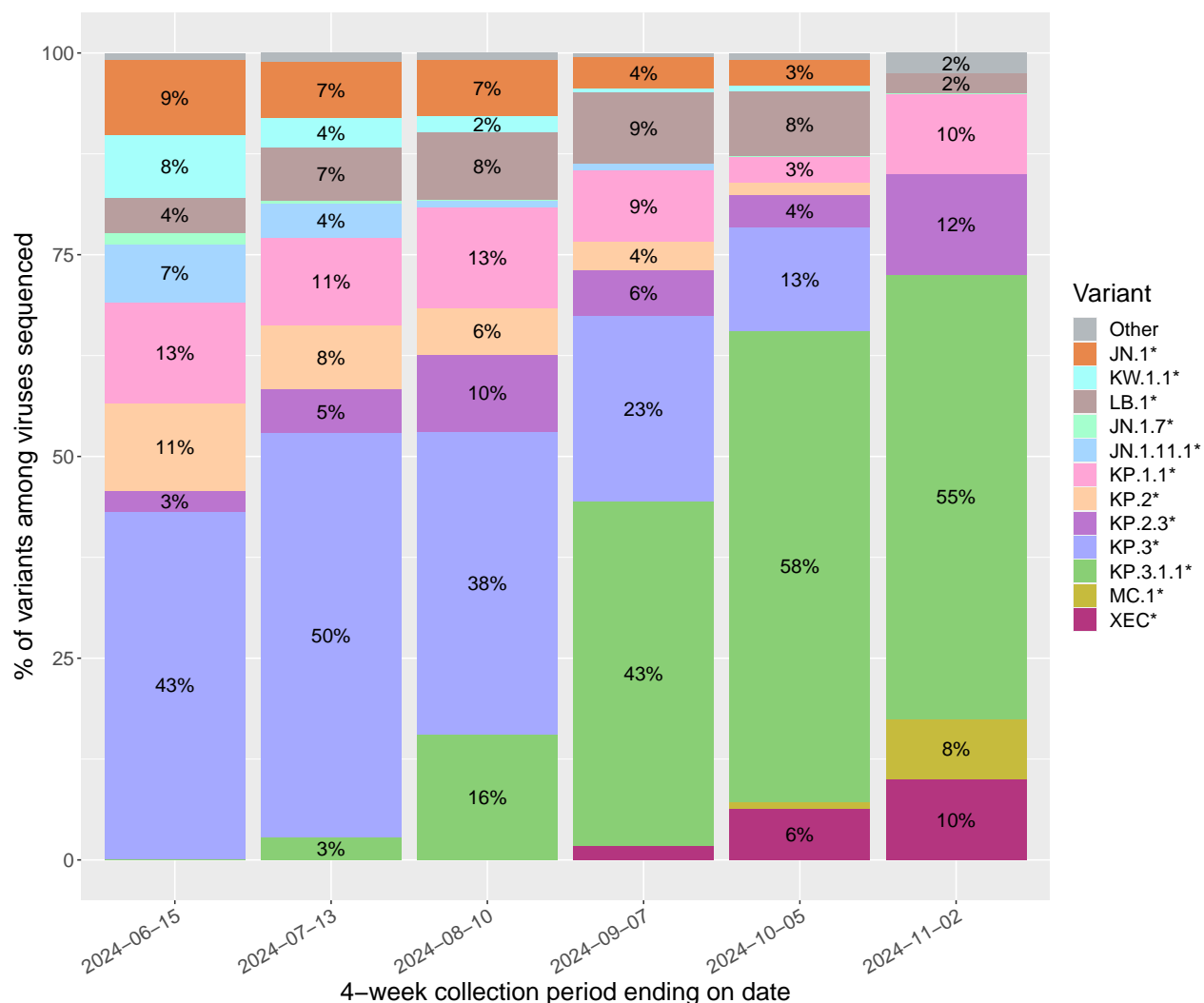


Figure Notes: Graph depicts an estimation of aggregated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Honolulu County, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant depicted is an aggregation of the parental lineage shown and its respective sub-lineages; an asterisk (*) indicates inclusion of sub-lineages. “Other”, when depicted, represents an aggregation of all other lineages not aggregated to the variants shown. The lineages aggregated to each variant can be deduced by the color gradient scheme in the previous figure.

Omicron Variants Detected in Honolulu County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				15763
	Other	01 Apr 2023	31 Oct 2023	6755
	XBB.1.5	17 Dec 2022	26 Aug 2023	1148
	BA.1.1	27 Nov 2021	11 May 2022	661
	BA.2	27 Jan 2022	08 Jul 2022	628
	BA.2.12.1	21 Mar 2022	29 Sep 2022	504
	BA.5.2.1	05 Jun 2022	03 Jan 2023	463
	BA.2.3	30 Jan 2022	24 Jun 2022	366
	JN.1	09 Nov 2023	11 Jun 2024	351
	JN.1.4	06 Nov 2023	30 May 2024	312
	BA.1.1.2	06 Dec 2021	31 Mar 2022	309
	BG.5	09 Apr 2022	21 Aug 2022	303
	HV.1	27 Jul 2023	06 Feb 2024	300
	KP.3.3	23 Apr 2024	02 Oct 2024	289
	BQ.1.1	07 Oct 2022	27 Mar 2023	247
	BA.5.2	22 Jun 2022	09 Jan 2023	229
	KP.3.1.1	29 May 2024	13 Nov 2024	205
	BQ.1	04 Oct 2022	13 Feb 2023	190
	BA.5.1	11 Jun 2022	29 Jan 2023	171
	XBB.1.16	20 Mar 2023	04 Nov 2023	170
	BA.5.5	29 May 2022	28 Oct 2022	168
	GJ.1.2	03 May 2023	14 Nov 2023	167
	BA.1.15	30 Nov 2021	07 Apr 2022	164
	EG.5.1.1	31 May 2023	05 Jan 2024	155
	BA.5.6	18 Jun 2022	04 Nov 2022	134
	KP.3.3.3	22 Apr 2024	30 Sep 2024	125
	KW.1.1	05 Mar 2024	13 Aug 2024	122
	BA.2.3.17	05 Feb 2022	02 Jun 2022	121
	KP.1.1.3	10 May 2024	01 Nov 2024	107
	ML.2	30 Apr 2024	24 Aug 2024	107
	KP.1.1	20 Feb 2024	03 Aug 2024	103
	XBB.1.16.6	02 May 2023	15 Nov 2023	92
	KP.2.3	03 Apr 2024	31 Oct 2024	91
	JN.1.4.5	06 Nov 2023	17 Mar 2024	90
	BA.4.6	26 Jun 2022	09 Dec 2022	86
	JN.1.1	27 Nov 2023	25 Mar 2024	86
	KP.2.2	02 Apr 2024	09 Sep 2024	83
	BA.4.1	22 May 2022	29 Nov 2022	81
	FU.1	02 Apr 2023	23 Sep 2023	80

