COVID-19 Variant of Concern (VOC) 2023 Annual Report

January 1, 2023-December 31, 2023

COVID-19 Genomic Surveillance

Monitoring COVID-19 variants is an important part of epidemiologic surveillance to track the impact of SARS-CoV-2 mutations, which naturally occur over time. As the virus evolves, many variants will emerge and be identified; however, only a small minority will be classified as variants being monitored (VBM), variants of interest (VOI), or variants of concern (VOC). Variants are classified in these groups depending on whether the new mutations cause changes in transmissibility (i.e., how well the virus spreads between people), disease severity, detection by current diagnostic tests, or ability to evade monoclonal antibody treatments, natural immunity, or vaccine-induced immunity. Only a small proportion of COVID-19 cases have been sequenced since standard diagnostic tests do not test for specific variant strains and must be sent to a laboratory for sequencing. Genetic sequencing requires coordinated effort and time and there is a lag time from specimen collection to reporting of approximately 3-4 weeks. This lag time means that results cannot be interpreted and acted upon immediately to influence public health policies.

In this report you will find information about variants of concern circulating in New Mexico in 2023 including the number of specimens sequenced, the associated health outcomes, variant distribution by county, race and ethnicity, and age group when available. Data presented in this report are not representative of all COVID-19 cases because at-risk populations were oversampled, like hospitalized patients, residents in congregate settings such as long-term care facilities and correctional facilities, and vaccine reinfection cases. Due to changing national and state public health priorities, testing practices, and policies such as the end of the COVID-19 public health emergency in May 2023, positive cases and sequenced specimens declined, therefore there are only 4,612 sequenced specimens reported to NMDOH in 2023. Throughout 2023 in New Mexico, Omicron sublineages were dominant. Of the Omicron sublineages, XBB.1.5 was the most common (2,033) after its emergence at the end of 2022, and BA.5 was the second most common (647). The contact tracing and case investigation program was terminated in November 2022; therefore, symptoms and underlying conditions were no longer being routinely collected by interview for COVID positive patients in 2023 and are not included in the 2023 annual report.

In 2023, the highest amount of weekly positive COVID cases were reported the week of November 13th, 2023 (n=2,154). Over the course of 2023 in NM, a total of 4,612 sequenced specimens were reported to NMDOH Epidemiology and Response Division (ERD). Of those, the Variant Investigation Team was able to match 4,196 (91%) specimens to their associated patient profile including social characteristics and health outcomes of interest, when reported. The total NM sequences for 2023 reported on GISAID[1] is 4,331, of which, 100% were reported to NMDOH[2]. Cases peaked in NM on November 6th, 2022, with 508 positive cases reported that day. The following sublineages[3] of Omicron are reported in the 2023 annual report: BA.2 (37), BA.2.86 (15), BA.5 (647), XBB (116), XBB.1.5 (2033), XBB.1.9.1 (209), XBB.1.9.2 (63), XBB.1.16 (585), XBB.2.3 (92), EG.5 (392), HV.1 (337), and JN.1 (86).[4,5] From January 1st to February 2nd 2023 BA.5 was the dominant sublineage (greater than 50% of sequenced specimens). From February 6th to July 3rd, 2023, XBB.1.5 was the dominant sublineage. The remainder of the year (July 4-December 31st 2023) no Omicron sublineage was sequenced at a proportion greater than 50%.

[1]Global Initiative on Sharing Influenza Data (GISAID) is a global repository for infectious disease sequencing results such as influenza, COVID-19, and MPox (gisaid.org).

[2]There are multiple reasons some sequences are not catalogued on GISAID: submissions are sometimes flagged and held until manual review of the sequence can be completed by the submitter; GISAID will flag sequences with anomalies including known deletions and mutations and will not post them until manual review has been completed; reported sequences may not have been uploaded into the GISAID repository by the time of this report.

