COVID-19 Variant of Concern (VOC) 2022 Annual Report

January 1, 2022-December 31, 2022

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 2022 including the number of specimens sequenced, the associated health outcomes, information about symptoms and underlying conditions, variant distribution by county, race and ethnicity, and age group. 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 reinfection cases. Throughout 2022 in New Mexico, Omicron and its sublineages[1] were dominant (greater than 50% of lineages sequenced). Of the Omicron sublineages, BA.1 was the most common (6,824), and BA.5 was the second most common (5,070). Because XBB and related sublineages like XBB.1.5 emerged at the end of 2022, they were observed infrequently, however they increased proportionally in 2023. 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-19 positive patients.

Early in 2022 NM saw the highest amount of positive COVID-19 cases reported increasing from 12,732 (December 26, 2021-January 1, 2022) to 24,550 (January 23, 2022-January 29, 2022) which coincided with the arrival of the more transmissible Omicron variant and its sublineages[1]. Over the course of 2022 in NM, a total of 18,169 sequenced specimens were reported to NMDOH Epidemiology and Response Division (ERD). Of those, the Variant Investigation Team was able to match 16,046 (89%) specimens to their associated patient profile including social characteristics and health outcomes of interest, when reported. The total NM sequences for 2022 reported on GISAID[2] is 20,480, of which, 89% were reported to NMDOH. Cases peaked in NM on January 18th, 2022, with 7,590 positive cases reported that day. Reported sequencing results followed a similar pattern and peaked in January 2022 with a total of 15,920 sequenced results reported. The following sublineages of Omicron are reported in the 2022 annual report: BA.1 (6,824), BA.2 (3,615), BA.4 (467), BA.4.6 (125), BA.5 (5,070), BF.7 (336), BQ.1 (929), BQ.1.1 (427), and XBB (37).[3,4] Additionally, there were 339 Delta sequenced and reported and Delta was last observed in circulation the week of February 21st, 2022.

[1]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)

[2]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).

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

[4]The total sequenced specimens are all sequencing results reported to NMDOH in 2022 and may include out of state residents.

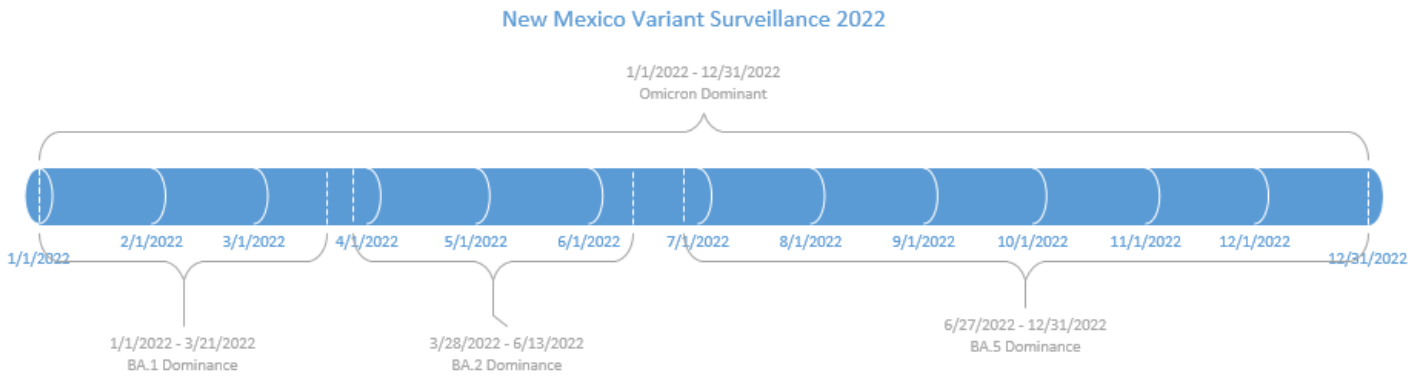


Figure 1: Timeline of CDC Variants of Concern Dominance Periods in New Mexico (2022)

