COVID-19 Variant of Concern Case Report
March 27, 2023

COVID-19 Genomic Surveillance

Monitoring COVID-19 variants is an important part of epidemiologic surveillance to track the accumulation 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 readily available diagnostic tests do not test for specific variant strains and must be sent to a lab for sequencing. Genetic sequencing requires coordinated effort and time, therefore there is a lag time from specimen collection to reporting of approximately 3-4 weeks.

CDC is monitoring one VOC currently in the US, Omicron. All other VOCs and VOIs are now classified as VBMs due to their low prevalence including Delta, Alpha, Beta, Gamma, Epsilon, Eta, Iota, Kappa, Zeta, and Mu. CDC designated Omicron a VOC on November 30, 2021. To date, 18,135 confirmed cases of Omicron have been sequenced in NM. Since the week of January 24, 2022, Omicron represented approximately 100% of sequenced samples in New Mexico. Sequenced specimens reported from February 13 to March 27, 2023 are incomplete but indicate a continued predominance of Omicron. Additional Omicron sublineages have been included in this report. To date, we have sequenced and identified 125 BA.4.6, 20 BF.11, 317 BF.7, 37 BN.1, 925 BQ.1, 494 BQ.1.1, 26 XBB, 266 XBB.1.5, 43 BA.5.2.6, and 16 CH.1.1 in New Mexico. DOH is monitoring these sublineage variants closely to ensure they are not causing increased cases or worse health outcomes. CDC Nowcast predictive modeling forecasts Omicron to represent 100% of US positive cases the week of March 25, 2023.[4] Studies indicate that vaccines and vaccine booster doses, including the new bivalent booster, authorized for use in the US are effective at preventing transmission, severe illness, and death caused by VOCs and are the recommended measure to slow the emergence of new variants.

NM COVID-19 Variant Epidemiologic Interpretation

CDC VARIANTS OF CONCERN (VOC)

Name	First Identified	Attributes[1]	New Mexico[2]
Omicron (B.1.1.529 and descendant sublineages)	South Africa	-May increase transmissibility -May reduce effectiveness of antibody treatments -May reduce natural and vaccine immunity	-Omicron became the dominant variant 12/27/21 representing 66% of cases. -18,135 confirmed cases of Omicron have been sequenced in NM.

CDC VARIANTS BEING MONITORED (VBM)

Name[3]	First Identified	Attributes[1]	New Mexico[2]
Delta (B.1.617.2 and AY sublineages)	India	-Increased transmissibility -May reduce effectiveness of antibody treatments -May cause more severe illness in unvaccinated persons -May reduce natural and vaccine immunity	-Delta remained the dominant variant from the week of 6/28/21 (56%) to 12/20/21 (72%). -The first Delta was sequenced the week of 4/19/21 and has not been observed in NM since 2/21/22
Alpha (B.1.1.7 and Q lineages)	United Kingdom	-50% more transmissible -Potential to cause more severe cases and deaths	-Alpha remained the dominant variant from the week of 3/29/21 (50%) to 6/21/21 (51%). -The first Alpha was sequenced the week of 12/28/20 and has not been observed in NM since 8/16/21.
Beta (B.1.351 and descendent lineages)	South Africa	-50% more transmissible -Reduced effectiveness of antibody treatments -Reduced response of natural and vaccine induced immunity	- Least reported VOC in NM. -Has not been observed in NM since 7/19/21.
Gamma (P.1 and descendent lineages)	Japan/Brazil	-Reduced effectiveness of some antibody treatments -Reduced response of natural and vaccine immunity	-First case sequenced in NM the week of 3/22/21 and has not been observed since 8/9/2021; Gamma peaked at 9% of sequenced NM specimens the week of 6/21/2021. -Currently has the highest proportion of hospitalizations (24%); oversampling of severe cases may skew these results.
Epsilon (B.1.427, and B.1.429)	California	-Downgraded from a VOI on September 21, 2021	-First case sequenced in NM the week of 10/12/20 and has not been observed since 6/7/21; Epsilon peaked at 27% of sequenced NM specimens the week of 3/15/21.
Iota (B.1.526)	U.S.	-Downgraded from a VOI on September 21, 2021	-First case sequenced in NM the week of 2/08/21 and has not been observed since 7/19/21; Iota peaked at 14% of sequenced NM specimens the week of 5/10/21
Mu (B.1.621, and B.1.621.1)	Colombia	-Designated a VBM on September 21, 2021	-First case sequenced in NM the week of 5/3/21 and has not been observed since 9/27/21; Mu peaked at 7% of sequenced NM specimens the week of 6/7/21.