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

Pre-Omicron Variants Detected in Honolulu County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha				514
	B.1.1.7	21 Jan 2021	14 Aug 2021	481
	Q.3	03 Apr 2021	02 Sep 2021	33
Beta	B.1.351	16 Feb 2021	22 Sep 2021	17
Gamma				98
	P.1.10	24 Apr 2021	13 Jul 2021	53
	P.1	24 Mar 2021	11 Jul 2021	16
	P.1.13	03 May 2021	07 Jun 2021	14
	P.1.17	29 Mar 2021	20 Jul 2021	14
	P.1.12	03 Apr 2021	03 Apr 2021	1
Delta				2635
	AY.103	20 Jun 2021	18 Dec 2021	732
	AY.44	07 Jun 2021	22 Dec 2021	416
	Other AY.*	01 Aug 2021	30 Nov 2021	289
	AY.54	28 May 2021	21 Nov 2021	282
	AY.3	24 Jun 2021	17 Dec 2021	237
	AY.25	21 Jun 2021	04 Jan 2022	204
	AY.1	30 Jun 2021	30 Nov 2021	107
	AY.100	23 Jul 2021	12 Dec 2021	88
	AY.117	15 Jul 2021	11 Nov 2021	73
	AY.26	07 Jun 2021	21 Nov 2021	69
	AY.25.1	18 Jul 2021	11 Dec 2021	61
	AY.119	06 Jul 2021	13 Dec 2021	50
	B.1.617.2	04 Jun 2021	25 Oct 2021	27
Epsilon				351
	B.1.429	05 Jan 2021	29 May 2021	320
	B.1.427	07 Jan 2021	05 Jun 2021	31
Zeta	P.2	06 Feb 2021	08 Feb 2021	2
Iota	B.1.526	08 Feb 2021	23 Jul 2021	26
Mu				25
	B.1.621	03 Jun 2021	28 Jul 2021	19
	B.1.621.1	27 May 2021	24 Aug 2021	6