[3]Sublineage is a term used to indicate closely related virus strains and their direct relationship to a common ancestor. E.g. BA.2.75 is a sublineage of BA.2, and both are sublineages of Omicron (B.1.1.529). SARS-CoV-2 Variant Classifications and Definitions (cdc.gov)

[4]Additional sublineages may be included in these parent lineages. When relevant, these are listed in the appendix.

[5]The total sequenced specimens are all sequencing results reported to NMDOH in 2023 and may include out of state residents.

NM COVID-19 Variant Epidemiologic Interpretation

CDC VARIANTS OF CONCERN (VOC) New Mexico 2023	
Name	New Mexico
Omicron (B.1.1.529 and BA sublineages)	-Omicron and its sublineages became dominant 12/27/21 representing 67% of cases and continued to remain dominant at 100% of sequenced specimens throughout 2023. -A total of 4612 specimens were sequenced in 2023.

[1]https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html

Number of specimens sequenced and matched to case investigations

Lineage	Sequenced Specimens	Matched Cases[1]	Percent Matched
BA.2 (Omicron)	37	32	86%
BA.2.86 (Omicron)	15	13	87%
BA.5 (Omicron)	647	589	91%
XBB (Omicron)	116	109	94%
XBB.1.5 (Omicron)	2033	1867	92%
XBB.1.9.1 (Omicron)	209	189	90%
XBB.1.9.2 (Omicron)	63	58	92%
XBB.1.16 (Omicron)	585	527	90%
XBB.2.3 (Omicron)	92	84	91%
EG.5 (Omicron)	392	360	92%
HV.1 (Omicron)	337	294	87%
JN.1 (Omicron)	86	74	86%
Total	4612	4196	91%

[1]Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 79 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico. These have been removed from the subsequent tables and figures.

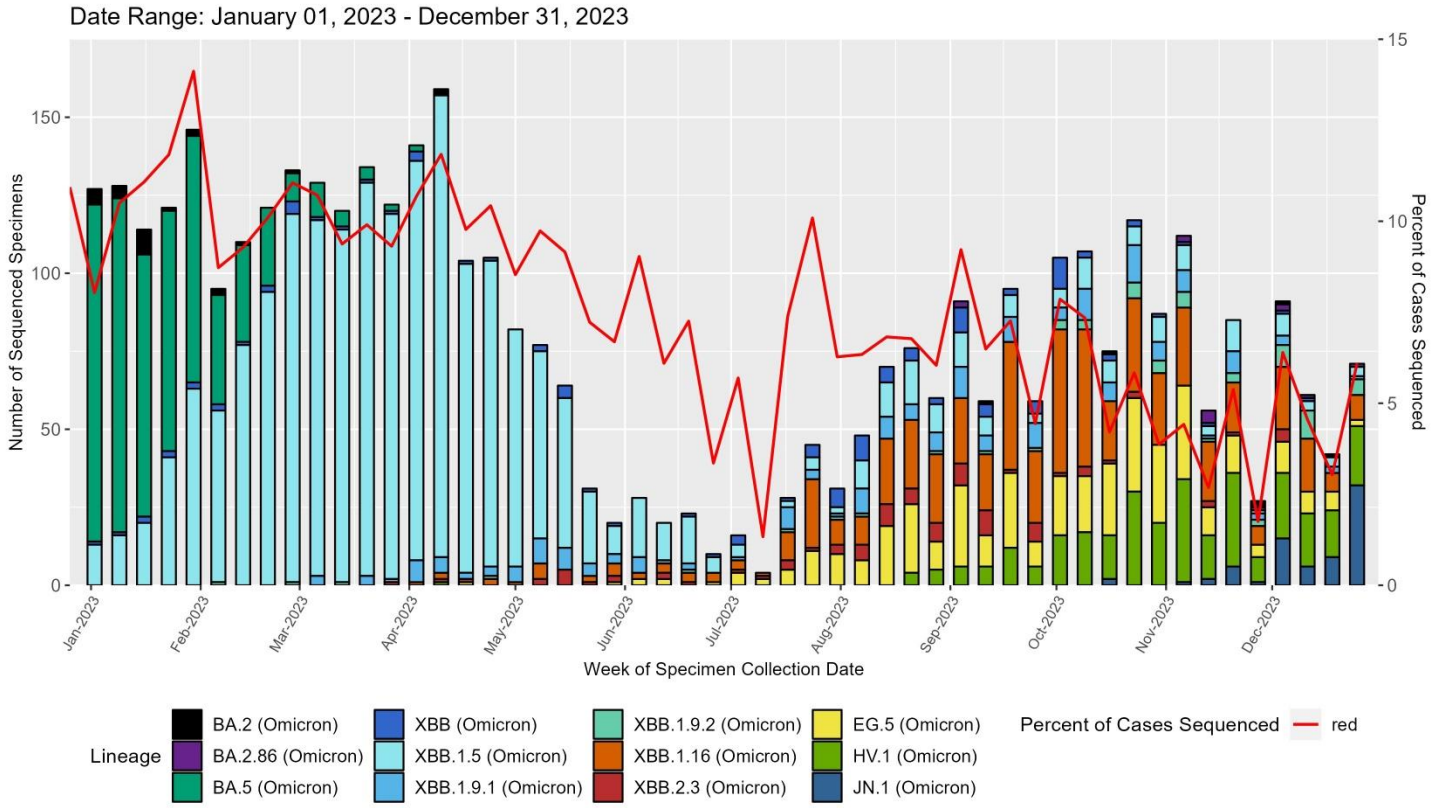
Health outcomes of matched New Mexico resident cases