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

[2] NM interpretations based on data collected >4 weeks ago to allow for lag in genomic sequencing.

[3] All other VBMs have either not been observed in NM or have had <10 sequenced specimens and are not included in this table.

[4] CDC COVID Data Tracker

Cumulative number of specimens sequenced and matched to case investigations

Lineage	Sequenced Cases	Matched Cases*	Percent Matched
BA.1 (Omicron)	7251	6826	94%
BA.2 (Omicron)	3434	2679	78%
BA.4 (Omicron)	432	352	81%
BA.5 (Omicron)	4749	3838	81%
BA.4.6 (Omicron)	125	107	86%
BF.11 (Omicron)	20	18	90%
BF.7 (Omicron)	317	273	86%
BN.1 (Omicron)	37	31	84%
BQ.1 (Omicron)	925	827	89%
BQ.1.1 (Omicron)	494	435	88%
XBB (Omicron)	26	25	96%
XBB.1.5 (Omicron)	266	242	91%
BA.5.2.6 (Omicron)	43	38	88%
CH.1.1 (Omicron)	16	13	81%
B.1.617.2 (Delta)	15653	14353	92%
B.1.1.7 (Alpha)	1870	1593	85%
B.1.351 (Beta)	10	5	50%
P.1 (Gamma)	108	91	84%
B.1.427/B.1.429 (Epsilon)	526	440	84%
B.1.525 (Eta)	5	5	100%
B.1.526 (Iota)	200	173	86%
B.1.617.1 (Kappa)	2	2	100%
P.2 (Zeta)	3	2	67%
B.1.621/B.1.621.1 (Mu)	35	32	91%
Other lineage	4128	3297	80%
Total	40675	35697	88%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 350 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.

**Sublineage variants BA.4.6, BF.11, BF.7, BN.1, BQ.1, BQ.1.1, XBB, XBB.1.5, BA.5.2.6, and CH.1.1 have been reaggregated into their parent lineages in the following tables due to small numbers.

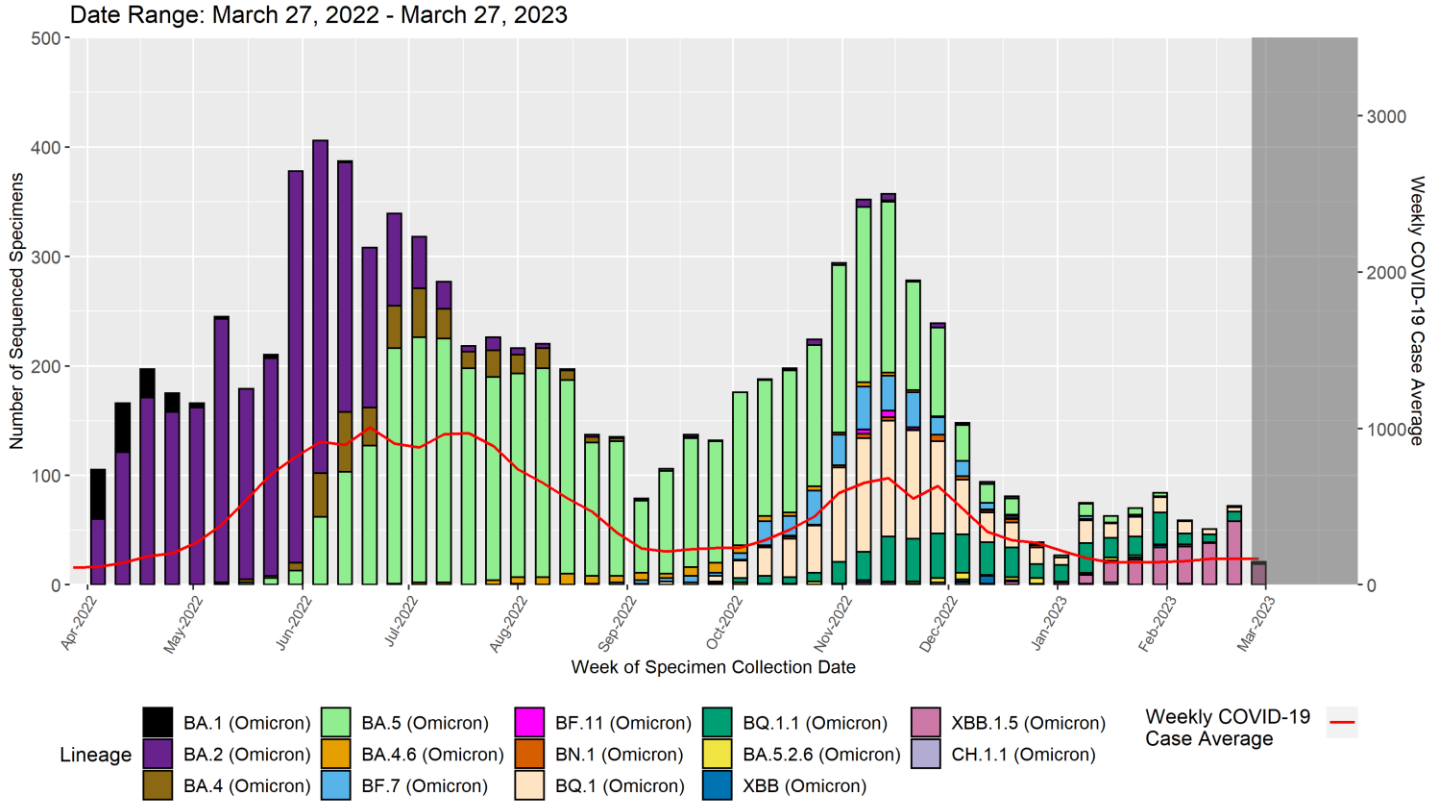
Health outcomes of cumulative matched specimens