NM COVID-19 Variant Epidemiologic Interpretation

CDC VARIANTS OF CONCERN (VOC) New Mexico 2022	
Name	New Mexico
Delta (B.1.617.2 and AY sublineages)	-Delta was the dominant variant from 6/28/21 to 12/20/21 and was 100% from 8/16/21 to 11/29/21. -A total of 339 were sequenced in 2022 and Delta was last sequenced the week of 2/21/22.
Omicron (B.1.1.529 and BA sublineages)	-Omicron became the dominant variant 12/27/21 representing 67% of cases. -A total of 17,830 Omicron sublineages were sequenced in 2022.

[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
B.1.617.2 (Delta)	339	322	95%
BA.1 (Omicron)	6824	6416	94%
BA.2 (Omicron)	3615	2758	76%
BA.4 (Omicron)	467	387	83%
BA.4.6 (Omicron)	125	112	90%
BA.5 (Omicron)	5070	4457	88%
BF.7 (Omicron)	336	304	90%
BQ.1 (Omicron)	929	864	93%
BQ.1.1 (Omicron)	427	390	91%
XBB (Omicron)	37	36	97%
Total	18169	16046	88%

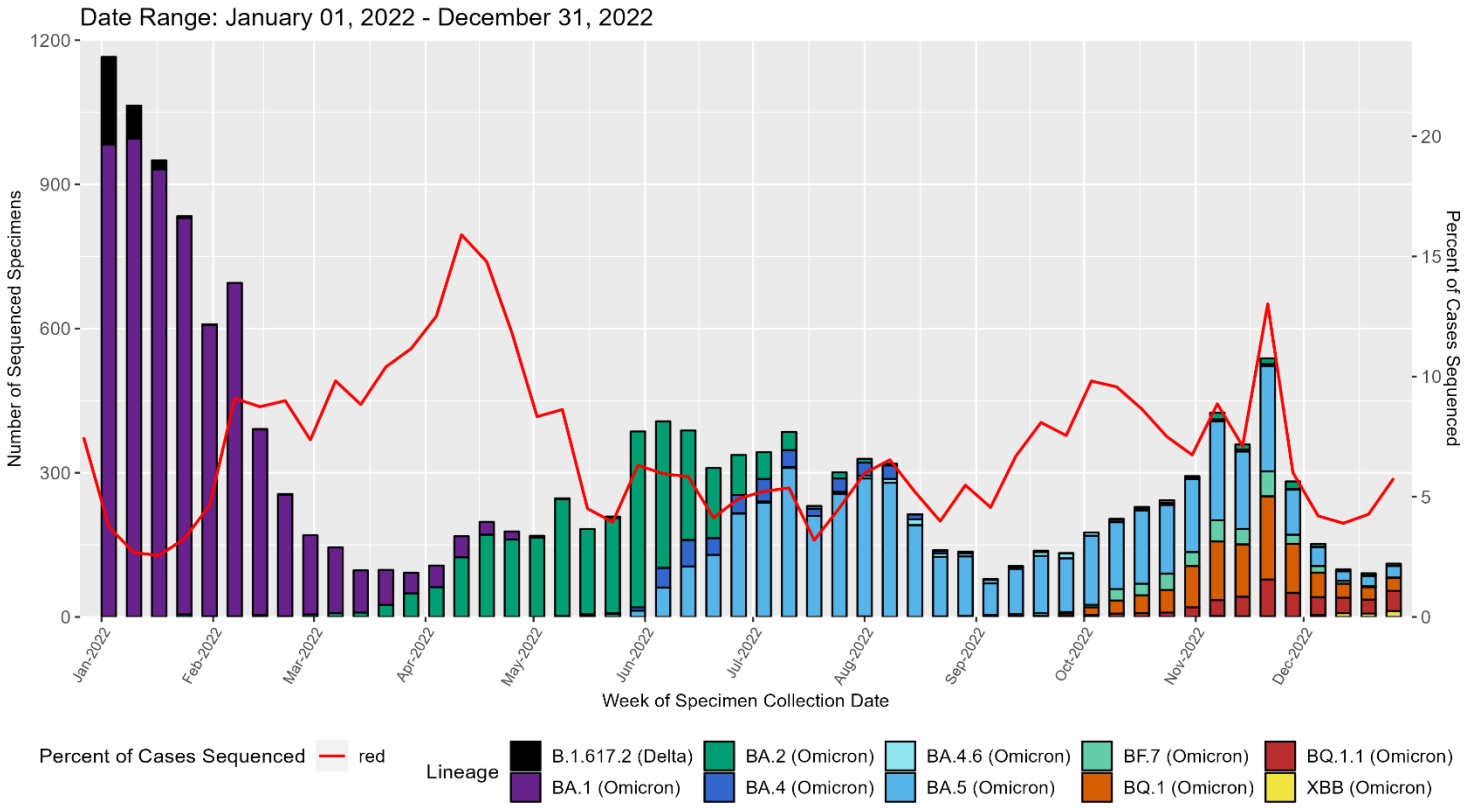
[1]Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 133 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico. These have been removed from the subsequent tables and figures.