Note: 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

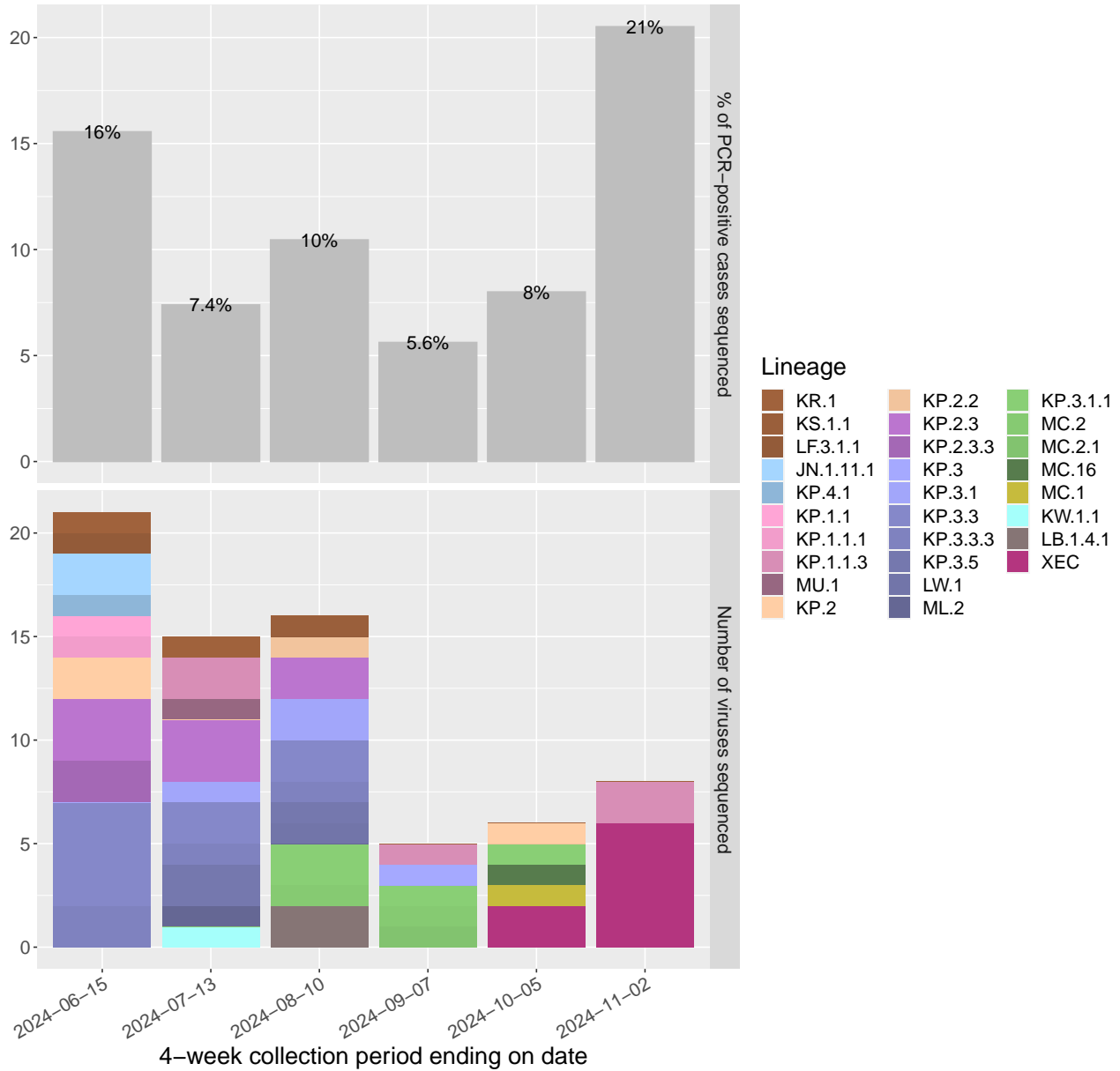


Figure Notes: Graph depicts SARS-CoV-2 variants by lineage identified in Maui County in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

Estimated Variant Proportions for Maui County

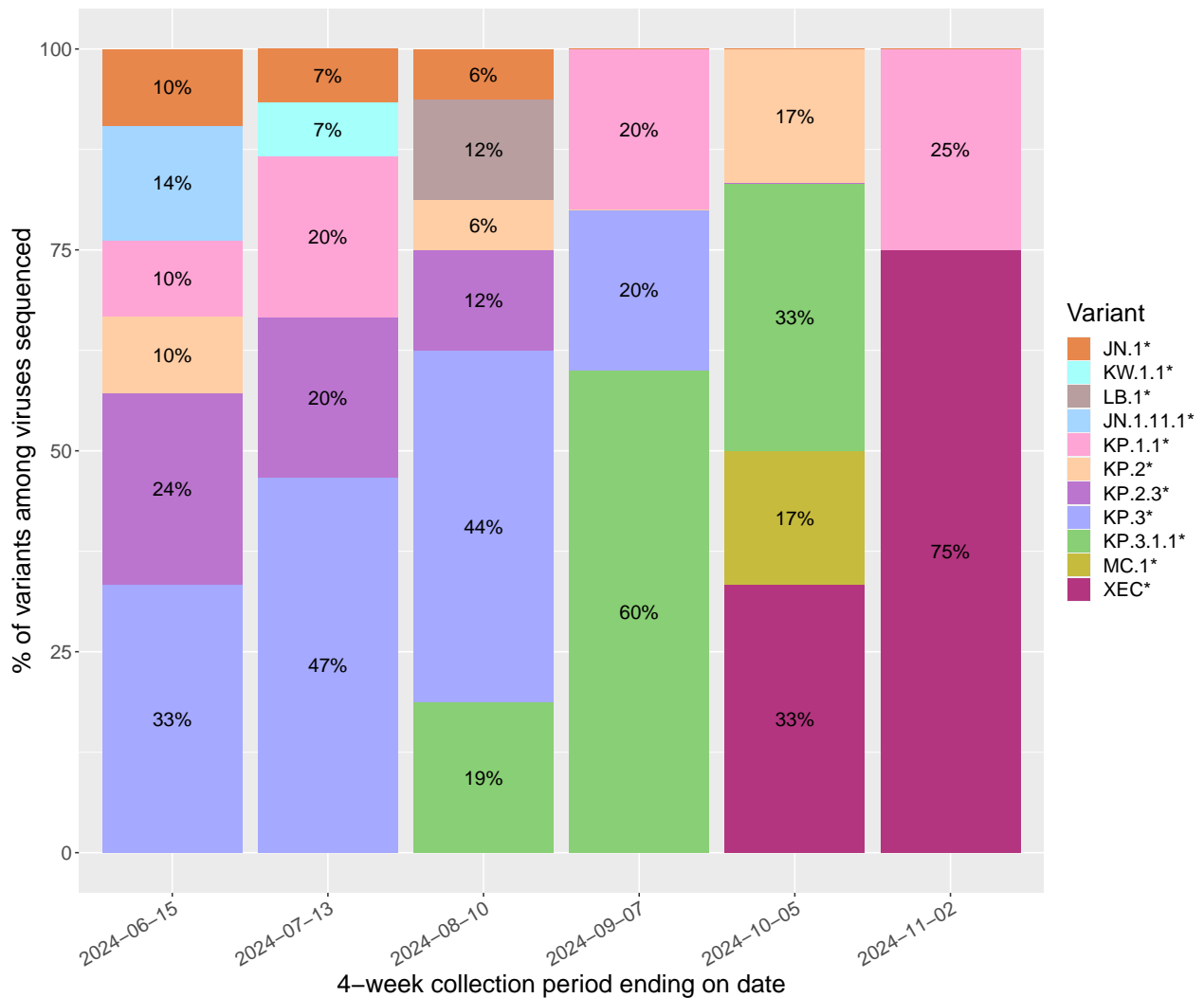


Figure Notes: Graph depicts an estimation of aggregated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Maui County, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant depicted is an aggregation of the parental lineage shown and its respective sub-lineages; an asterisk (*) indicates inclusion of sub-lineages. “Other”, when depicted, represents an aggregation of all other lineages not aggregated to the variants shown. The lineages aggregated to each variant can be deduced by the color gradient scheme in the previous figure.

