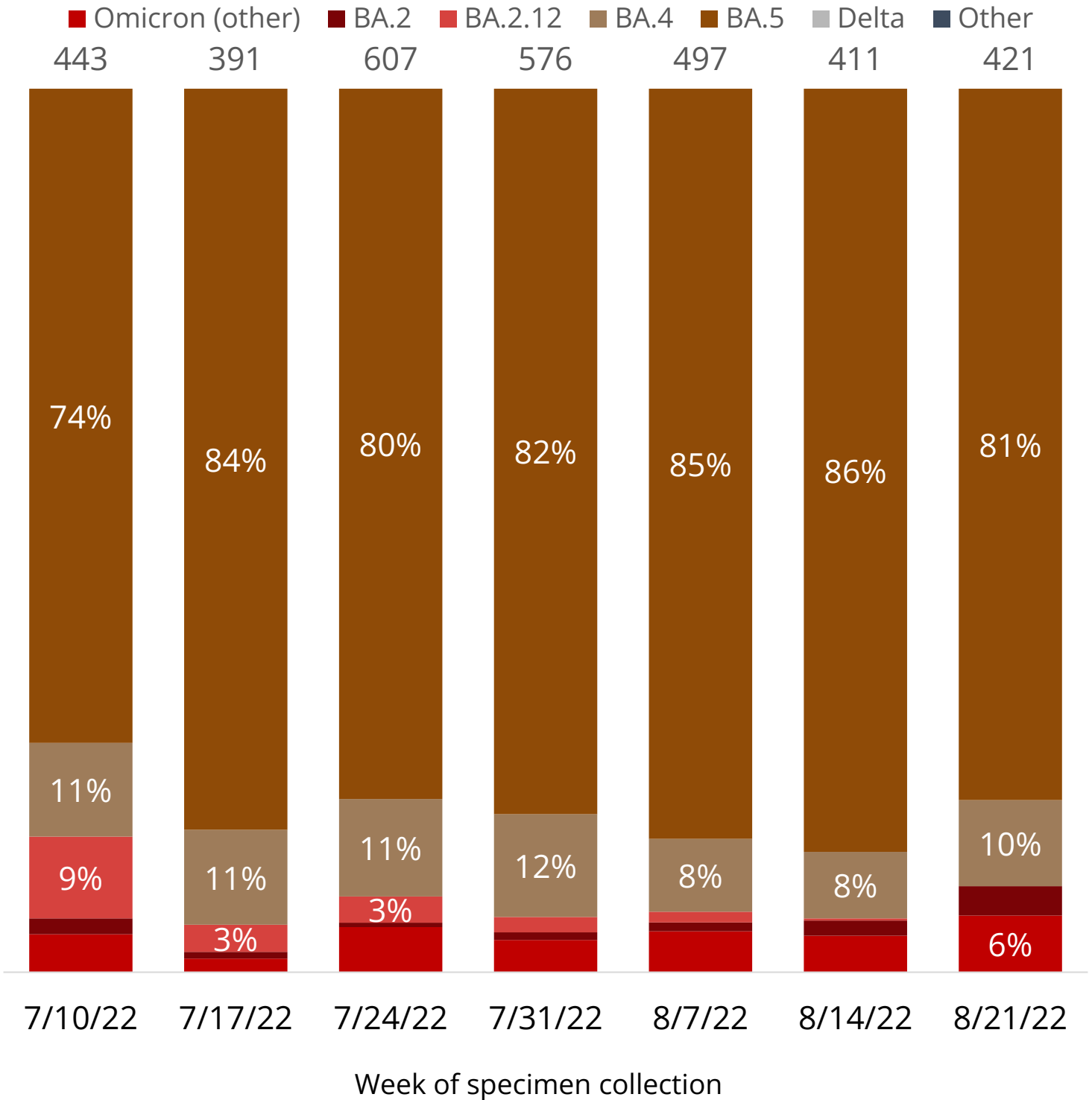