Health outcomes of matched New Mexico resident cases				
Lineage	Matched Cases[1]	Number Hospitalized (%)	Number Died (%)	Number Reinfections[2] (%)
B.1.617.2 (Delta)	314	78 (25%)	33 (11%)	8 (3%)
BA.1 (Omicron)	6374	326 (5%)	67 (1%)	573 (9%)
BA.2 (Omicron)	2726	243 (9%)	30 (1%)	248 (9%)
BA.4 (Omicron)	387	34 (9%)	4 (1%)	45 (12%)
BA.5 (Omicron)	4424	456 (10%)	51 (1%)	767 (17%)
BA.4.6 (Omicron)	111	5 (5%)	0 (0%)	24 (22%)
BF.7 (Omicron)	301	39 (13%)	4 (1%)	37 (12%)
BQ.1 (Omicron)	856	102 (12%)	16 (2%)	235 (27%)
BQ.1.1 (Omicron)	384	49 (13%)	6 (2%)	87 (23%)
XBB (Omicron)	36	8 (22%)	0 (0%)	7 (19%)

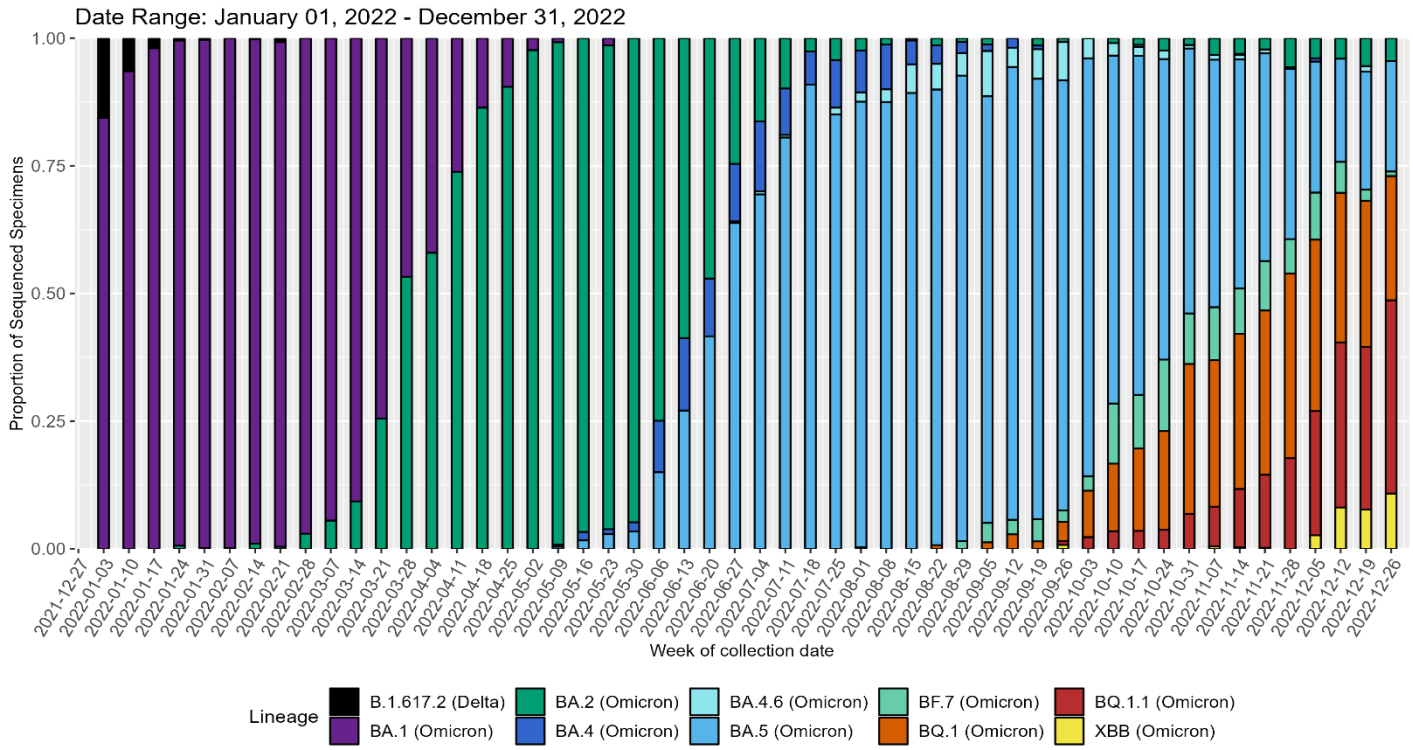
[1]Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table excludes 133 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico and are removed from subsequent tables and figures.