Lineage	Total Matched Cases	Number Hospitalized (%)	Number Died (%)	Number Vaccine Breakthrough (%)*
BA.1 (Omicron)	6779	323 (5%)	66 (1%)	3847 (57%)
BA.2 (Omicron)	2925	257 (9%)	29 (1%)	2099 (72%)
BA.4 (Omicron)	458	32 (7%)	4 (1%)	315 (69%)
BA.5 (Omicron)	5425	550 (10%)	66 (1%)	3760 (69%)
B.1.617.2 (Delta)	14249	1251 (9%)	456 (3%)	4403 (31%)
B.1.1.7 (Alpha)	1574	144 (9%)	20 (1%)	90 (6%)
B.1.351 (Beta)	5	0 (0%)	0 (0%)	0 (0%)
P.1 (Gamma)	89	21 (24%)	2 (2%)	4 (4%)
B.1.427/B.1.429 (Epsilon)	429	9 (2%)	2 (0%)	9 (2%)
B.1.525 (Eta)	5	0 (0%)	0 (0%)	0 (0%)
B.1.526 (Iota)	171	5 (3%)	1 (1%)	8 (5%)
B.1.617.1 (Kappa)	2	0 (0%)	0 (0%)	0 (0%)
P.2 (Zeta)	2	0 (0%)	0 (0%)	0 (0%)
B.1.621/B.1.621.1 (Mu)	32	1 (3%)	0 (0%)	5 (16%)
Other lineage	3202	191 (6%)	64 (2%)	47 (1%)