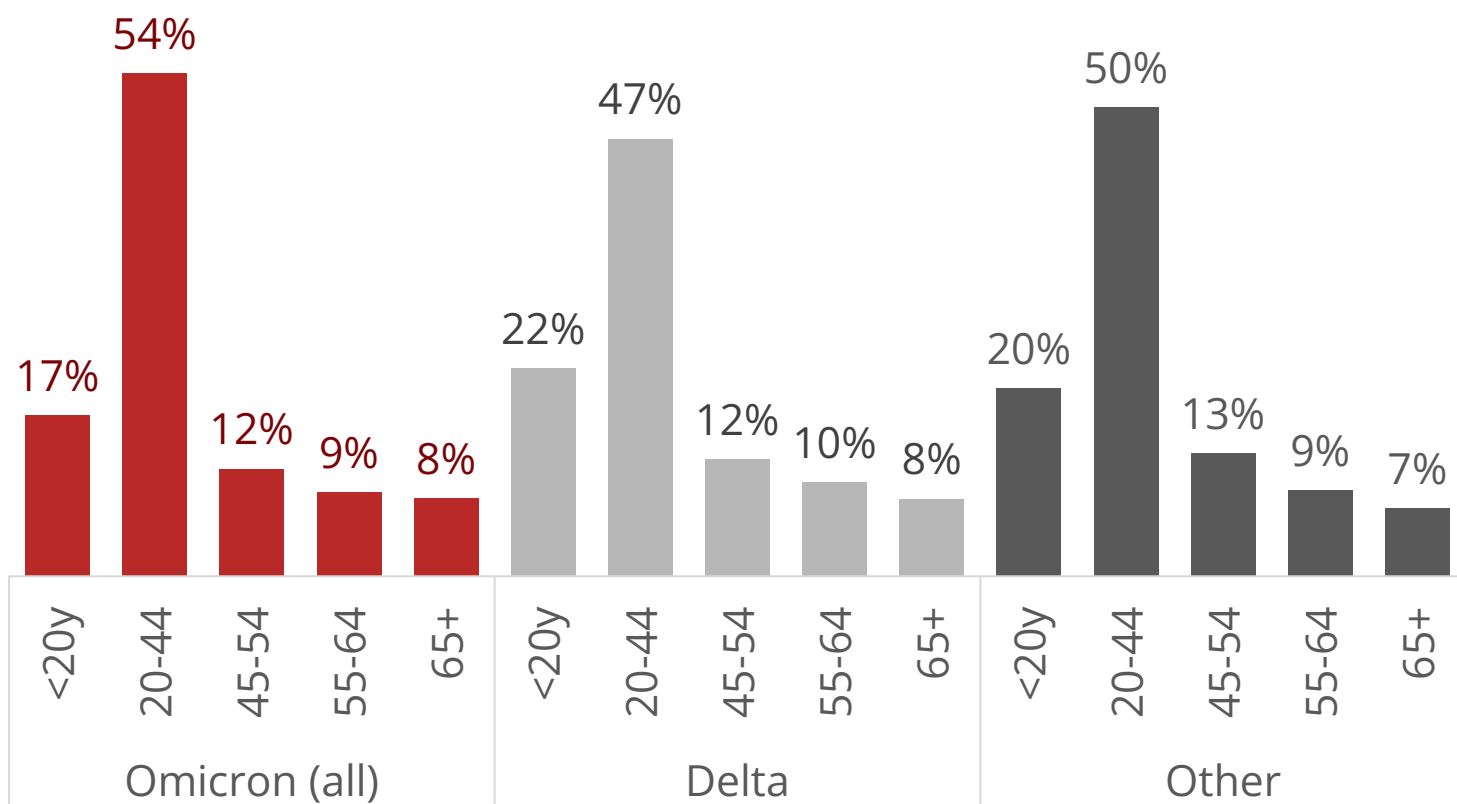