Omicron Variants Detected in Maui County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				3323
	Other	01 Aug 2022	31 May 2024	922
	BA.2.12.1	06 Apr 2022	26 Aug 2022	413
	BA.5.2.1	31 May 2022	01 Dec 2022	273
	BA.2	13 Feb 2022	12 Jul 2022	259
	BA.1.1	16 Dec 2021	19 Jun 2022	243
	BA.5.2	19 Jun 2022	28 Dec 2022	110
	XBB.1.5	27 Dec 2022	06 Jun 2023	110
	BA.5.1	17 Jun 2022	15 Dec 2022	102
	BA.5.5	02 Jun 2022	12 Oct 2022	95
	BA.1.15	14 Dec 2021	09 Apr 2022	86
	BA.2.3	28 Jan 2022	14 Jul 2022	72
	BF.5	16 Jul 2022	19 Nov 2022	66
	BQ.1	16 Sep 2022	31 Jan 2023	60
	BQ.1.1	06 Oct 2022	14 Mar 2023	48
	BA.5.6	27 May 2022	25 Oct 2022	44
	BA.5.2.9	01 Jul 2022	06 Nov 2022	39
	BG.5	19 Apr 2022	16 Jul 2022	37
	BA.4.1	09 May 2022	06 Sep 2022	35
	BA.5.1.23	23 Jun 2022	19 Oct 2022	31
	BQ.1.12	16 Oct 2022	08 Feb 2023	29
	BA.1	17 Dec 2021	25 Feb 2022	26
	BA.4.6	08 Jul 2022	23 Nov 2022	26
	BA.5.1.1	17 Jun 2022	17 Aug 2022	26
	BF.7	01 Aug 2022	17 Jan 2023	24
	BA.1.1.2	13 Dec 2021	15 Feb 2022	23
	BF.10	23 Jun 2022	12 Jan 2023	23
	JN.1	28 Dec 2023	15 May 2024	23
	BA.2.9	08 Mar 2022	25 Jul 2022	20
	DN.2	05 Nov 2022	19 Jan 2023	20
	BA.2.42	24 Apr 2022	23 Jun 2022	19
	BQ.1.1.3	01 Nov 2022	20 Feb 2023	19

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

Pre-Omicron Variants Detected in Maui County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha				41
	B.1.1.7	01 Mar 2021	11 Jul 2021	39
	Q.3	03 Apr 2021	28 May 2021	2
Beta	B.1.351	08 Jul 2021	08 Jul 2021	1
Gamma				43
	P.1	18 Apr 2021	20 Jun 2021	23
	P.1.12	21 Mar 2021	28 Apr 2021	19
	P.1.10	10 May 2021	10 May 2021	1
Delta				434
	AY.103	13 Jul 2021	23 Dec 2021	95
	AY.44	27 Jun 2021	27 Dec 2021	65
	AY.3	19 Jul 2021	01 Dec 2021	60
	Other AY.*	02 Aug 2021	30 Sep 2021	43
	AY.47	19 Aug 2021	07 Dec 2021	31
	AY.100	22 Jul 2021	18 Nov 2021	23
	AY.13	21 Jul 2021	13 Sep 2021	22
	AY.25	12 Aug 2021	19 Dec 2021	18
	AY.25.1	24 Jul 2021	10 Dec 2021	18
	AY.122	19 Jul 2021	01 Oct 2021	16
	AY.26	03 Aug 2021	28 Oct 2021	16
	AY.2	07 Jun 2021	06 Aug 2021	14
	AY.39	25 Sep 2021	31 Oct 2021	11
	B.1.617.2	02 Dec 2021	16 Dec 2021	2
Epsilon				273
	B.1.429	08 Jan 2021	18 May 2021	266
	B.1.427	27 Apr 2021	10 May 2021	7
Iota	B.1.526	12 Mar 2021	25 Jun 2021	16