Lineage	Matched Cases[1]	Number Hospitalized (%)	Number Died (%)	Number Reinfection[2] (%)
BA.2 (Omicron)	30	4 (13%)	1 (3%)	9 (30%)
BA.2.86 (Omicron)	13	1 (8%)	0 (0%)	6 (46%)
BA.5 (Omicron)	580	77 (13%)	7 (1%)	129 (22%)
XBB (Omicron)	106	18 (17%)	0 (0%)	30 (28%)
XBB.1.5 (Omicron)	1834	362 (20%)	11 (1%)	502 (27%)
XBB.1.9.1 (Omicron)	187	42 (22%)	0 (0%)	61 (33%)
XBB.1.9.2 (Omicron)	55	17 (31%)	0 (0%)	17 (31%)
XBB.1.16 (Omicron)	516	112 (22%)	0 (0%)	163 (32%)
XBB.2.3 (Omicron)	84	15 (18%)	0 (0%)	26 (31%)
EG.5 (Omicron)	347	101 (29%)	0 (0%)	99 (29%)
HV.1 (Omicron)	293	84 (29%)	0 (0%)	75 (26%)
JN.1 (Omicron)	72	12 (17%)	0 (0%)	18 (25%)

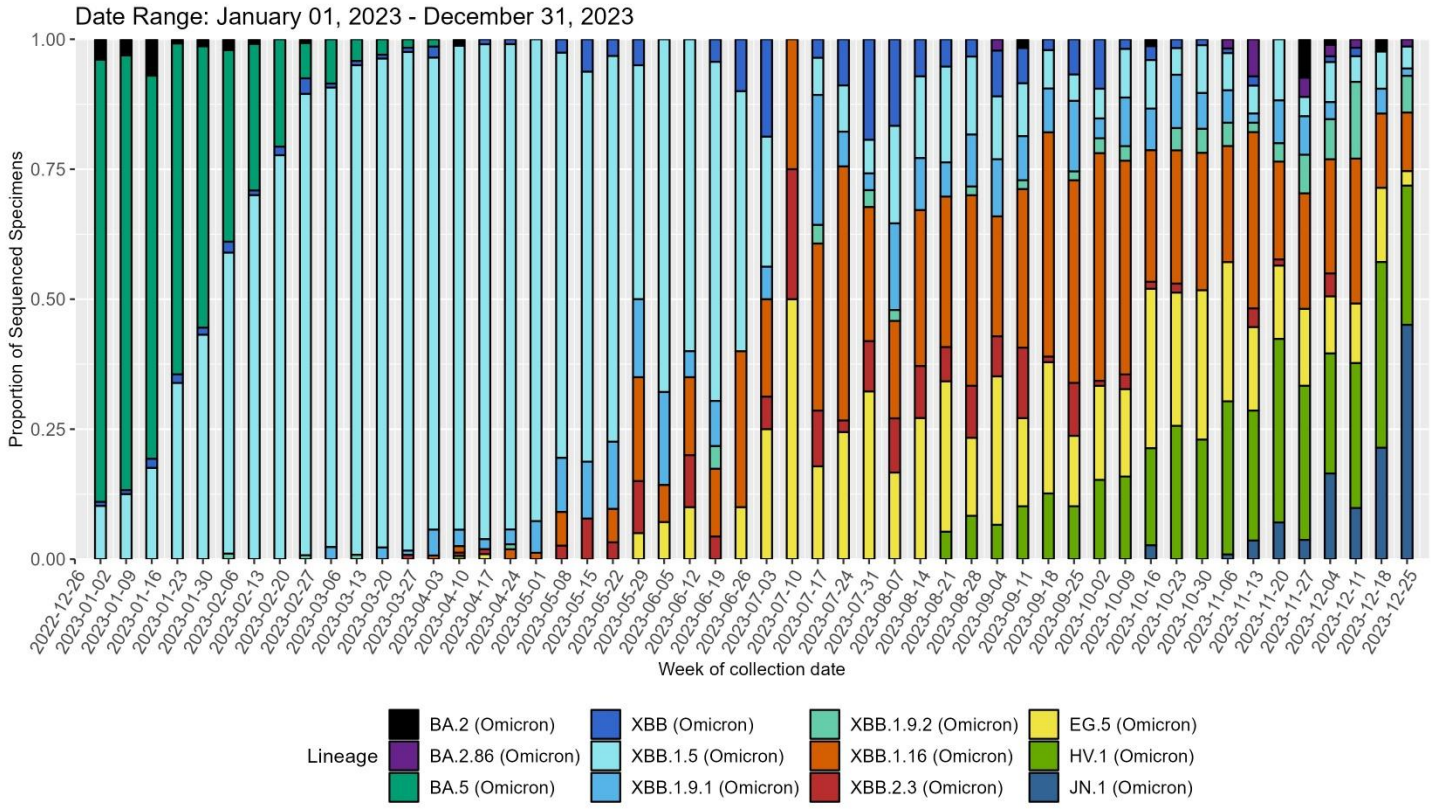
[1]Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table excludes 79 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico and are removed from subsequent tables and figures.

[2]A COVID Reinfection is defined by a laboratory confirmed positive case occurring in the same patient >90 days from a prior infection.