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

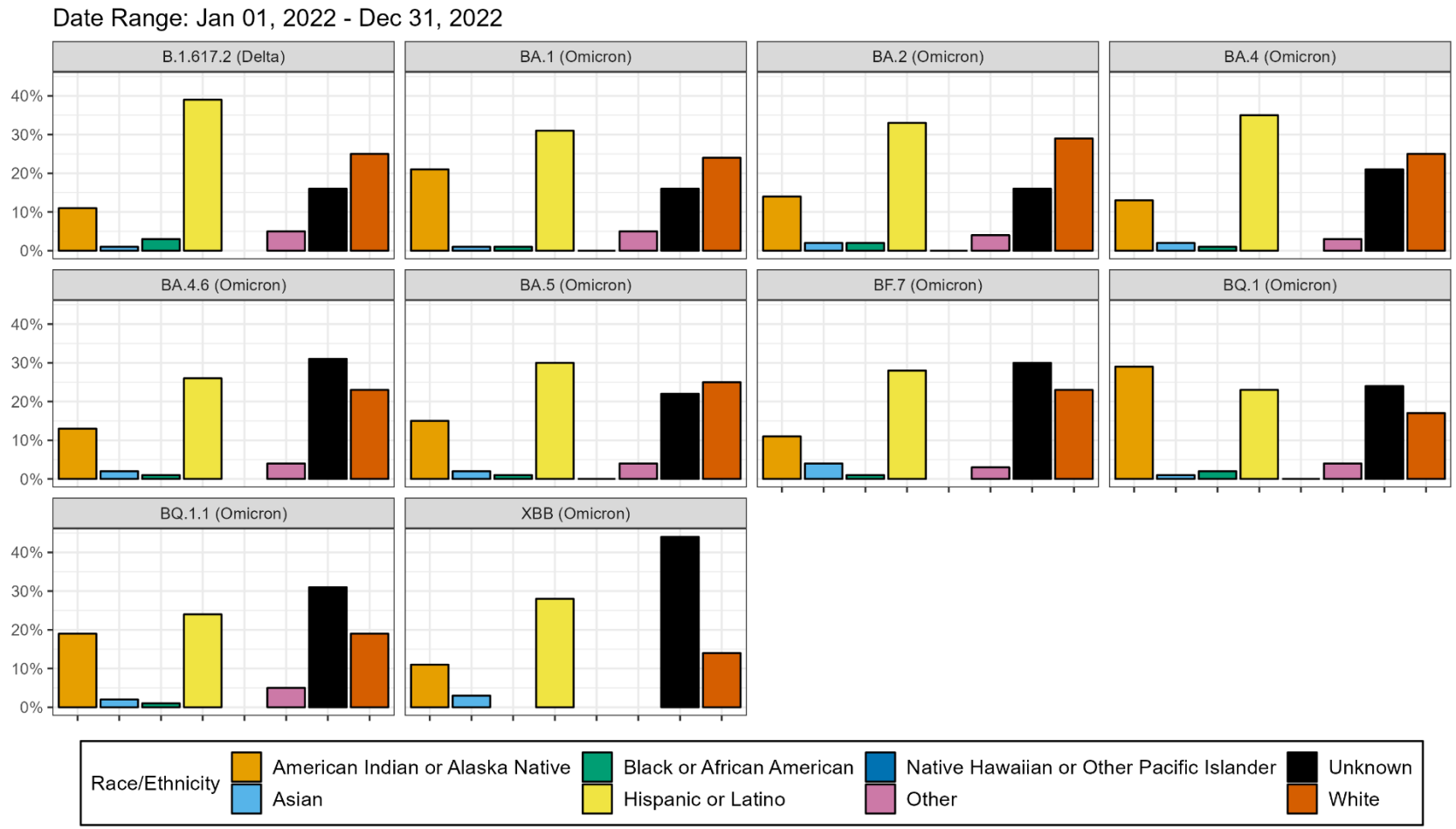
Identified SARS-CoV-2 lineages by week



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	B.1.617.2 (Delta)	BA.1 (Omicron)	BA.2 (Omicron)	BA.4 (Omicron)	BA.4.6 (Omicron)	BA.5 (Omicron)	BF.7 (Omicron)	BQ.1 (Omicron)	BQ.1.1 (Omicron)	XBB (Omicron)	Total
Bernalillo	140	2466	1138	186	37	1840	158	341	139	11	6456
Chaves	18	51	9	4	5	69	4	4	5	0	169
Cibola	14	206	132	14	4	77	8	12	8	1	476
Colfax	3	35	7	1	0	12	0	0	0	0	58
Curry	6	121	82	13	7	178	3	6	19	1	436
Dona Ana	14	287	150	19	11	196	3	28	23	0	731
Eddy	9	68	13	0	2	25	2	0	3	0	122
Grant	2	66	58	2	2	24	0	2	2	0	158
Lea	1	33	4	1	0	13	0	0	0	0	52
Lincoln	0	53	42	3	6	104	8	18	13	3	250
Los Alamos	0	35	18	1	1	10	1	1	2	0	69
Luna	0	66	19	0	2	11	0	1	1	0	100
McKinley	1	334	6	2	0	31	5	27	6	0	412
Otero	5	197	44	7	0	45	1	4	3	0	306
Quay	1	13	12	4	2	42	0	3	1	0	78
Rio Arriba	10	118	93	11	1	141	8	14	7	0	403
San Juan	21	943	208	31	8	534	21	204	73	3	2046
San Miguel	5	73	37	0	1	44	1	7	4	0	172
Sandoval	17	423	261	33	10	400	34	88	23	3	1292
Santa Fe	24	340	252	36	9	336	32	49	16	4	1098
Sierra	3	31	19	2	1	16	0	11	2	0	85
Socorro	1	22	20	0	0	63	1	8	9	1	125
Taos	0	44	37	2	0	36	1	10	2	0	132
Torrance	5	50	16	1	0	19	1	2	1	0	95
Valencia	15	247	63	12	2	143	11	20	11	3	527