Note: 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

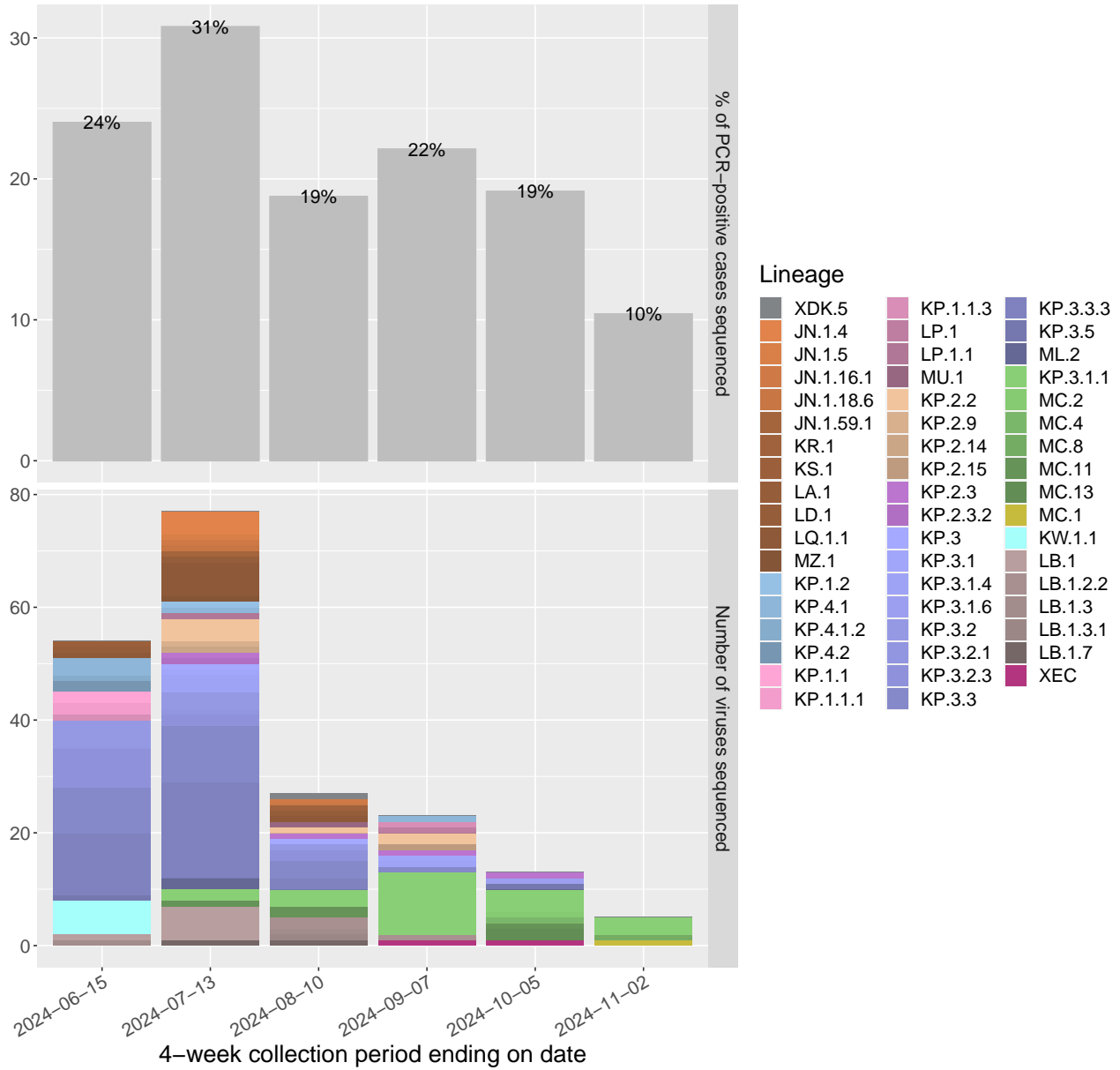


Figure Notes: Graph depicts SARS-CoV-2 variants by lineage identified in Hawaii County in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

Estimated Variant Proportions for Hawaii County

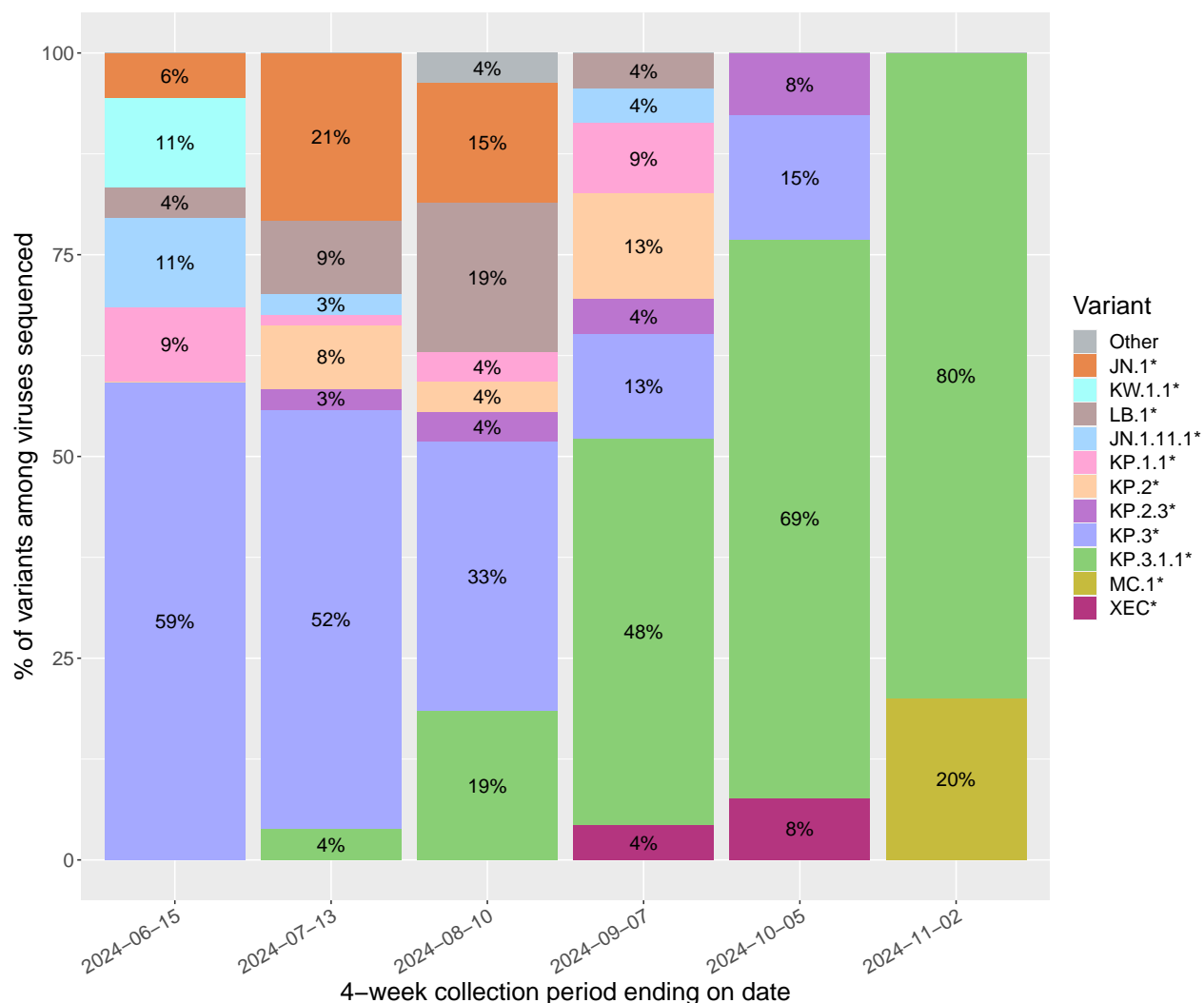


Figure Notes: Graph depicts an estimation of aggregated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Hawaii County, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant depicted is an aggregation of the parental lineage shown and its respective sub-lineages; an asterisk (*) indicates inclusion of sub-lineages. “Other”, when depicted, represents an aggregation of all other lineages not aggregated to the variants shown. The lineages aggregated to each variant can be deduced by the color gradient scheme in the previous figure.

