COVID-19 Variant of Concern (VOC) Case Report

May 30, 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. The first confirmed Omicron case was identified in NM December 12, 2021. To date, 7274 confirmed cases of Omicron have been sequenced in NM; of these, 397 confirmed cases are BA.2 sublineages. Since the week of January 24, 2022, Omicron represented approximately 100% of sequenced samples in New Mexico. Sequenced specimens reported from May 2 to May 30, 2022 are incomplete but indicate a continued predominance of Omicron, with a rising trend of BA.2 sublineages. CDC Nowcast predictive modeling forecasts Omicron to represent approximately 100% of US positive cases the week of May 28, 2022, and that BA.2 sublineages could represent more than 90% of current cases.[4] CDC currently classifies all BA sublineage variants with B.1.1.529 as Omicron. 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. -7274 confirmed cases of Omicron have been sequenced in NM; 397 of them are BA.2.

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 6/28/21 to 12/20/21 and represented 72% of sequences reported on 12/20/21. -CDC downgraded Delta to a VBM 4/14/22
Alpha (B.1.1.7 and Q lineages)	United Kingdom	-50% more transmissible -Potential to cause more severe cases and deaths	-Alpha has proportionally declined from 80% the week of 5/24/21 to 2% of samples collected the week of 7/19/21. -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

For the remainder of the report, Omicron BA.2 sublineages will be split from B.1.1.529 and BA.1 sublineages.

Lineage	Sequenced Cases	Matched Cases*	Percent Matched
BA.2 (Omicron)	397	370	93%
B.1.1.529 (Omicron)	6877	6261	91%
B.1.617.2 (Delta)	15839	14238	90%
B.1.1.7 (Alpha)	1900	1607	85%
B.1.351 (Beta)	10	5	50%
P.1 (Gamma)	109	95	87%
B.1.427/B.1.429 (Epsilon)	528	439	83%
B.1.525 (Eta)	5	4	80%
B.1.526 (Iota)	202	174	86%
B.1.617.1 (Kappa)	2	2	100%
P.2 (Zeta)	3	2	67%
B.1.621/B.1.621.1 (Mu)	36	31	86%
Other lineage	4042	3246	80%
Total	29950	26474	88%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 266 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.

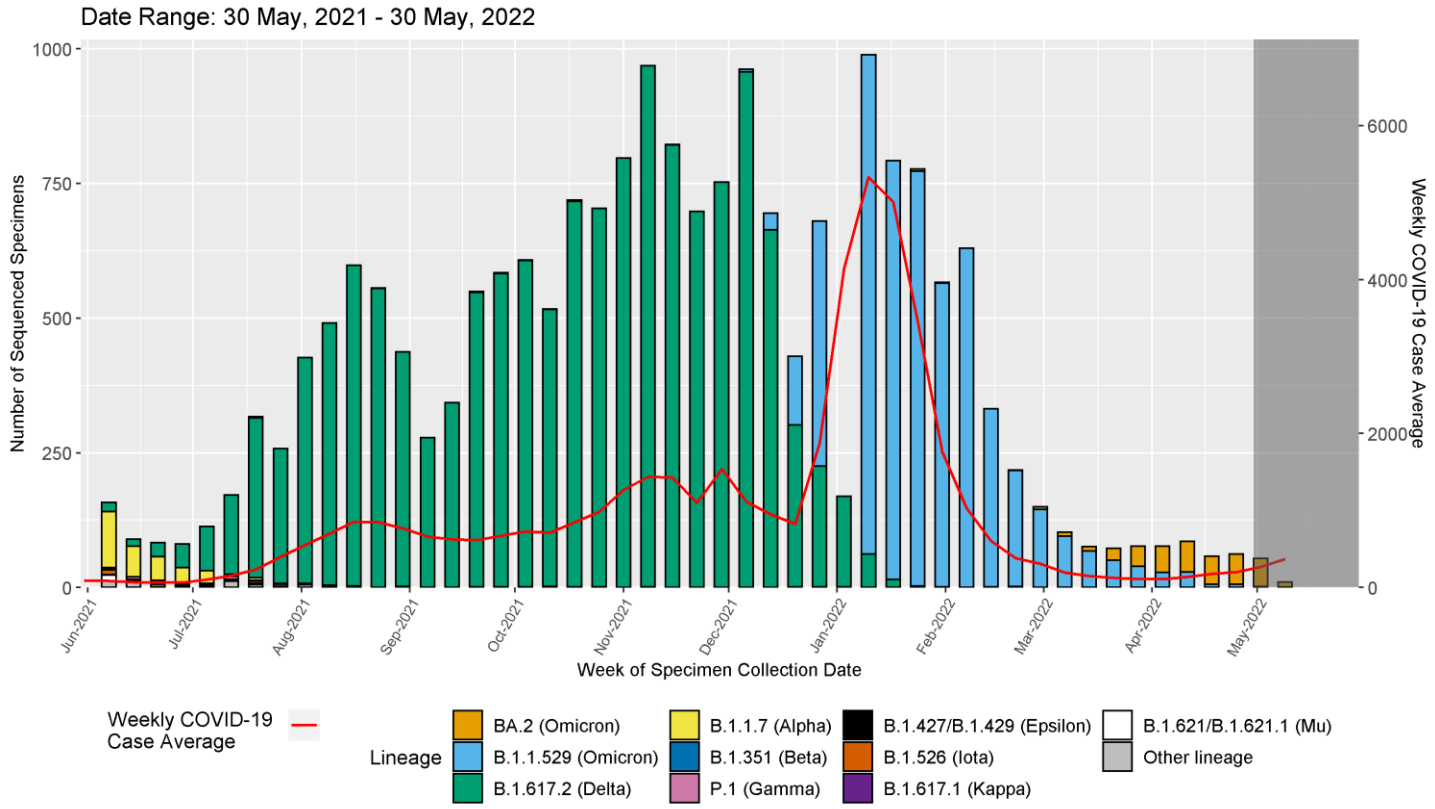
Cumulative number of variant cases, hospitalizations, and deaths