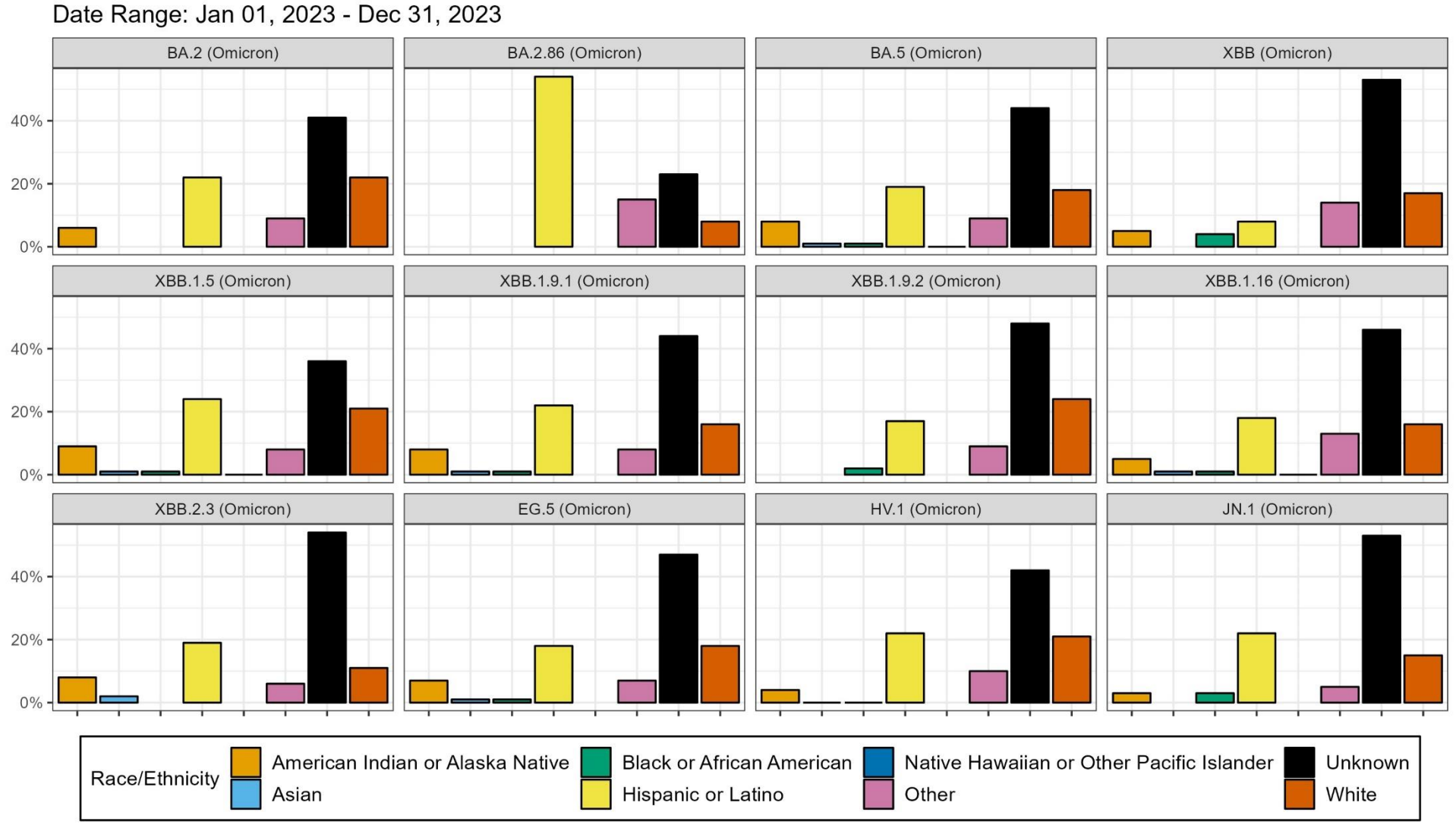
Identified SARS-CoV-2 lineages by week



Proportion of identified SARS-CoV-2 lineages by week



Cumulative percentage of sequenced specimens by variant and race/ethnicity[1]



[1]Sampling was consistent, but not random, so the absolute percentage of cases by race/ethnicity and age group do not reflect the distribution of all cases when a variant was dominant. However, the changes in the relative distribution can reflect differences in relative risk of infection during times when different variants were dominant. In variants of concern with small numbers of matched cases, group percentages may not reflect actual differences in risk among racial, ethnic, or age categories.