Omicron Variants Detected in Hawaii County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				2908
	Other	01 Aug 2022	31 Oct 2023	1020
	BA.2.12.1	13 Apr 2022	12 Aug 2022	213
	BA.2	19 Jan 2022	27 Jun 2022	181
	XBB.1.5	27 Dec 2022	04 Aug 2023	173
	BA.5.2.1	12 Jun 2022	11 Dec 2022	163
	BA.1.1	13 Dec 2021	09 May 2022	156
	BA.2.3	30 Jan 2022	22 Jul 2022	90
	BA.1.1.2	10 Dec 2021	01 Mar 2022	65
	BQ.1.1	07 Oct 2022	27 Feb 2023	65
	BA.5.1	07 Jun 2022	23 Nov 2022	64
	BA.5.2	17 Jun 2022	11 Jan 2023	53
	BA.5.1.1	14 May 2022	28 Sep 2022	41
	KP.3.3.3	17 Apr 2024	05 Aug 2024	39
	BA.5.6	21 May 2022	28 Sep 2022	32
	XBB.1.16.1	27 Apr 2023	26 Jun 2023	31
	JN.1	22 Nov 2023	02 Mar 2024	30
	HV.1	19 Aug 2023	18 Jan 2024	29
	XBB.1.16	31 Mar 2023	26 Sep 2023	28
	BA.5.5	03 May 2022	12 Sep 2022	27
	BQ.1	11 Oct 2022	23 Jan 2023	27
	BG.5	13 Apr 2022	12 Jul 2022	26
	KP.3.3	30 Apr 2024	12 Aug 2024	26
	BA.1	17 Dec 2021	02 Mar 2022	25
	BA.1.15	10 Dec 2021	22 Mar 2022	24
	FL.1.5.1	08 Aug 2023	04 Nov 2023	24
	KP.3.1.1	09 Jul 2024	01 Nov 2024	23
	BQ.1.1.3	04 Nov 2022	16 Feb 2023	22
	BA.2.9	28 Mar 2022	03 Jul 2022	21
	BF.5	07 Jul 2022	25 Nov 2022	20
	XBB.1.9.1	16 May 2023	21 Jul 2023	20
	BA.2.18	24 Apr 2022	24 Jun 2022	19
	JN.1.4	22 Dec 2023	20 Jun 2024	19
	BA.4.1	16 Jun 2022	01 Sep 2022	16
	BQ.1.1.32	11 Jan 2023	07 Mar 2023	16
	CH.1.1	21 Nov 2022	16 Feb 2023	16
	EG.5.1.1	08 Jul 2023	16 Oct 2023	16
	FL.25	13 May 2023	31 Jul 2023	16
	KP.3.2.3	30 Apr 2024	16 Jul 2024	16
	XBB.1.16.19	29 Jun 2023	30 Aug 2023	16

Note: 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.

Pre-Omicron Variants Detected in Hawaii County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha				71
	B.1.1.7	22 Feb 2021	22 Jul 2021	57
	Q.3	21 Mar 2021	20 Aug 2021	14
Gamma				17
	P.1.10	27 May 2021	13 Jun 2021	12
	P.1	10 May 2021	02 Jun 2021	4
	P.1.17	14 Jun 2021	14 Jun 2021	1
Delta				951
	AY.44	11 Jun 2021	16 Dec 2021	229
	AY.3	31 Jul 2021	16 Dec 2021	123
	AY.103	21 May 2021	16 Dec 2021	113
	AY.25	19 Jul 2021	09 Nov 2021	110
	Other AY.*	01 Jul 2021	30 Jul 2021	85
	AY.100	17 Jul 2021	12 Nov 2021	54
	AY.25.1	28 Jul 2021	17 Dec 2021	45
	AY.118	08 Jul 2021	27 Sep 2021	41
	AY.117	11 Aug 2021	17 Nov 2021	30
	AY.122	19 Jul 2021	22 Sep 2021	29
	AY.46.4	21 Jun 2021	06 Dec 2021	27
	AY.119	03 Aug 2021	24 Nov 2021	24
	AY.1	20 Jul 2021	03 Sep 2021	18
	AY.26	24 Jun 2021	03 Dec 2021	18
	B.1.617.2	15 Jul 2021	08 Nov 2021	5
Epsilon				44
	B.1.429	25 Jan 2021	26 May 2021	38
	B.1.427	04 Feb 2021	17 May 2021	6
Iota	B.1.526	06 Feb 2021	07 Jul 2021	73
Mu	B.1.621	13 Jun 2021	13 Jun 2021	1

