COVID-19 Variant of Concern (VOC) Case Report

February 14, 2022

Cases reported here include cases with specimens sequenced at the Scientific Laboratory Division (SLD), University of New Mexico, Centers for Disease Control and Prevention (CDC), Aegis, LabCorp, Fulgent, Gravity, and Helix Genetics. 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.

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 two VOCs currently in the US, Delta and Omicron. All other VOCs and VOIs are now classified as VBMs due to their low prevalence including Alpha, Beta, Gamma, Epsilon, Eta, Iota, Kappa, Zeta, and Mu. CDC designated B.1.1.529 (Omicron) a VOC on November 30, 2021. The first confirmed Omicron case was identified in NM December 12, 2021. To date, 2026 confirmed cases of Omicron have been sequenced in NM. Omicron represented approximately 97% of sequenced samples in New Mexico in the week of January 10, 2021. Sequenced specimens reported from January 17-February 14, 2022 are incomplete but indicate a predominance of Omicron compared to other variants. CDC Nowcast predictive modeling forecasts Omicron to represent approximately 100% of US positive cases the week of February 12, 2022.[4] CDC currently classifies all AY sublineage variants with B.1.617.2 as Delta, and 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 and spread of new variants.

NM COVID-19 Variant Epidemiologic Interpretation

CDC VARIANTS OF CONCERN (VOC)

Name	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 69% of sequences reported on 12/20/21. -Proportion of deaths is currently 3%.
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 70% of cases. -To date, 2026 confirmed cases of Omicron have been sequenced in NM.

CDC VARIANTS BEING MONITORED (VBM)			
Name[3]	First Identified	Attributes[1]	New Mexico[2]
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 78% the week of 5/24/21 to 3% 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 10% of sequenced NM specimens the week of 6/21/2021. -Currently has the highest proportion of hospitalizations (23%); 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 26% 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 6/28/21; Iota peaked at 15% 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 5/24/21 and has not been observed since 8/16/21; 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
B.1.617.2 (Delta)	11863	10361	87%
B.1.1.529 (Omicron)	2026	1901	94%
B.1.1.7 (Alpha)	1835	1524	83%
B.1.351 (Beta)	8	3	38%
P.1 (Gamma)	109	92	84%
B.1.427/B.1.429 (Epsilon)	521	418	80%
B.1.525 (Eta)	4	4	100%
B.1.526 (Iota)	191	162	85%
B.1.617.1 (Kappa)	2	2	100%
P.2 (Zeta)	3	2	67%
B.1.621/B.1.621.1 (Mu)	38	30	79%
Other lineage	4507	3129	69%
Total	21107	17628	84%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 220 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.

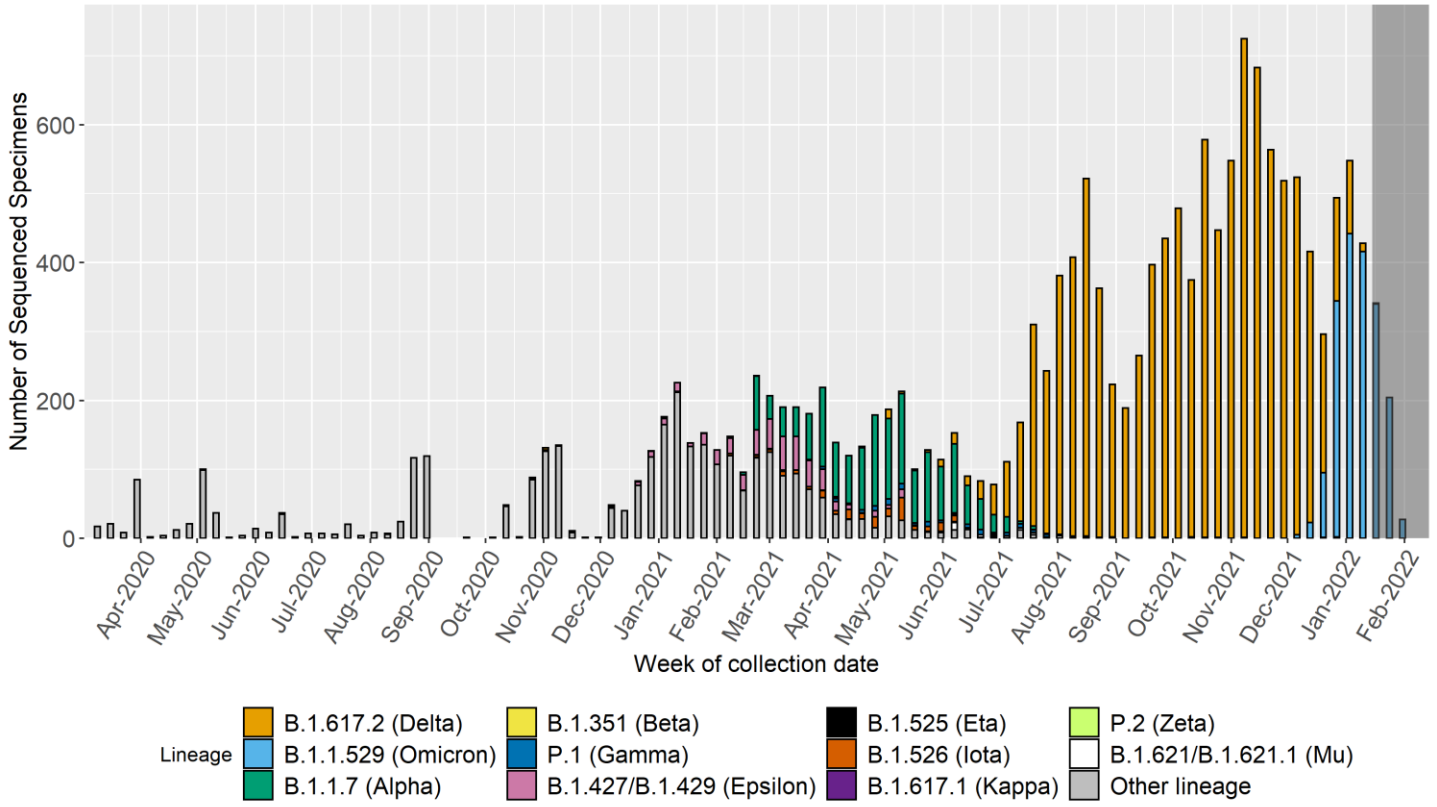
Cumulative number of variant cases, hospitalizations, and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
Delta	10361	940	9%	263	3%	3461
Omicron	1901	24	1%	1	0%	1101
Alpha	1524	151	10%	18	1%	95
Beta	3	0	0%	0	0%	0
Gamma	92	21	23%	2	2%	3
Epsilon	418	9	2%	2	0%	8
Eta	4	0	0%	0	0%	0
Iota	162	5	3%	1	1%	8
Kappa	2	0	0%	0	0%	0
Zeta	2	0	0%	0	0%	0
Mu	30	2	7%	0	0%	4
Other lineage	3129	206	7%	65	2%	24