Omicron has been the major circulating variant in Arizona since mid-December 2021. BA.4 and BA.5 became the predominant Omicron sub-variants in June 2022.



Data timeframe represented above: 7/10/2022 to 8/27/2022

Sequenced COVID-19 cases, by variant, for each age group and county



County of Residence	Omicron (other)	Omicron BA.2	Delta	Other	Total Sequenced
Apache	39.1%	5.4%	40.3%	14.9%	570
Cochise	42.1%	7.5%	36.5%	13.5%	889
Coconino	43.6%	4.4%	32.0%	19.9%	9,332
Gila	12.8%	3.1%	54.3%	29.6%	256
Graham	24.5%	13.2%	36.8%	25.5%	212
Greenlee	12.2%	7.3%	75.6%	4.8%	41
La Paz	34.1%	12.2%	34.1%	19.5%	41
Maricopa	38.5%	7.9%	32.6%	20.8%	59,075
Mohave	26.4%	2.1%	53.7%	17.3%	1,928
Navajo	36.7%	7.3%	41.1%	14.4%	1,247
Pima	32.5%	7.6%	41.8%	17.1%	11,230
Pinal	26.0%	4.0%	46.7%	22.5%	4,069
Santa Cruz	42.4%	5.2%	36.4%	16.2%	462
Yavapai	22.8%	4.0%	57.6%	14.2%	1,351
Yuma	33.1%	3.5%	45.5%	16.6%	1,794
Totals	34,223	6,489	32,965	18,434	92,497

Data timeframe represented above: 1/1/2021 to 8/27/2022

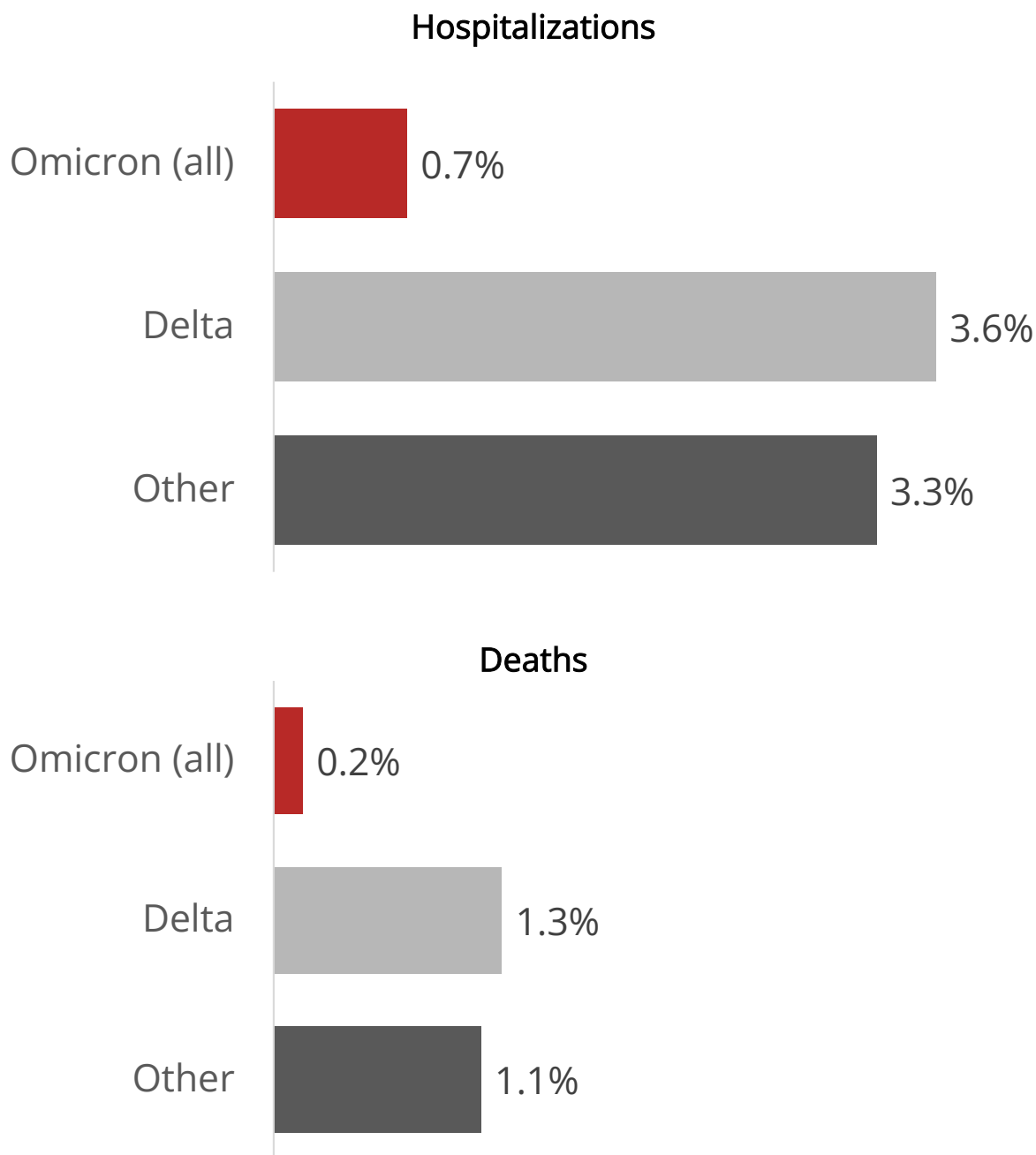
NOTE: BA.2.12 & BA.2.12.1 are included under the BA.2 column.