Lineage	Total Cases	Number Hospitalized	Number Died	Vaccine Breakthrough Cases*
BA.2 (Omicron)	363	11 (3%)	1 (0%)	268 (74%)
B.1.1.529 (Omicron)	6228	262 (4%)	52 (1%)	3484 (56%)
B.1.617.2 (Delta)	14140	1221 (9%)	425 (3%)	4377 (31%)
B.1.1.7 (Alpha)	1589	150 (9%)	19 (1%)	96 (6%)
B.1.351 (Beta)	5	0 (0%)	0 (0%)	0 (0%)
P.1 (Gamma)	93	22 (24%)	2 (2%)	4 (4%)
B.1.427/B.1.429 (Epsilon)	428	9 (2%)	2 (0%)	9 (2%)
B.1.525 (Eta)	4	0 (0%)	0 (0%)	0 (0%)
B.1.526 (Iota)	172	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)	31	1 (3%)	0 (0%)	4 (13%)
Other lineage	3151	195 (6%)	65 (2%)	22 (1%)

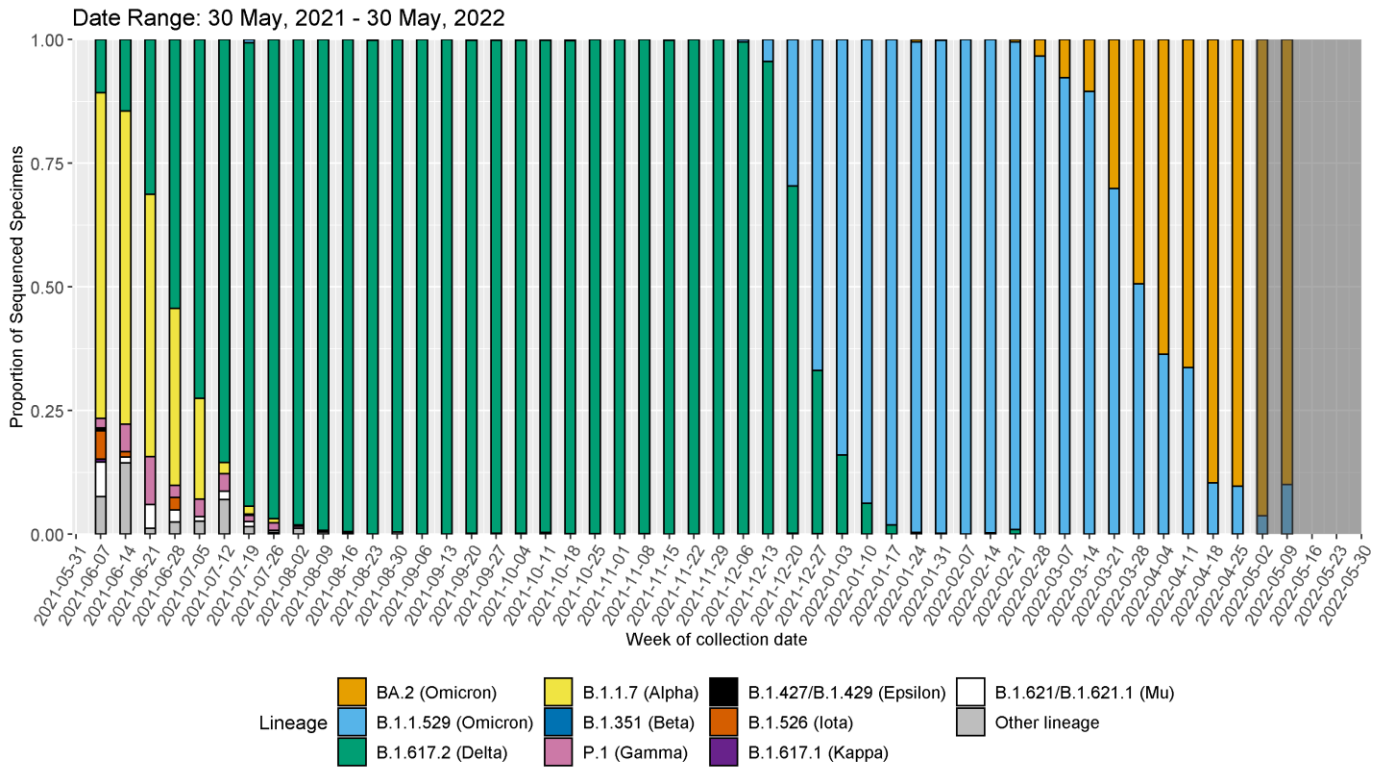
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. *Because samples collected from VBT cases are more frequently sequenced compared to samples from 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*