Note: 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

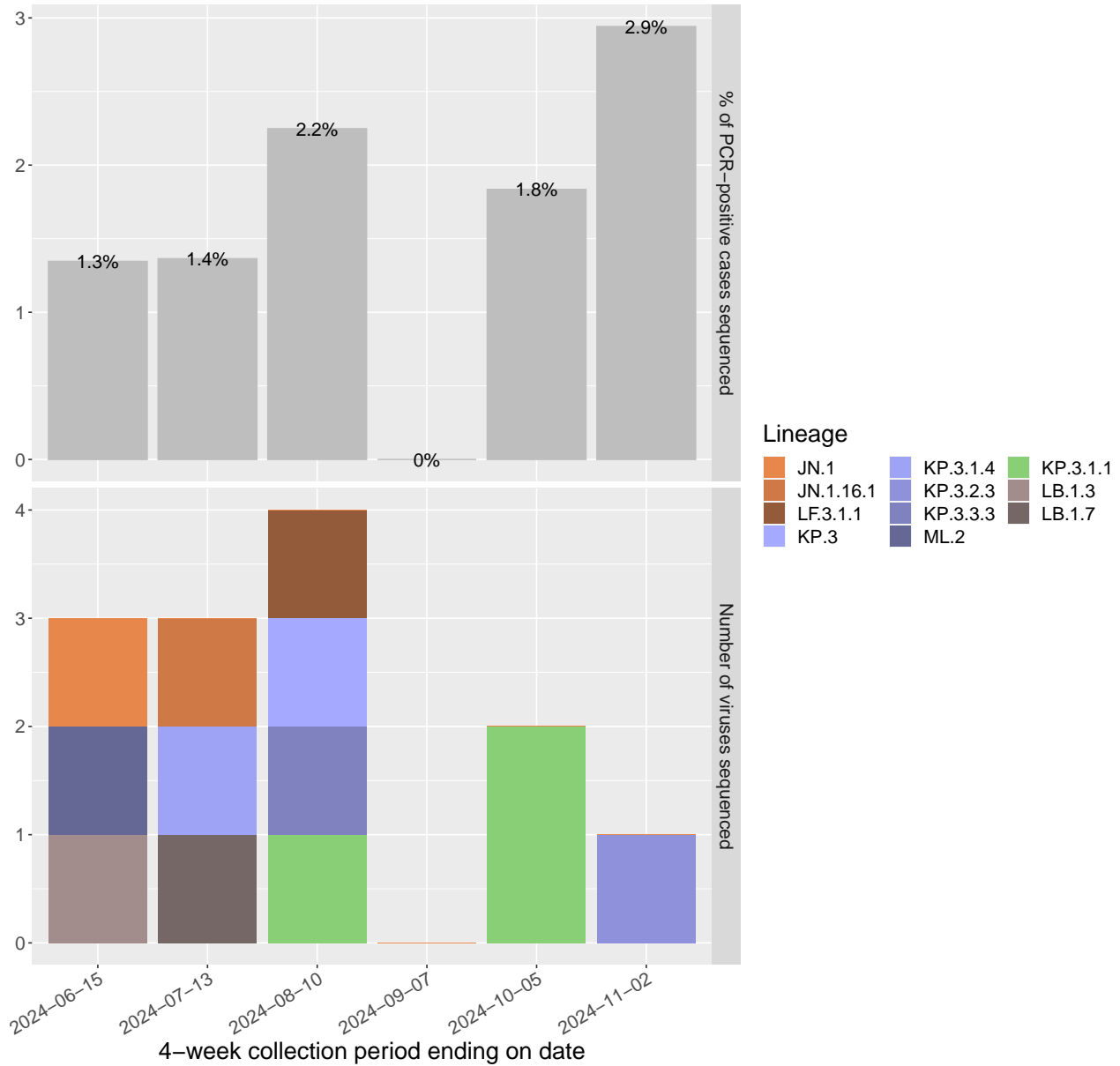


Figure Notes: Graph depicts SARS-CoV-2 variants by lineage identified in Kauai County in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

Due to its small population size and low case counts, very few PCR-positive specimens have been received for sequencing from Kauai County since Dec 2023.