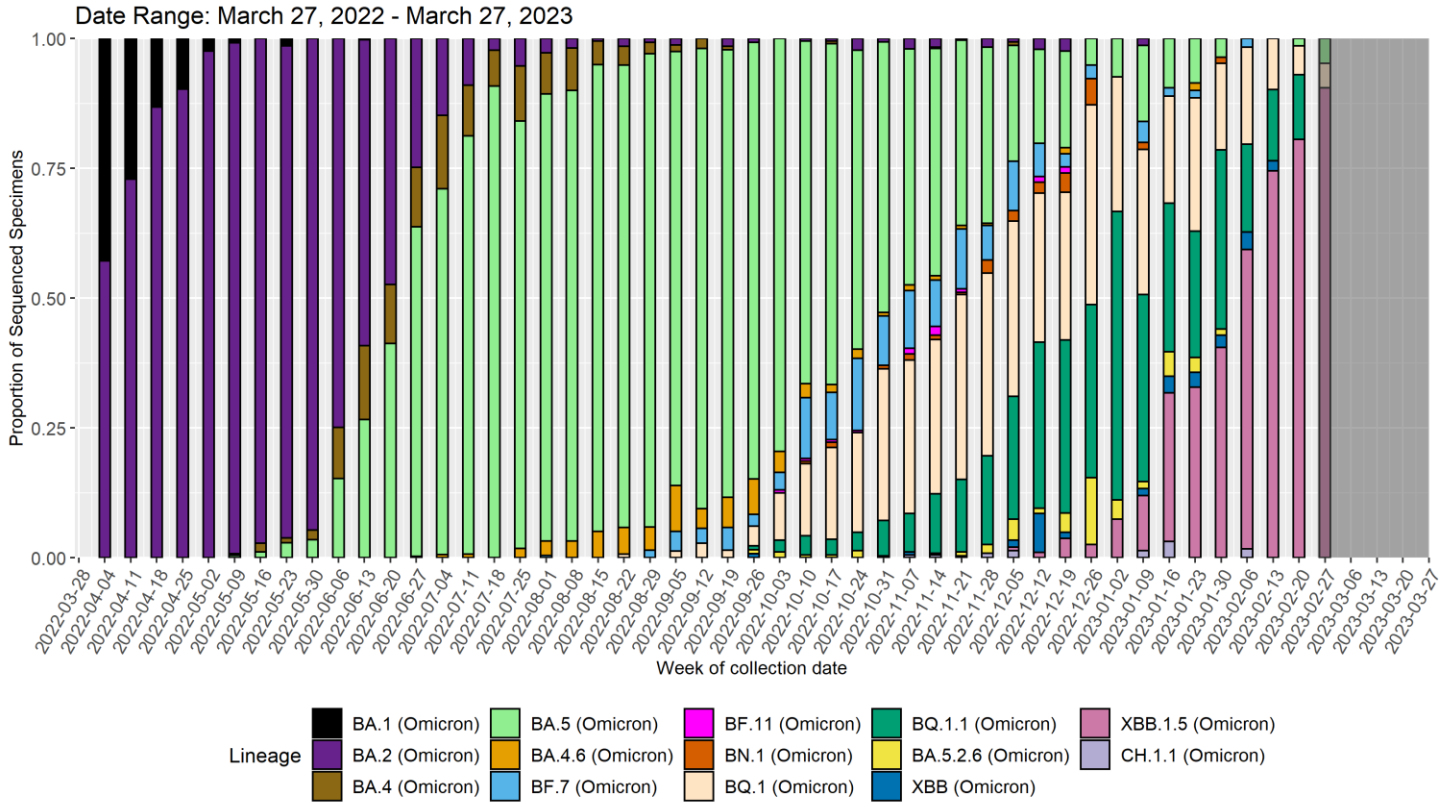
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. *Because samples collected from VBT cases are more frequently sequenced compared to samples from other COVID-19 cases, these counts should not be used to evaluate the frequency with which VOCs cause vaccine breakthrough.*

**The specimen submission process for sequencing is not representative. A large proportion of P.1 (Gamma) cases were collected from a single hospital in San Juan County that submitted specimens on hospital admissions, rather than on a representative set of cases in the county. This is likely increasing the apparent severity of this VOC.

