COVID-19 Variant of Concern Case Report

November 28, 2022

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, 13,846 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 October 31 to November 28, 2022 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 84 BA.4.6, 85 BF.7, 101 BQ.1, and 141 BQ.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 November 26, 2022.[4] Studies indicate that vaccines and vaccine booster doses 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 BA 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. -13,846 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)	7221	6651	92%
BA.2 (Omicron)	2636	2453	93%
BA.4 (Omicron)	375	334	89%
BA.5 (Omicron)	3203	2856	89%
BA.4.6 (Omicron)	84	81	96%
BF.7 (Omicron)	85	83	98%
BQ.1 (Omicron)	101	101	100%
BQ.1.1 (Omicron)	141	138	98%
B.1.617.2 (Delta)	15653	14465	92%
B.1.1.7 (Alpha)	1870	1621	87%
B.1.351 (Beta)	10	5	50%
P.1 (Gamma)	108	94	87%
B.1.427/B.1.429 (Epsilon)	526	441	84%
B.1.525 (Eta)	5	5	100%
B.1.526 (Iota)	200	175	88%
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	4047	3254	80%
Total	36305	32793	90%

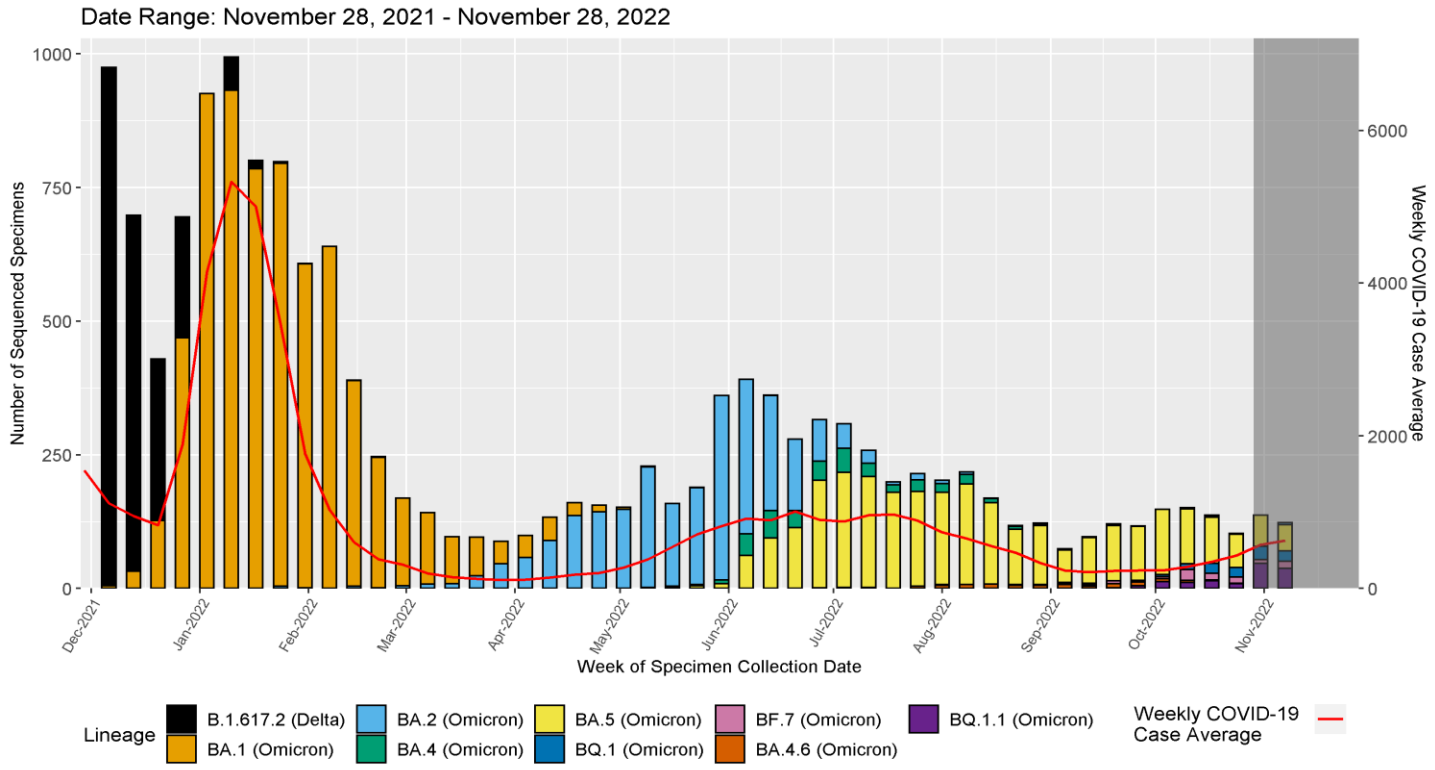
*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 320 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico. These have been removed from the subsequent tables and figures.
**Sublineage variants BA.4.6, BF.7, BQ.1, and BQ.1.1 have been reaggregated into their parent lineages in the following tables due to small numbers.