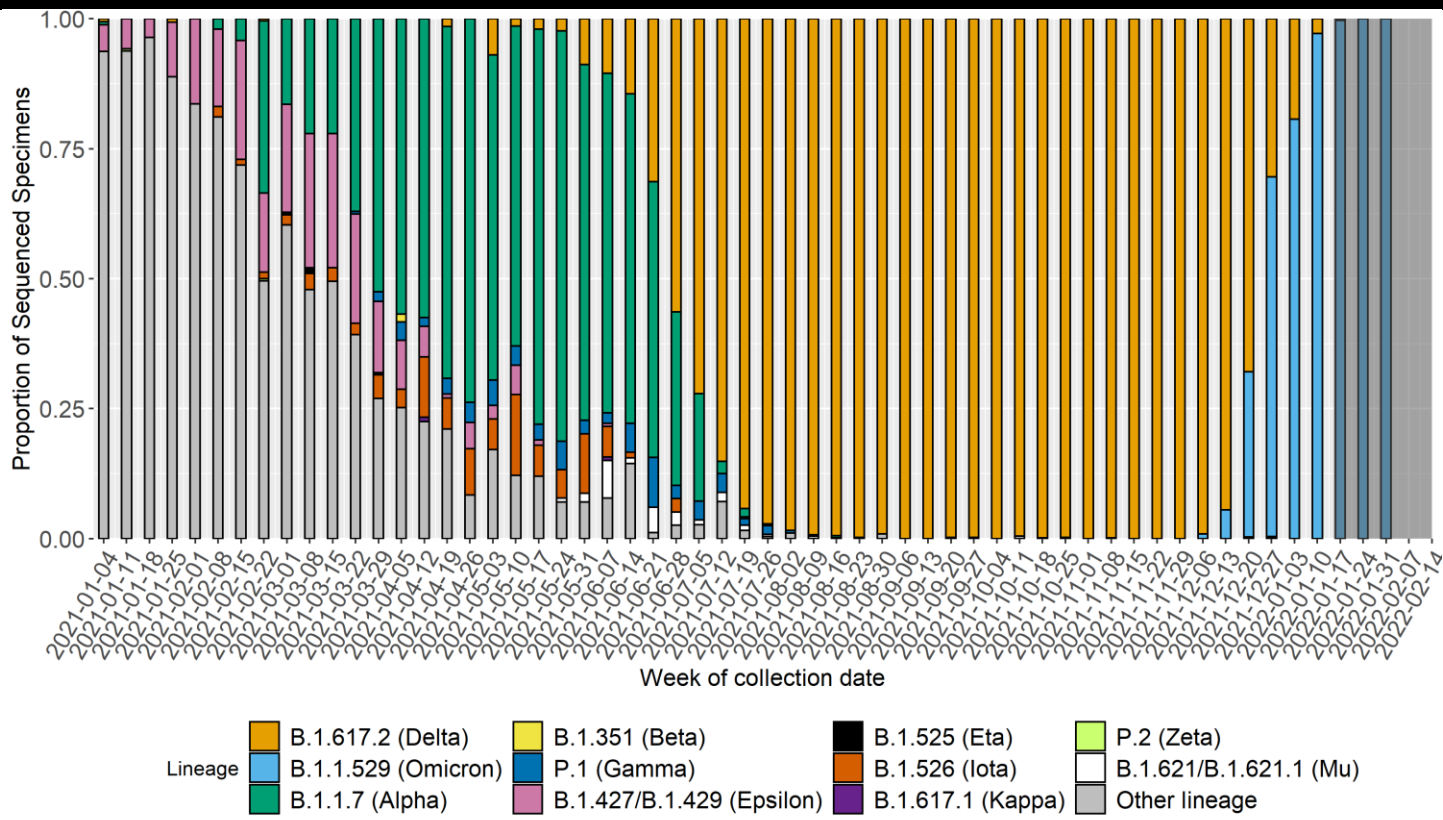
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. *Because samples collected from VBT cases are more frequently sequenced compared to samples from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