Identified SARS-CoV-2 lineages by week*



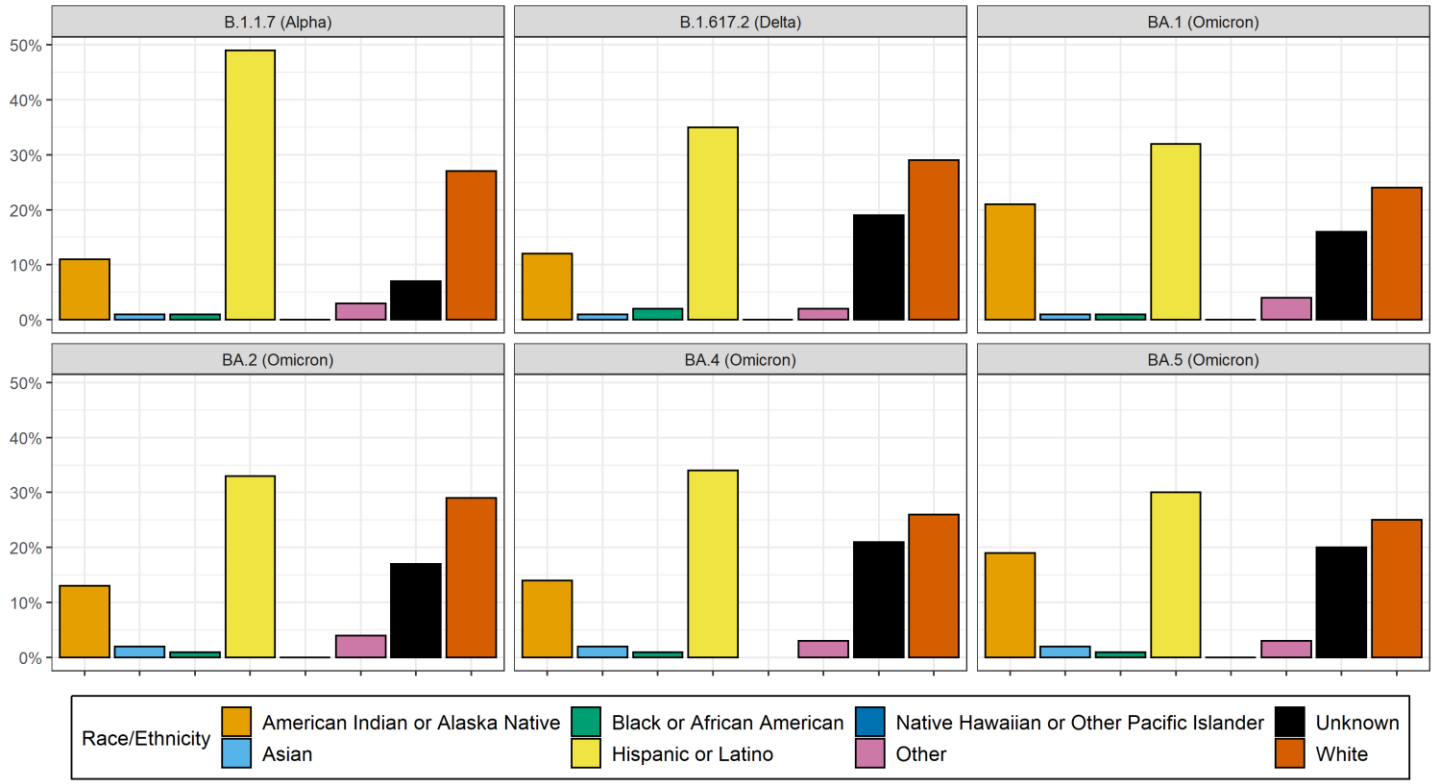
Proportion of identified SARS-CoV-2 lineages by week*



*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

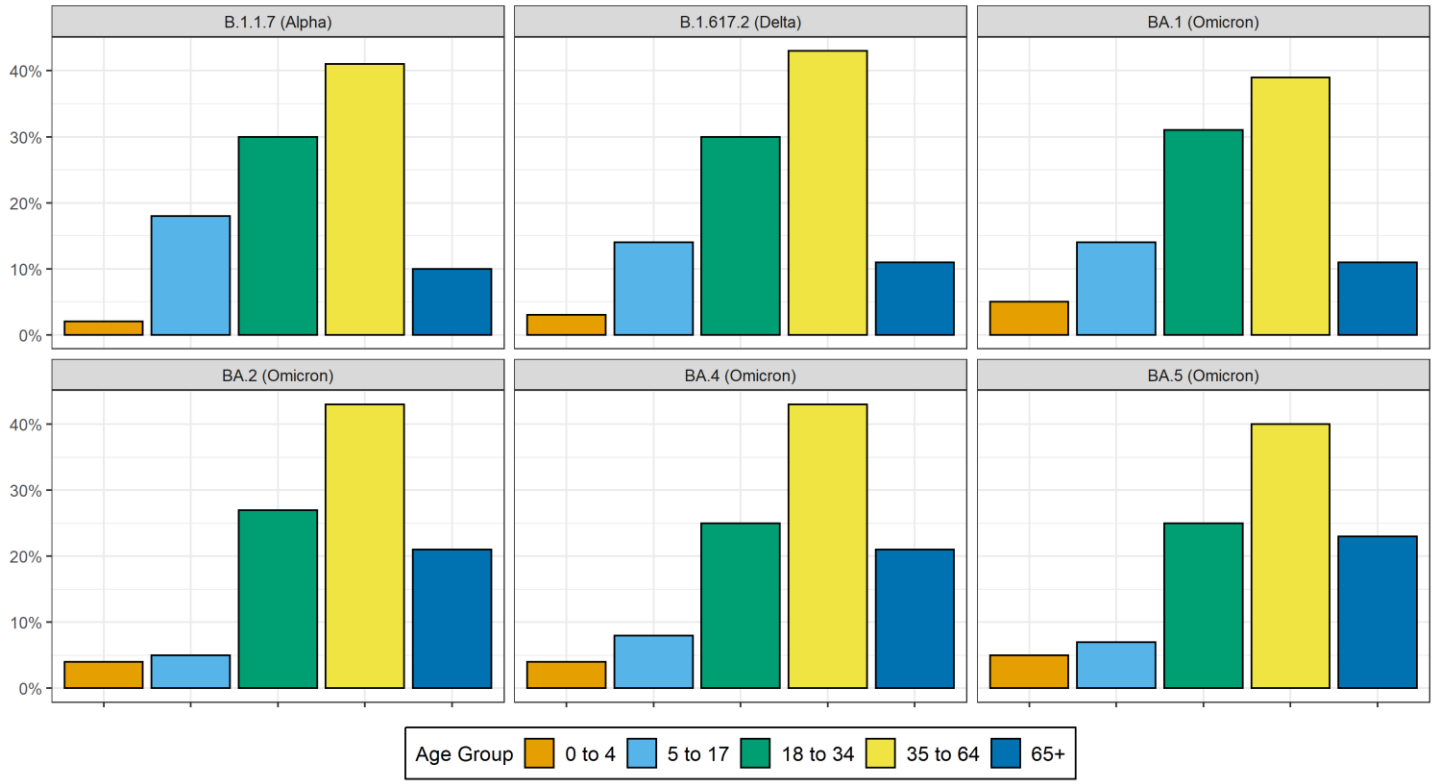
Cumulative proportion of variant cases by race/ethnicity