Cumulative percentage of sequenced specimens by variant and age group[1]

[1]Sampling was consistent, but not random, so the absolute percentage of cases by race/ethnicity and age group do not reflect the distribution of all cases when a variant was dominant. However, the changes in the relative distribution can reflect differences in relative risk of infection during times when different variants were dominant. In variants of concern with small numbers of matched cases, group percentages may not reflect actual differences in risk among racial, ethnic, or age categories.

Cumulative number of sequenced specimens by variant and county of residence													
County	BA.2 (Omicron)	BA.2.86 (Omicron)	BA.5 (Omicron)	EG.5 (Omicron)	HV.1 (Omicron)	JN.1 (Omicron)	XBB (Omicron)	XBB.1.16 (Omicron)	XBB.1.5 (Omicron)	XBB.1.9.1 (Omicron)	XBB.1.9.2 (Omicron)	XBB.2.3 (Omicron)	Total
Bernalillo	12	1	189	107	98	29	23	177	735	62	17	21	1471
Chaves	1	9	10	19	12	1	2	38	14	7	1	3	117
Cibola	0	0	20	10	5	1	1	9	71	4	0	3	124
Curry	3	0	71	24	8	4	31	40	117	9	7	16	330
Dona Ana	2	0	28	23	8	1	2	19	72	8	6	3	172
Grant	1	0	14	2	4	0	5	5	24	1	1	1	58
Lincoln	2	0	28	17	10	5	5	20	62	9	3	5	166
Luna	0	0	3	7	6	3	3	15	13	3	2	1	56
Otero	0	0	6	14	3	1	2	12	13	6	2	1	60
Quay	0	0	8	5	2	2	3	16	31	2	2	2	73
Rio Arriba	0	2	23	19	29	3	5	38	95	13	2	4	233
San Juan	0	1	11	3	9	1	2	8	52	7	0	3	97
San Miguel	0	0	6	2	3	0	3	5	30	2	1	4	56
Sandoval	3	0	53	50	29	11	7	48	182	22	6	4	415
Santa Fe	5	0	54	19	31	5	8	27	152	17	4	6	328
Socorro	1	0	23	5	10	2	1	12	42	2	1	2	101
Valencia	0	0	7	15	8	2	1	16	58	6	1	2	116
Lincoln	2	0	28	17	10	5	5	20	62	9	3	5	166

Counties with less than 50 matched sequenced cases are not included in the table above.

Appendix

List of additional sublineages and their parent sublineage categorization[1], when relevant.