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

Number (%) of matched and sequenced COVID-19 cases reporting any symptoms by variant					
Lineage	Total	Total Investigated (%)	No	Yes	Percent Symptomatic
B.1.617.2 (Delta)	322	119 (37%)	8	111	93%
BA.1 (Omicron)	6416	2328 (36%)	135	2193	94%
BA.2 (Omicron)	2758	1397 (51%)	69	1328	95%
BA.4 (Omicron)	387	171 (44%)	3	168	98%
BA.4.6 (Omicron)	112	32 (29%)	1	31	97%
BA.5 (Omicron)	4457	1492 (33%)	81	1411	95%
BF.7 (Omicron)	304	52 (17%)	6	46	88%
BQ.1 (Omicron)	864	116 (13%)	23	93	80%
BQ.1.1 (Omicron)	390	49 (13%)	5	44	90%
XBB (Omicron)	36	8 (22%)	1	7	88%

Number (%) of specific symptoms reported by symptom category and variant

The table below includes data ONLY from symptomatic cases.

Variant	Upper Respiratory (Runny nose, sore throat)	Lower Respiratory (Cough, shortness of breath)	Gastrointestinal (Nausea/Vomiting, abdominal pain, diarrhea)	Systemic (Fever, chills, muscle aches, headache, fatigue, loss of appetite)	Loss of Taste and Smell
B.1.617.2 (Delta)	57 (51%)	100 (90%)	45 (41%)	89 (80%)	41 (37%)
BA.1 (Omicron)	1,862 (85%)	1,802 (82%)	905 (41%)	1,973 (90%)	456 (21%)
BA.2 (Omicron)	1,136 (86%)	1,137 (86%)	552 (42%)	1,204 (91%)	261 (20%)
BA.4 (Omicron)	140 (83%)	143 (85%)	86 (51%)	156 (93%)	40 (24%)
BA.4.6 (Omicron)	26 (84%)	29 (94%)	10 (32%)	27 (87%)	6 (19%)
BA.5 (Omicron)	1,100 (78%)	1,229 (87%)	684 (48%)	1,251 (89%)	294 (21%)
BF.7 (Omicron)	24 (52%)	37 (80%)	17 (37%)	37 (80%)	5 (11%)
BQ.1 (Omicron)	40 (43%)	75 (81%)	30 (32%)	67 (72%)	15 (16%)
BQ.1.1 (Omicron)	14 (32%)	38 (86%)	10 (23%)	33 (75%)	1 (2%)
XBB (Omicron)	1 (14%)	4 (57%)	2 (29%)	3 (43%)	0 (0%)

Number (%) of matched and sequenced specimens by any underlying condition and variant					
Lineage	Total	Total Investigated (%)	No	Yes	Percent Underlying Conditions (%)
B.1.617.2 (Delta)	322	125 (39%)	65	60	48%
BA.1 (Omicron)	6416	1892 (29%)	1376	516	27%
BA.2 (Omicron)	2758	811 (29%)	219	592	73%
BA.4 (Omicron)	387	54 (14%)	10	44	81%
BA.4.6 (Omicron)	112	10 (9%)	4	6	60%
BA.5 (Omicron)	4457	656 (15%)	117	539	82%
BF.7 (Omicron)	304	41 (13%)	7	34	83%
BQ.1 (Omicron)	864	107 (12%)	14	93	87%
BQ.1.1 (Omicron)	390	48 (12%)	3	45	94%
XBB (Omicron)	36	8 (22%)	1	7	88%

Number (%) of sequenced specimens for cases reporting underlying conditions by specific condition and variant

Data below includes ONLY cases who report having a pre-existing condition.