Cumulative up to March 27, 2023



Cumulative proportion of variant cases by age group

Cumulative up to March 27, 2023



Cumulative number of variant cases by county of residence*

County	BA.1 (Omicron)	BA.2 (Omicron)	BA.4 (Omicron)	BA.5 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Bernalillo	2628	1212	203	2233	4809	463
Chaves	57	13	9	87	354	12
Cibola	213	133	17	122	293	15
Colfax	40	7	1	9	224	28
Curry	113	91	16	143	336	28
Dona Ana	319	157	30	262	911	81
Eddy	68	10	2	28	374	21
Grant	84	62	4	30	135	16
Guadalupe	22	0	0	2	65	1
Hidalgo	11	3	0	12	27	0
Lea	32	4	1	11	222	16
Lincoln	46	39	5	90	117	6
Los Alamos	34	17	2	15	49	9
Luna	67	19	2	16	59	14
McKinley	342	9	3	66	346	17
Otero	218	42	7	42	742	27
Quay	12	8	3	27	79	4
Rio Arriba	114	100	10	133	199	95
Roosevelt	17	5	1	9	79	1
San Juan	982	218	39	817	1655	319
San Miguel	76	39	1	54	158	10
Sandoval	458	281	39	485	966	77
Santa Fe	369	278	43	390	742	100
Sierra	31	15	3	30	124	5
Socorro	19	19	0	57	92	9
Taos	48	37	2	48	233	17
Torrance	48	16	1	19	176	16
Valencia	265	72	13	154	567	70

* Counties with less than 50 matched sequenced cases are not included in the table below. Excludes all VBMs other than Alpha and Delta.

Percentage of variant cases reporting any symptoms

Lineage	Total	Total Investigated (%)	No	Yes	Percent Symptomatic
BA.1 (Omicron)	6779	2370 (35%)	142	2228	94%
BA.2 (Omicron)	2925	1395 (48%)	69	1326	95%
BA.4 (Omicron)	458	189 (41%)	3	186	98%
BA.5 (Omicron)	5423	1549 (29%)	102	1447	93%
B.1.617.2 (Delta)	14249	5689 (40%)	389	5300	93%
B.1.1.7 (Alpha)	1574	1206 (77%)	115	1091	90%

Percentage of specific symptoms reported by symptomatic variant cases

The table below includes data only from symptomatic cases.