Health outcomes of cumulative matched specimens

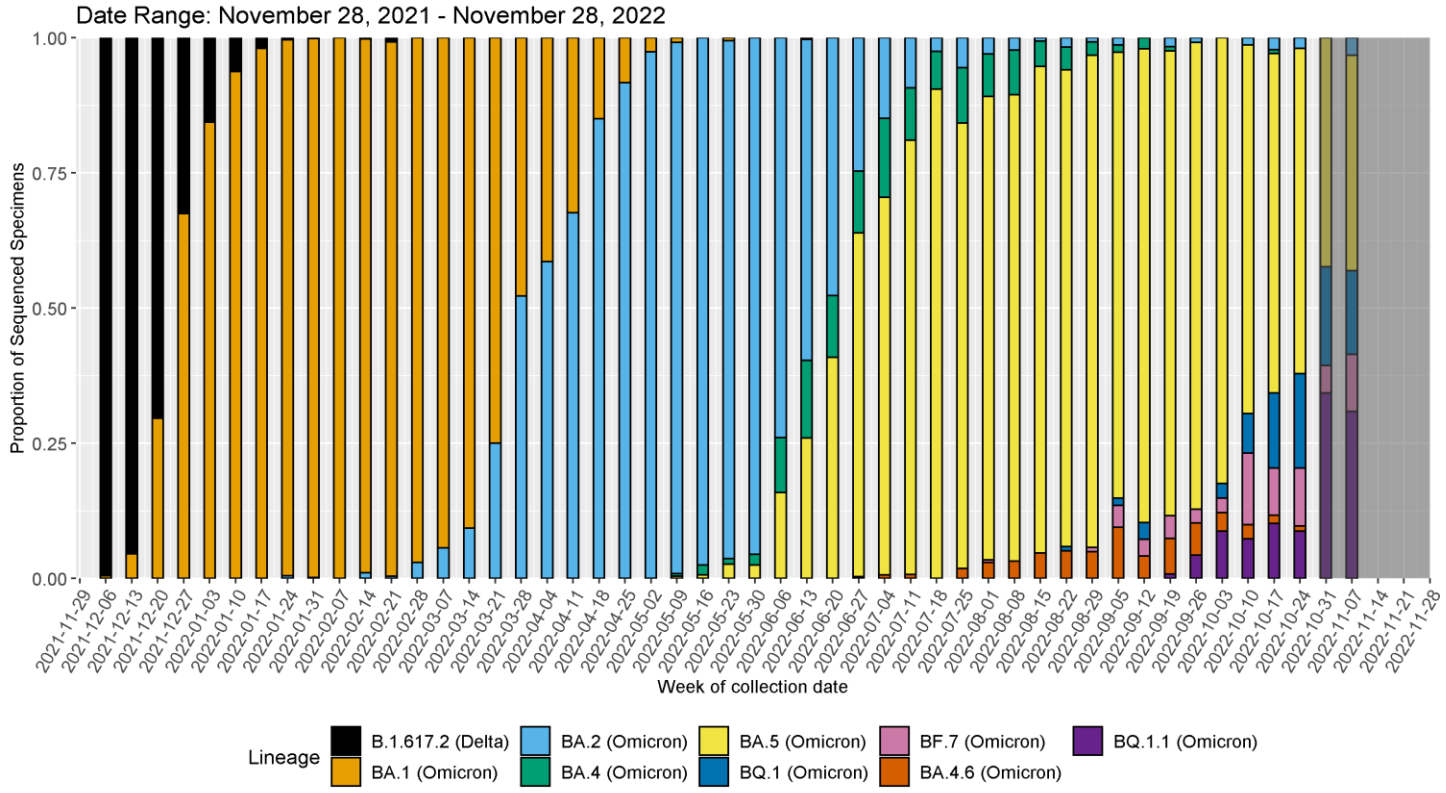
Lineage	Total Matched Cases	Number Hospitalized (%)	Number Died (%)	Number Vaccine Breakthrough (%)*
BA.1 (Omicron)	6612	281 (4%)	61 (1%)	3748 (57%)
BA.2 (Omicron)	2423	207 (9%)	21 (1%)	1733 (72%)
BA.4 (Omicron)	414	26 (6%)	3 (1%)	288 (70%)
BA.5 (Omicron)	3162	234 (7%)	25 (1%)	2239 (71%)
B.1.617.2 (Delta)	14362	1259 (9%)	459 (3%)	4439 (31%)
B.1.1.7 (Alpha)	1602	153 (10%)	21 (1%)	96 (6%)
B.1.351 (Beta)	5	0 (0%)	0 (0%)	0 (0%)
P.1 (Gamma)	92	22 (24%)	2 (2%)	4 (4%)
B.1.427/B.1.429 (Epsilon)	430	9 (2%)	2 (0%)	9 (2%)
B.1.525 (Eta)	5	0 (0%)	0 (0%)	0 (0%)
B.1.526 (Iota)	173	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	3157	190 (6%)	65 (2%)	27 (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*