Variant	Chronic Lung Disease	Chronic Liver Disease	Chronic Renal Disease	Diabetes Mellitus	Cardiovascular Disease	Autoimmune Disease	Neurological Disability	Current or Former Smoker
B.1.617.2 (Delta)	6 (13%)	5 (11%)	7 (15%)	24 (52%)	20 (43%)	4 (9%)	5 (11%)	6 (13%)
BA.1 (Omicron)	130 (29%)	17 (4%)	57 (13%)	135 (30%)	176 (40%)	14 (3%)	56 (13%)	183 (41%)
BA.2 (Omicron)	144 (30%)	25 (5%)	52 (11%)	122 (25%)	196 (40%)	22 (5%)	58 (12%)	221 (45%)
BA.4 (Omicron)	9 (22%)	1 (2%)	5 (12%)	13 (32%)	15 (37%)	3 (7%)	7 (17%)	15 (37%)
BA.4.6 (Omicron)	1 (20%)	1 (20%)	0 (0%)	1 (20%)	2 (40%)	1 (20%)	1 (20%)	3 (60%)
BA.5 (Omicron)	130 (29%)	26 (6%)	78 (18%)	140 (32%)	192 (43%)	30 (7%)	68 (15%)	178 (40%)
BF.7 (Omicron)	5 (20%)	1 (4%)	3 (12%)	14 (56%)	8 (32%)	1 (4%)	5 (20%)	9 (36%)
BQ.1 (Omicron)	16 (21%)	7 (9%)	24 (32%)	35 (46%)	33 (43%)	1 (1%)	13 (17%)	14 (18%)
BQ.1.1 (Omicron)	11 (28%)	3 (8%)	8 (20%)	17 (42%)	17 (42%)	3 (8%)	12 (30%)	12 (30%)
XBB (Omicron)	4 (80%)	0 (0%)	0 (0%)	2 (40%)	2 (40%)	0 (0%)	0 (0%)	2 (40%)