Estimated Variant Proportions for Kauai County

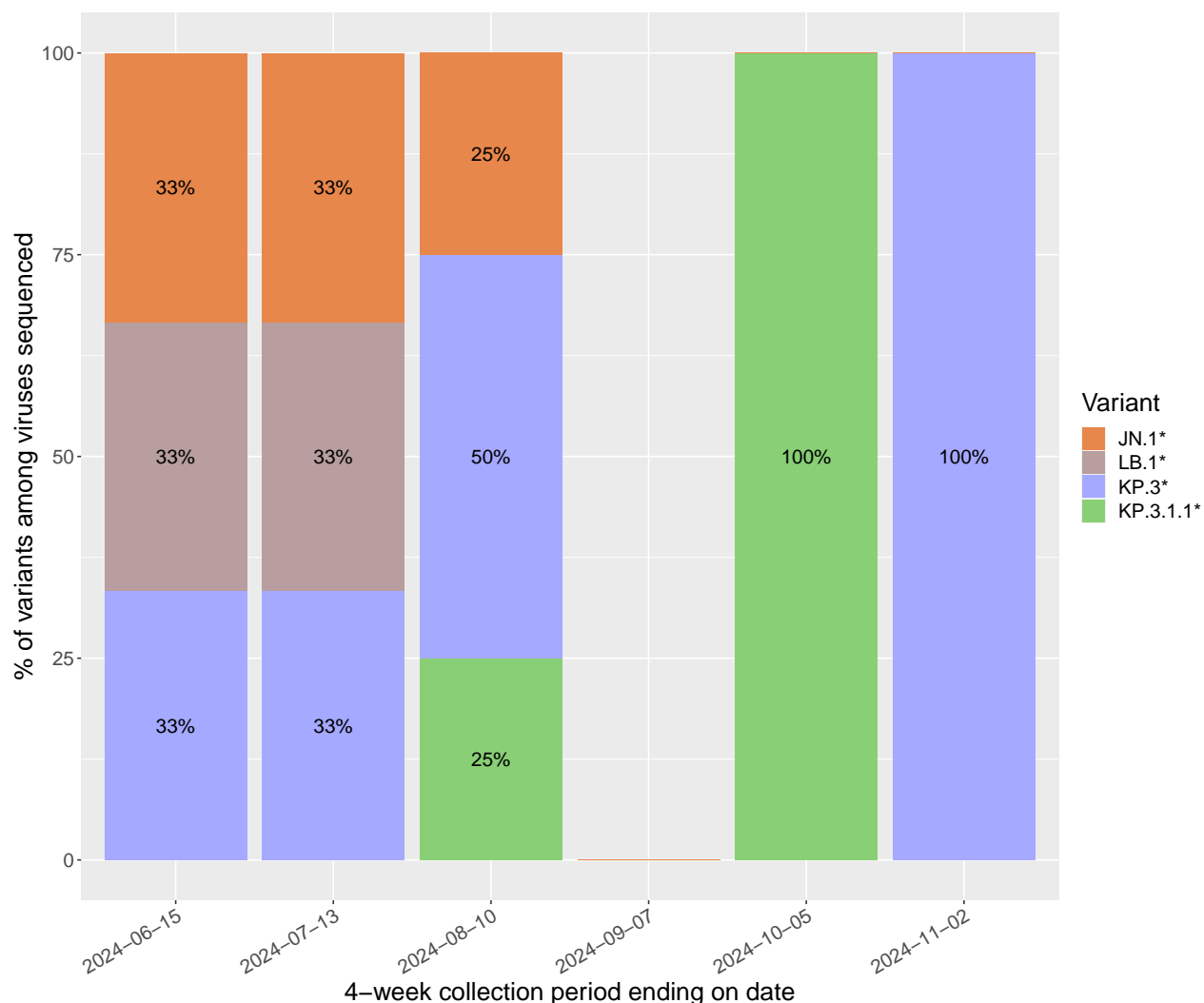


Figure Notes: Graph depicts an estimation of aggregated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Kauai County, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant depicted is an aggregation of the parental lineage shown and its respective sub-lineages; an asterisk (*) indicates inclusion of sub-lineages. “Other”, when depicted, represents an aggregation of all other lineages not aggregated to the variants shown. The lineages aggregated to each variant can be deduced by the color gradient scheme in the previous figure.

Due to its small population size and low case counts, very few PCR-positive specimens have been received for sequencing from Kauai County since Dec 2023.

Omicron Variants Detected in Kauai County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				609
	Other	01 Aug 2024	31 Oct 2023	145
	BA.2	17 Mar 2022	28 Jun 2022	82
	BA.2.12.1	30 Mar 2022	29 Jun 2022	61
	BA.1.1	15 Dec 2021	19 Apr 2022	60
	BA.5.2.1	03 Jun 2022	02 Nov 2022	32
	BA.2.3	09 Mar 2022	24 May 2022	19
	BA.5.5	13 Jun 2022	31 Aug 2022	18
	BA.1.15	28 Dec 2021	23 Mar 2022	13
	BA.5.1	23 Jun 2022	29 Sep 2022	13
	BA.1	16 Dec 2021	07 Feb 2022	12
	BA.5.2	02 Jul 2022	17 Nov 2022	10
	XAC	28 Apr 2022	14 Jun 2022	9
	XBB.1.5	11 Jan 2023	14 Jun 2023	9
	BA.1.1.18	28 Dec 2021	21 Mar 2022	8
	BA.1.1.2	15 Dec 2021	09 Feb 2022	8
	BA.2.18	24 Apr 2022	16 Jun 2022	8
	BA.2.42	07 May 2022	02 Jul 2022	8
	BQ.1.1	04 Nov 2022	27 Jan 2023	8
	BG.5	03 May 2022	13 Jun 2022	7
	BQ.1	30 Sep 2022	06 Feb 2023	7
	BA.4.1	08 Jun 2022	26 Jun 2022	6
	BF.10	13 Jun 2022	19 Aug 2022	6
	BA.1.18	15 Dec 2021	04 Jan 2022	5
	BA.2.9	17 Mar 2022	09 May 2022	5
	EG.5.1.1	12 Sep 2023	18 Oct 2023	5
	EG.5.1.14	22 May 2023	29 Jun 2023	5
	BA.4.6	23 Aug 2022	04 Nov 2022	4
	BA.4.6.5	23 Aug 2022	04 Nov 2022	4
	BA.5.2.9	27 Jun 2022	30 Aug 2022	4
	BA.5.6	16 Jun 2022	29 Aug 2022	4
	BE.3	15 Jun 2022	17 Oct 2022	4
	BF.5	21 Jun 2022	17 Oct 2022	4
	HF.1	09 Aug 2023	28 Sep 2023	4
	HV.1	30 Aug 2023	05 Dec 2023	4
	XBB.1.5.72	20 Jul 2023	03 Oct 2023	4
	XBB.1.9.2	14 Apr 2023	08 May 2023	4

Note: 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.

Pre-Omicron Variants Detected in Kauai County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha	B.1.1.7	05 Apr 2021	13 Jul 2021	20
Gamma				2
	P.1	31 May 2021	31 May 2021	1
	P.1.10	14 May 2021	14 May 2021	1
Delta				246
	AY.25	16 Jul 2021	10 Nov 2021	70
	AY.44	29 Jun 2021	21 Dec 2021	37
	AY.119	28 Aug 2021	21 Dec 2021	35
	Other AY.*	03 Nov 2021	29 Nov 2021	25
	AY.47	27 Jul 2021	29 Nov 2021	19
	AY.1	09 Aug 2021	30 Aug 2021	18
	AY.103	01 Aug 2021	15 Dec 2021	17
	AY.3	30 Sep 2021	15 Dec 2021	8
	AY.54	06 Jul 2021	09 Nov 2021	8
	AY.67	06 Jun 2021	30 Jun 2021	7
	B.1.617.2	21 Sep 2021	18 Oct 2021	2
Epsilon				31
	B.1.429	07 Jan 2021	08 May 2021	29
	B.1.427	27 Apr 2021	27 Apr 2021	2
Iota	B.1.526	14 Apr 2021	14 Apr 2021	1
Mu	B.1.621	29 Jun 2021	06 Jul 2021	2

Note: 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.