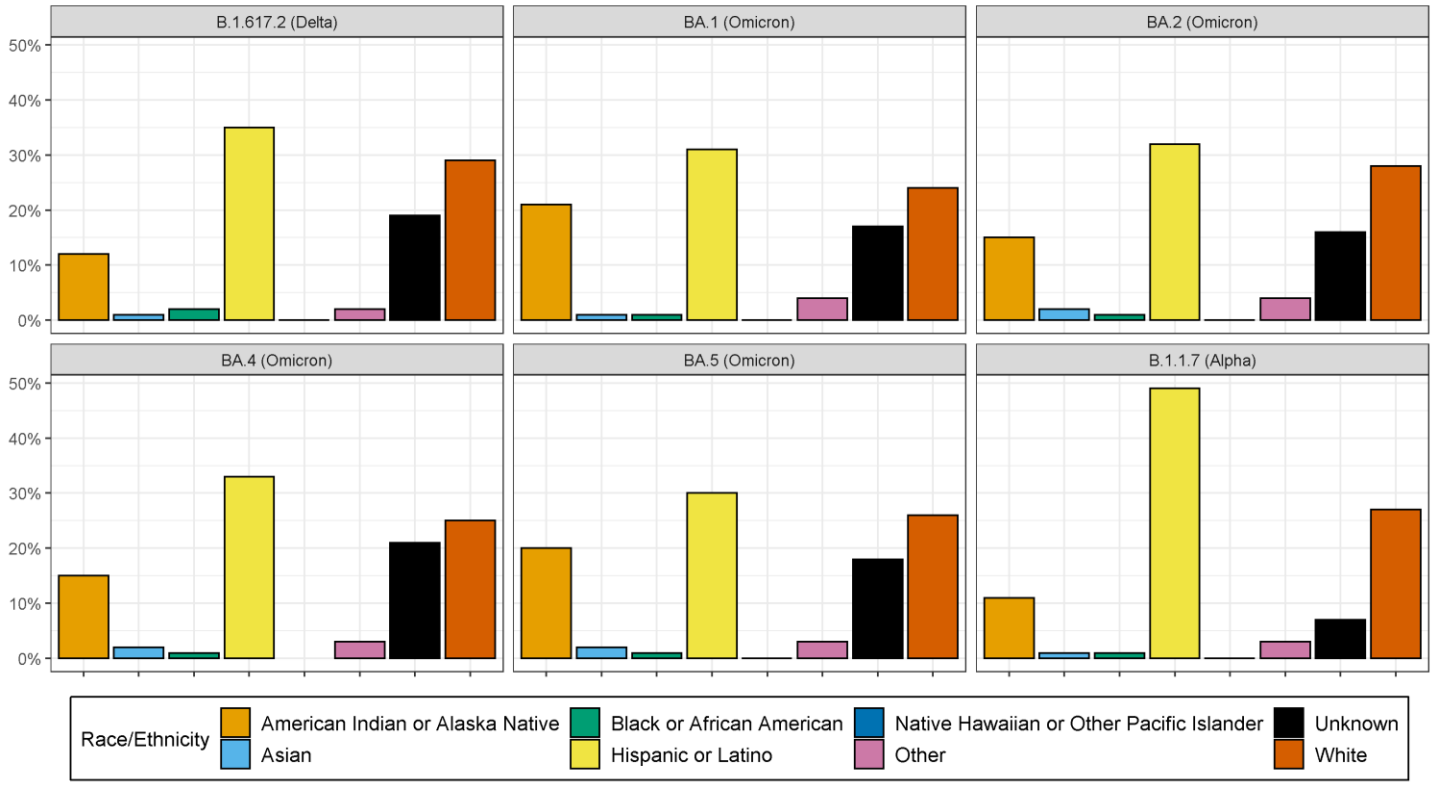
Proportion of identified SARS-CoV-2 lineages by week*