Hospitalizations and deaths of COVID-19 cases, by variant

These graphs show the proportion of sequenced cases for each variant that were hospitalized or died due to COVID-19.

At this time, cases with the Omicron variant were less likely to be hospitalized or die compared to other sequenced cases.

Omicron includes all of its circulating sub-variants in AZ.

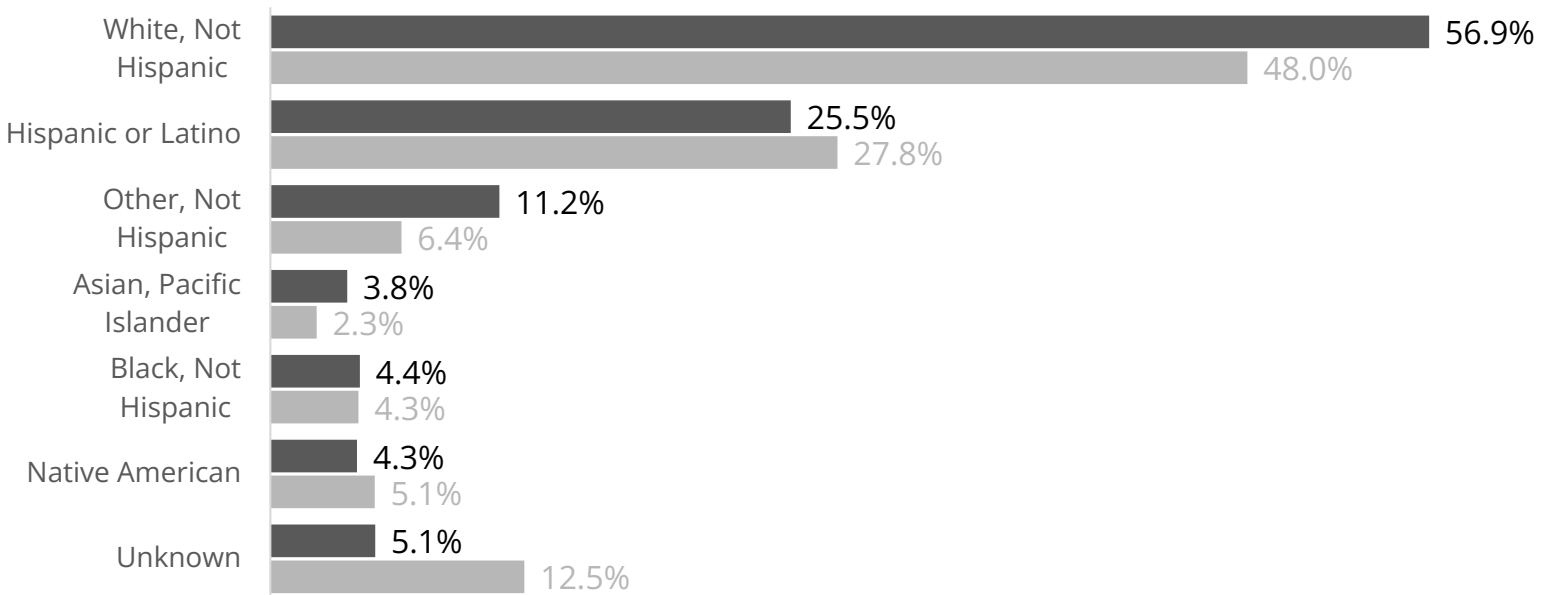
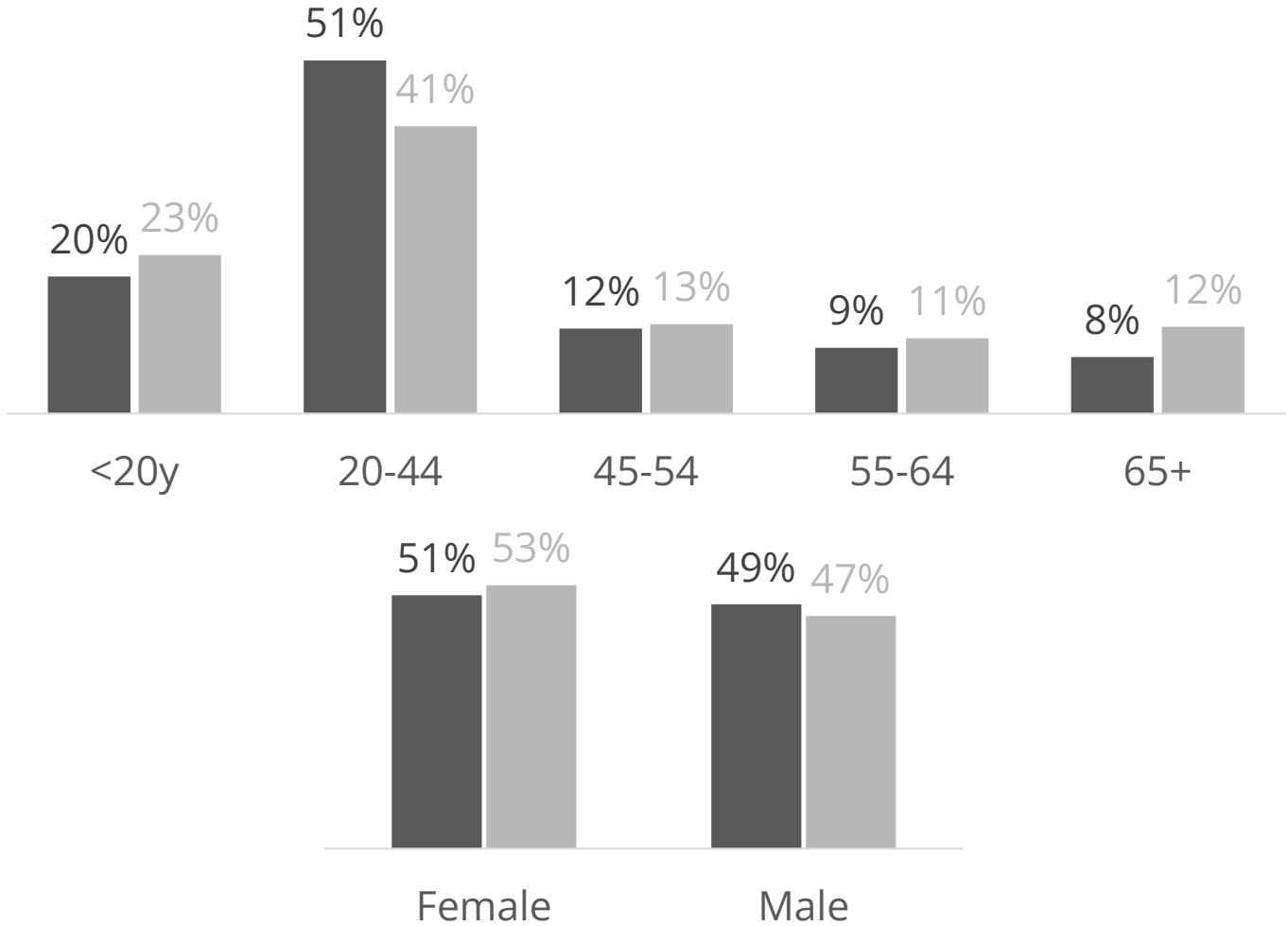