Sublineage	New Mexico
BA.2	-BA.2 includes the following sublineages of Omicron: BA.4.6, BM.2, BN.1, BN.1.3, BN.1.3.1, BN.1.5, BN.1.9, CH.1.1, CH.1.1.1, CH.1.1.3, DF.1.1, DV.1.1, DV.7.1, and DV.7.1.5.
BA.2.86	BA.2.86 includes the following sublineages of Omicron: BA.2.86, BA.2.86.1, and XDD.
XBB	-XBB includes the following sublineages of Omicron: FE.1, FE.1.1, FE.1.1.1, FY.1, FY.2, FY.3, FY.3.1, FY.4, FY.4.1, FY.4.2, FY.5, GD.1, XBB.1, XBB.1.19.1, XBB.1.4, XBB.1.41, XBB.1.42, XBB.1.42.1, XBB.1.42.2, XBB.1.6, and XBB.2
BA.5	-BA.5 includes the following sublineages of Omicron: BA.5.1.30, BA.5.2, BA.5.2.1, BA.5.2.20, BA.5.2.23, BA.5.2.26, BA.5.2.35, BA.5.2.59, BA.5.2.6, BA.5.2.9, BA.5.3.1, BE.1.1, BF.10, BF.21, BF.26, BF.32, BF.7, BF.7.21, BF.7.4, BF.7.4.1, BF.7.5.1, BF.7.6, BQ.1, BQ.1.1, BQ.1.1.1, BQ.1.1.11, BQ.1.1.13, BQ.1.1.18, BQ.1.1.22, BQ.1.1.23, BQ.1.1.24, BQ.1.1.28, BQ.1.1.3, BQ.1.1.31, BQ.1.1.32, BQ.1.1.4, BQ.1.1.40, BQ.1.1.41, BQ.1.1.44, BQ.1.1.45, BQ.1.1.5, BQ.1.1.52, BQ.1.1.61, BQ.1.1.63, BQ.1.1.65, BQ.1.1.69, BQ.1.1.7, BQ.1.1.8, BQ.1.10, BQ.1.11, BQ.1.12, BQ.1.13, BQ.1.13.1, BQ.1.14, BQ.1.15, BQ.1.16, BQ.1.18, BQ.1.2, BQ.1.2.3, BQ.1.22, BQ.1.23, BQ.1.24, BQ.1.25, BQ.1.25.1, BQ.1.26.1, BQ.1.28, BQ.1.3, BQ.1.5, BQ.1.6, BQ.1.8, BQ.1.9, BU.1, BW.1.1, BW.1.1.1, CK.1, CK.1.5, CQ.2, DE.2, DQ.1, DT.2, DU.1, and XBF.
EG.5	EG.5 includes the following sublineages of Omicron: EG.1, EG.1.7, EG.10, EG.10.1, EG.11, EG.2, EG.5, EG.5.1, EG.5.1.1, EG.5.1.13, EG.5.1.16, EG.5.1.3, EG.5.1.4, EG.5.1.6, EG.5.1.8, EG.5.2, EG.5.2.1, EG.5.2.3, EG.6.1, and EG.7
HV.1	HV.1 includes the following sublineages of Omicron: HV.1, HV.1.1, HV.1.10, HV.1.11, and HV.1.6.1.
JN.1	JN.1 includes the following sublineages of Omicron: JN.1, JN.1.1, JN.1.4, JN.1.5, and JN.1.9.