*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.

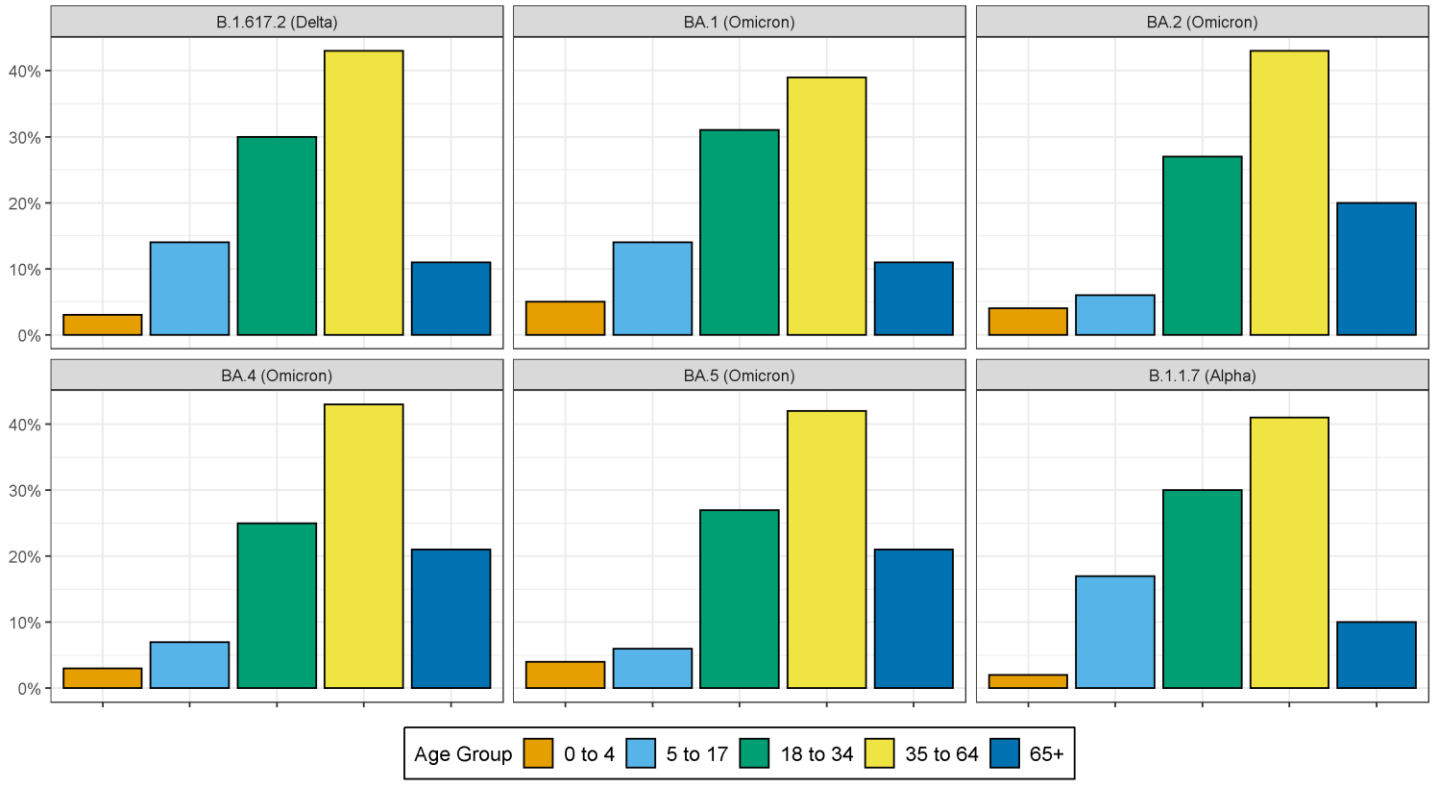
Cumulative proportion of variant cases by race/ethnicity