Symptom	BA.1 (Omicron)	BA.2 (Omicron)	BA.4 (Omicron)	BA.5 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Upper Respiratory (Runny nose, sore throat)	1902 (85%)	1127 (85%)	155 (83%)	1063 (73%)	3467 (65%)	731 (67%)
Lower Respiratory (Cough, shortness of breath)	1828 (82%)	1126 (85%)	159 (85%)	1249 (86%)	4176 (79%)	828 (76%)
Gastrointestinal (Nausea/vomiting, abdominal pain, diarrhea)	917 (41%)	550 (41%)	92 (49%)	680 (47%)	2351 (44%)	466 (43%)
Systemic (Fever, chills, muscle aches, headache, fatigue, loss of appetite)	2005 (90%)	1203 (91%)	171 (92%)	1254 (87%)	4706 (89%)	963 (88%)
Loss of Taste and Smell	480 (22%)	257 (19%)	46 (25%)	297 (21%)	2557 (48%)	424 (39%)

* Excludes all VBMs other than Alpha and Delta.

Percentage of variant cases reporting underlying conditions

Lineage	Total	Total Investigated (%)	No	Yes	Percent Underlying Conditions
BA.1 (Omicron)	6327	1941 (31%)	1440	501	26%
BA.2 (Omicron)	2344	818 (35%)	217	601	73%
BA.4 (Omicron)	324	59 (18%)	14	45	76%
BA.5 (Omicron)	4660	776 (17%)	127	649	84%
B.1.617.2 (Delta)	14249	5596 (39%)	4303	1293	23%
B.1.1.7 (Alpha)	1574	1199 (76%)	620	579	48%

Percentage of specific underlying conditions reported by variant cases

Data below includes ONLY cases who report having a preexisting condition.

Symptom	BA.1 (Omicron)	BA.2 (Omicron)	BA.4 (Omicron)	BA.5 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Chronic Lung Disease	119 (28%)	142 (29%)	9 (23%)	144 (28%)	247 (24%)	133 (26%)
Chronic Liver Disease	16 (4%)	24 (5%)	2 (5%)	32 (6%)	54 (5%)	15 (3%)
Chronic Renal Disease	51 (12%)	55 (11%)	3 (8%)	92 (18%)	125 (12%)	18 (3%)
Diabetes Mellitus	121 (29%)	124 (26%)	12 (31%)	186 (36%)	394 (38%)	90 (17%)
Cardiovascular Disease	162 (39%)	194 (40%)	14 (36%)	229 (44%)	379 (36%)	167 (32%)
Autoimmune Disease	12 (3%)	20 (4%)	2 (5%)	25 (5%)	58 (6%)	39 (8%)
Neurological Disability	52 (12%)	59 (12%)	7 (18%)	93 (18%)	76 (7%)	29 (6%)
Current or Former Smoker	179 (43%)	221 (46%)	15 (38%)	192 (37%)	355 (34%)	279 (54%)

* Excludes all VBMs other than Alpha and Delta.

**Beginning January 2022, case investigation interviews conducted via webform survey no longer collected underlying conditions, and have been excluded from the underlying conditions tables.

Data Sources

- **COVID-19 data**
  - **New Mexico Electronic Disease Surveillance System (NM-EDSS)**, Infectious Disease Epidemiology Bureau, Epidemiology and Response Division, New Mexico Department of Health.
  - **Salesforce/MTX COVID-19 Case Investigation Platform.**
- **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 labs 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: https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html.
- **CDC COVID Data Tracker:** CDC COVID Data Tracker

Data Notes

- **The data reported in this weekly update may not match the daily numbers that are reported in the New Mexico Department of Health (NMDOH) press releases and/or the NMDOH COVID-19 data dashboard. This may be due to variation in the date and time of data extraction from NM-EDSS, corrections after quality assurance review, and differences in the exclusion criteria.**

- **New Mexico Electronic Disease Surveillance System (NM-EDSS).** Disease incidence data are derived from reports of notifiable infectious diseases. 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 due to of lack of awareness about reporting requirements or lack of compliance with those requirements. Not all cases of infectious diseases can be detected for various reasons including lack of access to health care services, lack of laboratory testing or concerns about confidentiality. Specific and standardized national case definitions are used to classify disease reports by case status.

- **Race/Ethnicity.** Race/Ethnicity are reported as a single variable according to the selection of the case. Any case who is Hispanic is in the Hispanic category and all other races are non-Hispanic.

- **Gender**. Gender refers to a person's internal sense of being male, female, some combination of male and female, or neither male nor female. Sex refers to the biological anatomy of an individual's reproductive system, and secondary sex characteristics.