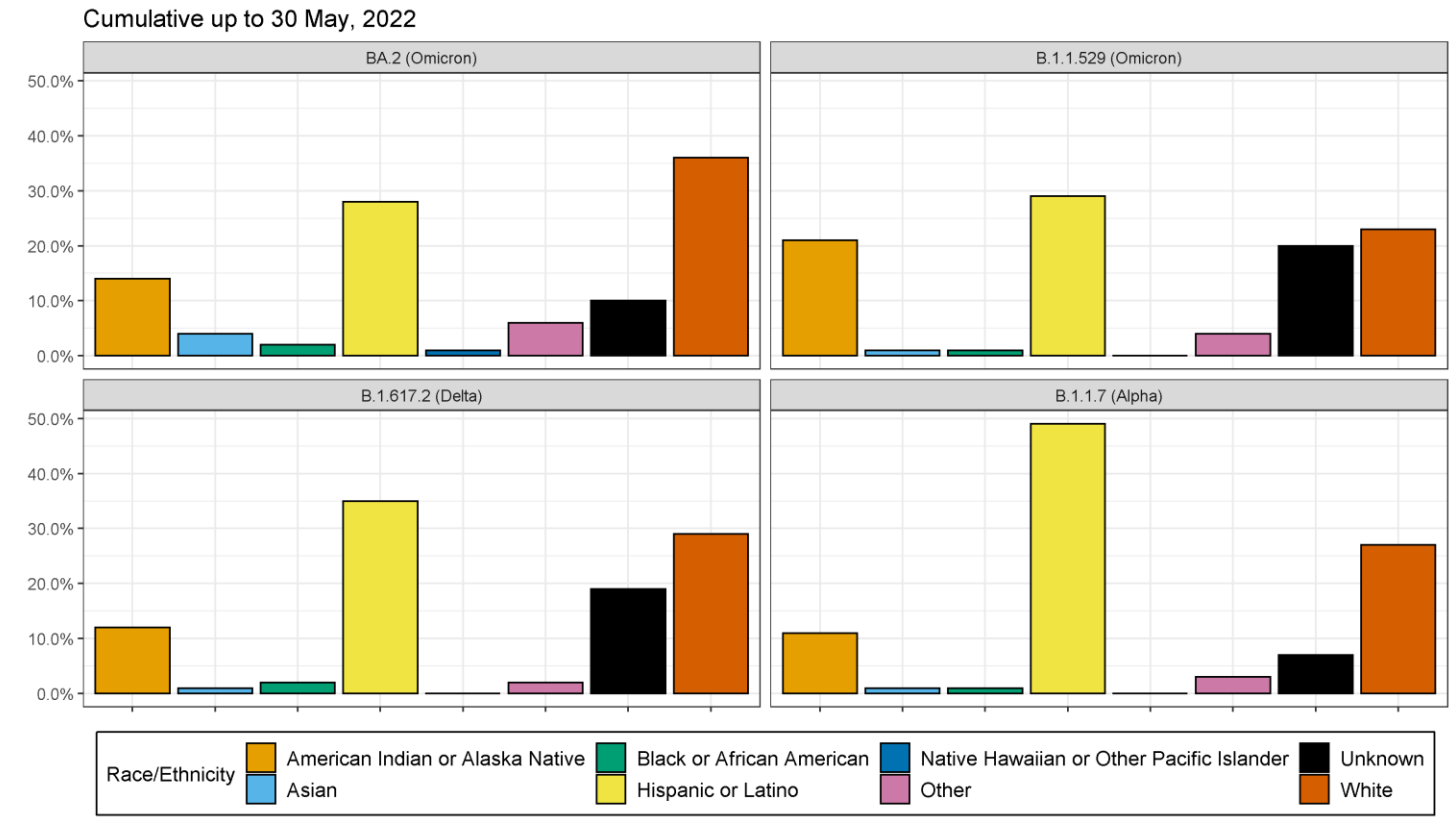


Proportion of identified SARS-CoV-2 lineages by week*

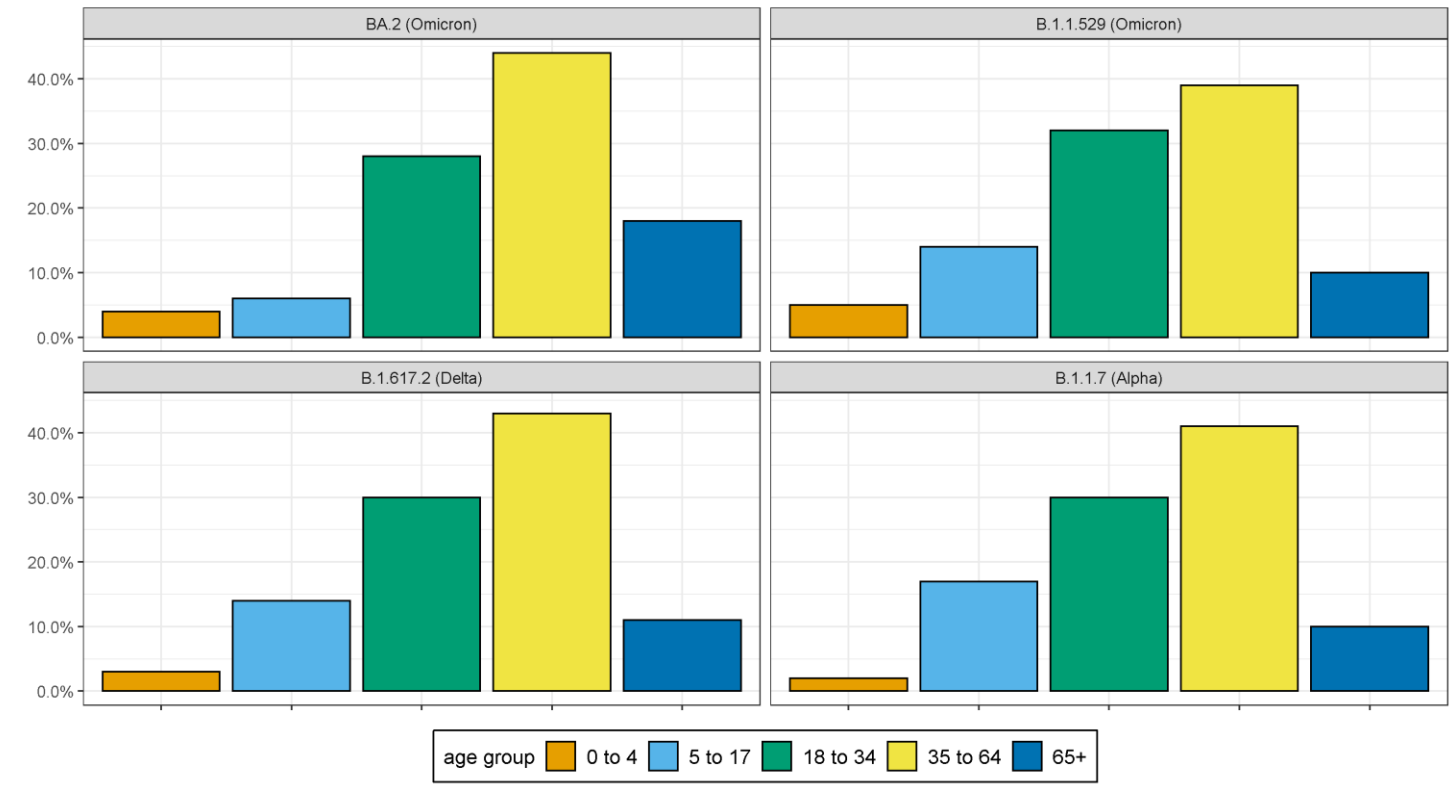


*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

Cumulative proportion of variant cases by race/ethnicity



Cumulative proportion of variant cases by age group



Cumulative number of variant cases by county of residence*

County	BA.2 (Omicron)	B.1.1.529 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Bernalillo	149	2381	4755	468
Chaves	2	57	344	13
Cibola	32	180	290	14
Colfax	1	33	206	28
Curry	15	116	331	30
Dona Ana	24	283	904	83
Eddy	2	60	378	21
Grant	4	81	132	16
Guadalupe	0	21	67	1
Lea	1	30	223	16
Lincoln	12	40	119	6
Los Alamos	8	29	48	9
Luna	0	65	59	14
McKinley	0	335	357	18
Otero	7	211	773	26
Quay	1	12	79	4
Rio Arriba	11	93	193	92
Roosevelt	0	16	78	1
San Juan	15	956	1624	324
San Miguel	0	64	158	10
Sandoval	28	413	958	77
Santa Fe	34	339	739	101
Sierra	1	28	124	5
Socorro	2	17	92	9
Taos	5	43	230	17
Torrance	1	47	171	16