Cumulative up to November 28, 2022



Cumulative proportion of variant cases by age group

Cumulative up to November 28, 2022



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	2486	990	180	1216	4816	470
Chaves	57	9	9	51	354	13
Cibola	209	132	16	61	292	14
Colfax	40	7	1	6	224	28
Curry	116	79	15	82	337	30
Dona Ana	319	122	27	147	915	83
Eddy	67	11	2	21	383	21
Grant	84	56	4	16	135	16
Guadalupe	22	0	0	2	67	1
Lea	11	2	0	9	28	0
Lincoln	32	3	1	7	226	17
Los Alamos	44	34	5	55	119	6
Luna	34	17	2	10	49	9
McKinley	67	19	0	6	59	15
Otero	343	6	2	38	360	19
Quay	219	36	7	27	782	27
Rio Arriba	12	6	3	16	79	4
Roosevelt	113	89	9	97	203	96
San Juan	17	3	1	7	79	1
San Miguel	981	208	41	542	1662	327
Sandoval	78	31	1	24	160	10
Santa Fe	452	248	38	289	974	77
Sierra	361	188	35	247	749	101
Socorro	31	14	2	14	124	5
Taos	18	16	0	29	92	9
Torrance	47	25	2	32	234	17
Valencia	47	14	1	11	176	16

* 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)	6612	2318 (35%)	140	2178	94%
BA.2 (Omicron)	2423	1244 (51%)	55	1189	96%
BA.4 (Omicron)	414	173 (42%)	2	171	99%
BA.5 (Omicron)	3162	1134 (36%)	45	1089	96%
B.1.617.2 (Delta)	14362	5752 (40%)	392	5360	93%
B.1.1.7 (Alpha)	1602	1226 (77%)	117	1109	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)	1863 (86%)	1022 (86%)	143 (84%)	898 (82%)	3513 (66%)	744 (67%)
Lower Respiratory (Cough, shortness of breath)	1787 (82%)	1017 (86%)	145 (85%)	961 (88%)	4223 (79%)	844 (76%)
Gastrointestinal (Nausea/vomiting, abdominal pain, diarrhea)	894 (41%)	503 (42%)	84 (49%)	536 (49%)	2373 (44%)	476 (43%)
Systemic (Fever, chills, muscle aches, headache, fatigue, loss of appetite)	1964 (90%)	1080 (91%)	159 (93%)	994 (91%)	4757 (89%)	979 (88%)
Loss of Taste and Smell	471 (22%)	230 (19%)	43 (25%)	256 (24%)	2582 (48%)	428 (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)	6174	1907 (31%)	1420	487	26%
BA.2 (Omicron)	1889	713 (38%)	194	519	73%
BA.4 (Omicron)	290	54 (19%)	13	41	76%
BA.5 (Omicron)	2512	461 (18%)	104	357	77%
B.1.617.2 (Delta)	14362	5653 (39%)	4345	1308	23%
B.1.1.7 (Alpha)	1602	1219 (76%)	628	591	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	115 (28%)	124 (30%)	7 (19%)	81 (28%)	248 (23%)	136 (26%)
Chronic Liver Disease	15 (4%)	20 (5%)	2 (6%)	12 (4%)	53 (5%)	17 (3%)
Chronic Renal Disease	45 (11%)	43 (10%)	2 (6%)	40 (14%)	126 (12%)	20 (4%)
Diabetes Mellitus	117 (28%)	106 (25%)	11 (31%)	89 (31%)	400 (38%)	95 (18%)
Cardiovascular Disease	157 (38%)	166 (40%)	12 (33%)	120 (42%)	388 (37%)	172 (32%)
Autoimmune Disease	13 (3%)	19 (5%)	2 (6%)	13 (5%)	61 (6%)	41 (8%)
Neurological Disability	50 (12%)	46 (11%)	7 (19%)	36 (13%)	80 (8%)	31 (6%)
Current or Former Smoker	175 (42%)	195 (47%)	14 (39%)	121 (42%)	362 (34%)	285 (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.