XBB.1.5	XBB.1.5 includes the following sublineages of Omicron: EL.1, EU.1.1, FD.1.1, FD.2, ,FD.4, FH.1, FK.1.1, FK.1.3.2, FT.3.1, FT.3.1.1, GB.1, GK.1, GK.1.1, GK.1.4, GK.2, GK.2.1, GK.3, GK.3.1, GK.7, GN.1, GN.1.1, GR.1, GV.1, HS.1.1, HT.1, HY.1, HZ.1, JD.1, JD.1.1, JD.1.1.1, JD.1.1.3, XBB.1.5, XBB.1.5.1, XBB.1.5.10, XBB.1.5.100, XBB.1.5.11, XBB.1.5.110, XBB.1.5.12, XBB.1.5.13, XBB.1.5.14, XBB.1.5.15, XBB.1.5.16, XBB.1.5.17, XBB.1.5.18, XBB.1.5.19, XBB.1.5.2, XBB.1.5.20, XBB.1.5.21, XBB.1.5.25, XBB.1.5.27, XBB.1.5.28, XBB.1.5.3, XBB.1.5.30, XBB.1.5.31, XBB.1.5.32, XBB.1.5.33, XBB.1.5.35, XBB.1.5.36, XBB.1.5.37, XBB.1.5.39, XBB.1.5.4, XBB.1.5.40, XBB.1.5.44, XBB.1.5.45, XBB.1.5.48, XBB.1.5.49, XBB.1.5.50, XBB.1.5.51, XBB.1.5.59, XBB.1.5.60, XBB.1.5.62, XBB.1.5.63, XBB.1.5.66, XBB.1.5.67, XBB.1.5.68, XBB.1.5.7, XBB.1.5.70, XBB.1.5.72, XBB.1.5.77, XBB.1.5.8, XBB.1.5.86, XBB.1.5.9, XCF, XCH, and XCH.1.
XBB.1.9.1	XBB.1.9.1 includes the following sublineages of Omicron: FL.1, FL.1.1, FL.1.3, FL.1.4, FL.1.5, FL.1.5.1, FL.1.5.2, FL.10.1, FL.12, FL.13, FL.15, FL.15.1.1, FL.16, FL.2, FL.2.3, FL.2.5, FL.20, FL.20.1, FL.20.2, FL.21, FL.24, FL.25, FL.4, FL.5, FL.7, FL.8, HN.1, and HN.4.
XBB.1.9.2	XBB.1.9.2 includes the following sublineages of Omicron: HK.1, HK.17, HK.3, HK.3.1, HK.3.11, HK.3.12, HK.3.2, HK.6, HK.8, JG.1, JG.3, JG.3.1, JG.3.2, KB.1, and KB.4.
XBB.1.16	XBB.1.16 includes the following sublineages of Omicron: FU.1, FU.2, FU.2.1, GF.1, GY.5, HF.1, HF.1.1, HF.1.2, HW.1.1, JF.1, JF.1.1, JM.2, XBB.1.16.1, XBB.1.16.11, XBB.1.16.13, XBB.1.16.14, XBB.1.16.15, XBB.1.16.16, XBB.1.16.2, XBB.1.16.20, XBB.1.16.4. XBB.1.16.5, XBB.1.16.6, XBB.1.16.8, and XBB.1.16.9.
XBB.2.3	XBB.2.3 includes the following sublineages of Omicron: GE.1, GJ.1, GJ.1.2, GJ.1.2.2, GJ.1.2.6, GJ.1.2.8, GS.1, GS.3, GZ.1, HG.2, HH.1, HH.1.1, HH.2, JE.1.1, XBB.2.3.11, XBB.2.3.2, XBB.2.3.3, XBB.2.3.4, and XBB.2.3.8.