Valencia	6	237	564	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	Symptomatic (%)
BA.2 (Omicron)	363	211 (58%)	6	205	97%
B.1.1.529 (Omicron)	6228	1254 (20%)	94	1160	93%
B.1.617.2 (Delta)	14140	5582 (39%)	375	5207	93%
B.1.1.7 (Alpha)	1589	1216 (77%)	115	1101	91%

Percentage of specific symptoms reported by symptomatic variant cases

The table below includes data ONLY from symptomatic cases.

Symptom	BA.2 (Omicron)	B.1.1.529 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Upper Respiratory (Runny nose, sore throat)	190 (93%)	937 (81%)	3425 (66%)	738 (67%)
Lower Respiratory (Cough, shortness of breath)	172 (84%)	949 (82%)	4112 (79%)	836 (76%)
Gastrointestinal (Nausea/vomiting, abdominal pain, diarrhea)	78 (38%)	450 (39%)	2315 (44%)	474 (43%)
Systemic (Fever, chills, muscle aches, headache, fatigue, loss of appetite)	187 (91%)	1037 (89%)	4631 (89%)	971 (88%)
Loss of Taste and Smell	38 (19%)	250 (22%)	2530 (49%)	424 (39%)

* Excludes all VBMs other than Alpha and Delta.

Percentage of variant cases reporting underlying conditions