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.2.1, BA.2.10, BA.2.10.1, BA.2.12, BA.2.12.1, BA.2.13, BA.2.13.1, BA.2.17, BA.2.18, BA.2.2.1, BA.2.20, BA.2.21, BA.2.22, BA.2.23, BA.2.29, BA.2.3, BA.2.3.10, BA.2.3.14, BA.2.3.17, BA.2.3.2, BA.2.3.20, BA.2.3.14, BA.2.3.17, BA.2.3.2, BA.2.3.20, BA.2.3.4, BA.2.31, BA.2.36, BA.2.37, BA.2.38, BA.2.47, BA.2.48, BA.2.5, BA.2.56, BA.2.61, BA.2.65, BA.2.7, BA.2.72, BA.2.75, BA.2.75.1, BA.2.75.2, BA.2.76, BA.2.81, BA.2.9, BA.2.9.3, BA.2.9.7, BG.2, BG.5, BM.1.1, BM.1.1.1, BM.1.1.3, BM.2, BM.4.1.1, BN.6, BR.1, BS.1.1, BY.1, CM.2, CM.5, CM.8.1, CP.2, CP.3, DF.1, and DF.1.1 , CH.1.1, BN.1, BN.1.1, BN.1.2, BN.1.3, and BN.1.5
XBB	-XBB includes the following sublineages of Omicron: XBB.1, XBB.1.2, XBB.1.5, and XBB.2
BA.4	-BA.4 includes the following sublineages of Omicron: BA.4.1, BA.4.1.1, BA.4.1.6, BA.4.1.8, BA.4.2, and BA.4.4
BA.4.6	-BA.4.6 includes the following sublineages of Omicron: BA.4.6.5
BA.5	-BA.5 includes the following sublineages of Omicron: BA.5.1, BA.5.1.1, BA.5.1.10, BA.5.1.16, BA.5.1.18, BA.5.1.2, BA.5.1.21. BA.5.1.22, BA.5.1.23, BA.5.1.24, BA.5.1.25, BA.5.1.27, BA.5.1.3, BA.5.1.30, BA.5.1.5. BA.5.1.6, BA.5.1.7, BA.5.10, BA.5.10.1, BA.5.2, BA.5.2.1, BA.5.2.12, BA.5.2.13, BA.5.2.16, BA.5.2.18, BA.5.2.19, BA.5.2.2, BA.5.2.20, BA.5.2.21, BA.5.2.22, BA.5.2.23, BA.5.2.24, BA.5.2.25, BA.5.2.27, BA.5.2.28, BA.5.2.29, BA.5.2.3, BA.5.2.31, BA.5.2.32, BA.5.2.33, BA.5.2.34, BA.5.2.35, BA.5.2.37, BA.5.2.4, BA.5.2.8, BA.5.2.9, BA.5.3, BA.5.3.1, BA.5.5, BA.5.5.1, BA.5.5.2, BA.5.5.3, BA.5.6, BA.5.6.1, BA.5.6.2, BA.5.6.3, BA.5.8, BA.5.9, BE.1, BE.1.1, BE.1.1.1, BE.1.2, BE.1.2.1, BE.1.4, BE.2, BE.3, BE.4, BE.5, BF.1, BF.10, BF.11, BF.11.3, BF.13, BF.14, BF.16, BF.20, BF.21, BF.25, BF.26, BF.27, BF.28, BF.29, BF.3, BF.31.1, BF.32, BF.4, BF.5, BF.6, BF.8, BK.1, BU.1, BU.2, BU.3, BW.1, BW.1.1, CA.1, CD.2, CK.1, CK.2, CK.2.1.1, CN.1, CN.2, CR.1.1, CT.1, DB.2, DE.2, DK.1, and XAS
BF.7	-BF.7 includes the following sublineages of Omicron: BF.7.12, BF.7.21, BF.7.4, BF.7.4.1, BF.7.4.2, BF.7.5, BF.7.6, BF.7.7, and BF.7.8
BQ.1	-BQ.1 includes the following sublineages of Omicron: BQ.1.10, BQ.1.10.1, BQ.1.11, BQ.1.12, BQ.1.13, BQ.1.13.1, BQ.1.14, BQ.1.15, BQ.1.19, BQ.1.2, BQ.1.2.3, BQ.1.21, BQ.1.22, BQ.1.23, BQ.1.24, BQ.1.25, BQ.1.25.1, BQ.1.28, BQ.1.3, BQ.1.3.1, BQ.1.3.2, BQ.1.5, BQ.1.6, BQ.1.8, and BQ.1.9
BQ.1.1	-BQ.1.1 includes the following sublineages of Omicron: BQ.1.1, BQ.1.1.1, BQ.1.1.10, BQ.1.1.11, BQ.1.1.13, BQ.1.1.15, BQ.1.1.17, BQ.1.1.18, BQ.1.1.19, BQ.1.1.22, BQ.1.1.23, BQ.1.1.24, BQ.1.1.27, BQ.1.1.28, BQ.1.1.3, BQ.1.1.32, BQ1.1.36, BQ.1.1.4, BQ.1.1.5, BQ.1.1.61, BQ.1.1.69, BQ.1.1.7, and BQ.1.1.8

[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.
- **Salesforce/MTX COVID-19 Case Investigation Platform,** many case investigation were conducted on the Salesforce Software Platform to capture symptoms and underlying conditions. Not all cases were investigated. The Contact Tracing and Case Investigation Unit (CTCI) was operating at peak capacity from November 2019 to December 2020. Over the course of 2021 the program gradually pared down. In October 2022, the program was terminated. Therefore, reporting of symptoms and underlying conditions is not complete and may not reflect the experience of all cases.

- **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.