These numbers will change as more information about hospitalizations and deaths is received by ADHS for sequenced cases.

Data timeframe represented above: 1/1/2021 to 8/27/2022

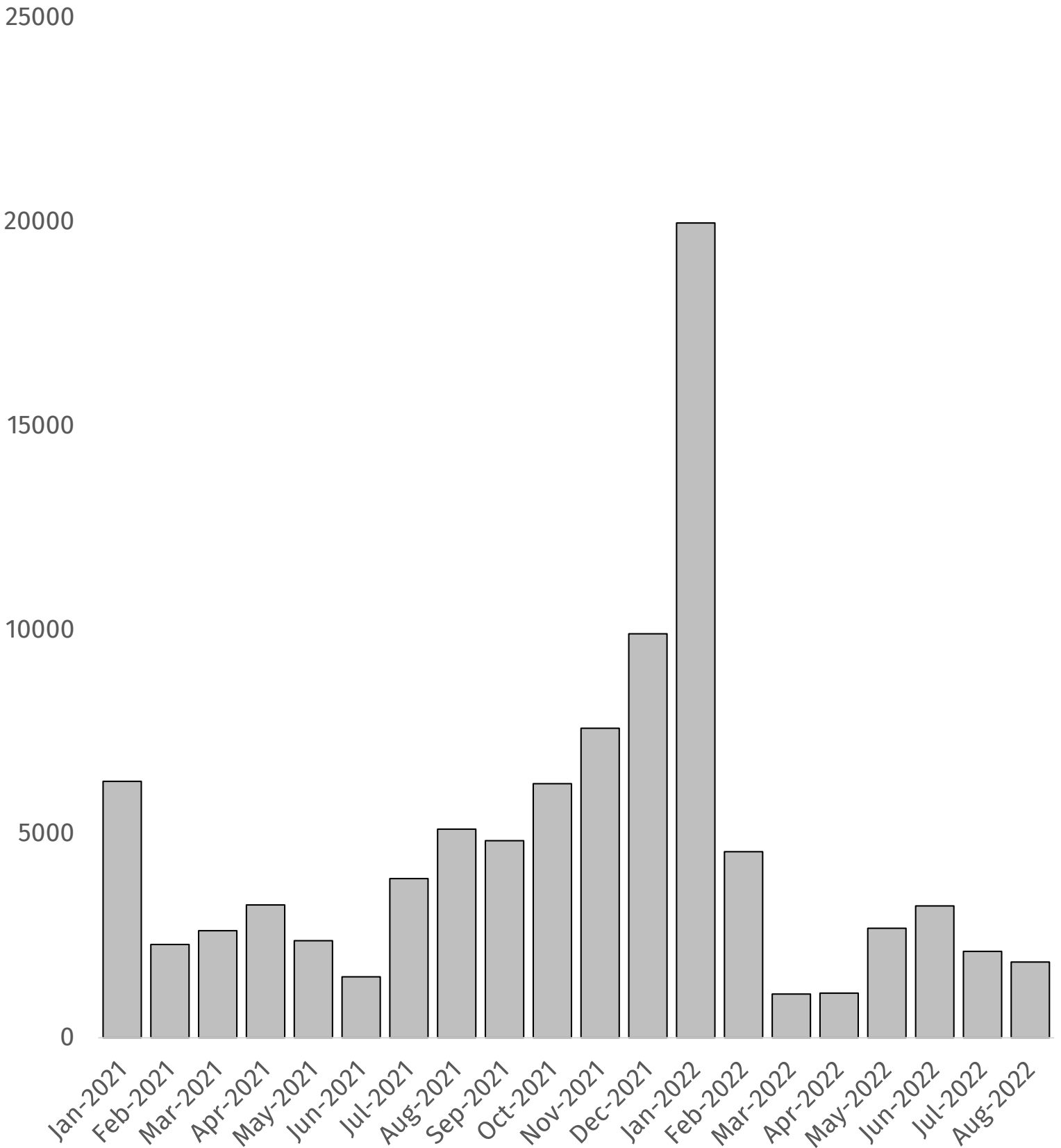
Proportion of COVID-19 cases sequenced compared to case demographics