Lineage	Total	Total Investigated (%)	No	Yes	Underlying Conditions (%)
BA.2 (Omicron)	363	205 (56%)	63	142	69%
B.1.1.529 (Omicron)	6228	1254 (20%)	850	404	32%
B.1.617.2 (Delta)	14140	5401 (38%)	4125	1276	24%
B.1.1.7 (Alpha)	1589	1210 (76%)	622	588	49%

Percentage of specific underlying conditions reported by variant cases

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

Symptom	BA.2 (Omicron)	B.1.1.529 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Chronic Lung Disease	36 (32%)	103 (30%)	241 (23%)	136 (26%)
Chronic Liver Disease	4 (4%)	15 (4%)	53 (5%)	18 (3%)
Chronic Renal Disease	11 (10%)	40 (11%)	124 (12%)	21 (4%)
Diabetes Mellitus	23 (20%)	101 (29%)	391 (38%)	96 (18%)
Cardiovascular Disease	45 (39%)	134 (38%)	375 (36%)	170 (32%)
Autoimmune Disease	2 (2%)	11 (3%)	60 (6%)	41 (8%)
Neurological Disability	11 (10%)	40 (11%)	80 (8%)	31 (6%)
Current or Former Smoker	58 (51%)	139 (40%)	354 (34%)	284 (54%)

* Excludes all VBMs other than Alpha and Delta.

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.