[1]Categoirizations of Omicron sublineages and their parent sublineages can be found on https://cov-spectrum.org/

Data Sources

- **COVID-19 data**

  New Mexico Electronic Disease Surveillance System (NMEDSS), *Infectious Disease Epidemiology Bureau, Epidemiology and Response Division, New Mexico Department of Health*. Disease incidence data (counts) are derived from reports of notifiable infectious diseases. NMEDSS includes hospitalization counts for those reported with COVID-19. NMDOH relies on health care providers, laboratories, hospitals, clinics, institutions and individuals to report suspected and confirmed notifiable infectious diseases in accordance with New Mexico Administrative Code 7.4.3.13. Under-reporting can occur from lack of awareness about reporting requirements or lack of compliance with those requirements. Not all cases of infectious diseases are detected for various reasons including lack of access to health care services and lack of laboratory testing. Specific and standardized national case definitions are used to classify disease reports by case status.
- **New Mexico Statewide Immunization Information System (NMSIIS)** is the immunization registry for the New Mexico Department of Health which includes patient and vaccination data submitted by healthcare providers, hospitals, schools and other vaccinating partners following administration of approved vaccines.
- **Sequencing data**
  - Cases reported here include cases with specimens sequenced at the Scientific Laboratory Division (SLD), the University of New Mexico, and the following partnering laboratories with the Centers for Disease Control and Prevention (CDC): Aegis Sciences Corporation, Fulgent Genetics, Gravity Diagnostics, Helix/Illumina, LabCorp, Quest Diagnostics, and Infinity BiologiX/Sampled.
- **Variants of concern (VOC)** are defined by Centers for Disease Control and Prevention: Variants of the Virus | CDC.
- **CDC COVID Data Tracker** CDC COVID Data Tracker.

Data Notes

The data presented here on the New Mexico Department of Health (NMDOH) dashboard may differ from data on Centers for Disease Control and Prevention (CDC) sites. This likely represents differing levels of data completeness. Data presented by the state are likely to be more complete.

Race/Ethnicity are reported as a single value. If a case is identified as Hispanic then the single category value is Hispanic. If a case is not identified as Hispanic, then the case is categorized by the reported race category.