Demographics for Arizona's sequenced cases resemble those for all 2021 through August 27, 2022 COVID-19 cases, although a higher proportion of cases aged 20-44 years have been sequenced.



Data timeframe represented above: 1/1/2021 to 8/27/2022

Number of COVID-19 cases sequenced, by month of specimen collection



Data timeframe represented above: 1/1/2021 to 8/27/2022

About the data:

- Facilities performing laboratory tests for COVID-19 report positive COVID-19 test results to ADHS pursuant to Arizona Administrative Code R9-6-204.
- Laboratories collect specimens from across the state. Sequencing is performed by specialized laboratories on a sample of specimens. The sequencing results are sent to ADHS and matched to case data.
- The sequencing data shown in this report represent lineage data that has been matched to reported and confirmed COVID-19 cases. Only one sequencing result is shown for a case with multiple results.
- The data timeframe on page 1 (cases with sequenced specimens collected July 10, 2022 to August 27, 2022) was selected to show the prevalence of Omicron and emergence of the Omicron sub-variants BA.4 and BA.5.
 - BA.2 includes all sub-variants (BA.2.3, BA.2.9, etc.), except those beginning with BA.2.12.
 - BA.2.12 includes all sub-variants (BA.2.12.1, BG.2,etc.).
 - BA.4 and BA.5 include all sub-variants respectively (BF.1, BE.1, etc.).
- The remainder of the report includes the total accumulated cases with sequenced specimens collected January 1, 2021 to August 27, 2022.
 - This data was compiled, verified, and matched by ADHS .
- Sequencing data is derived from whole genome sequencing performed on a proportion of positive COVID-19 samples in Arizona. Not every positive sample for COVID-19 is sequenced.
- ADHS receives data from various partners, affecting the timing of when summarized sequencing data will be available for any given period. Samples are collected, tested for COVID-19, delivered to the respective laboratories then sequenced. ADHS partners validate the quality of the data and report the results. There is time between each step of the process for matching sequence data to case data.
- COVID-19 sequencing data is reported to ADHS at a rapid rate. Interpretation of the data presented should consider that sequencing data is continuously updated.
- Please consult with public health if making clinical decisions based on circulating variant proportions.