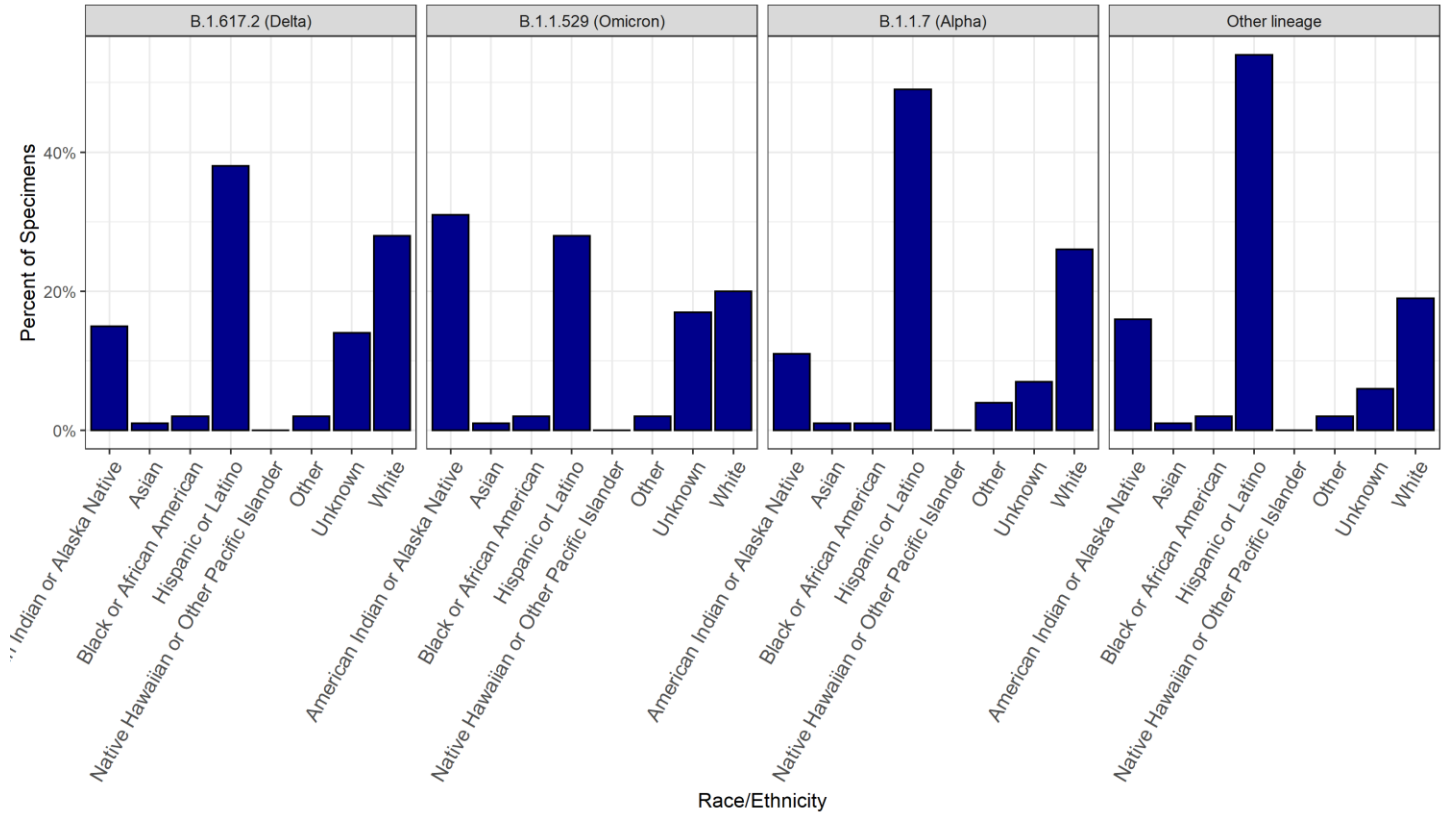


Proportion of identified SARS-CoV-2 lineages by week*

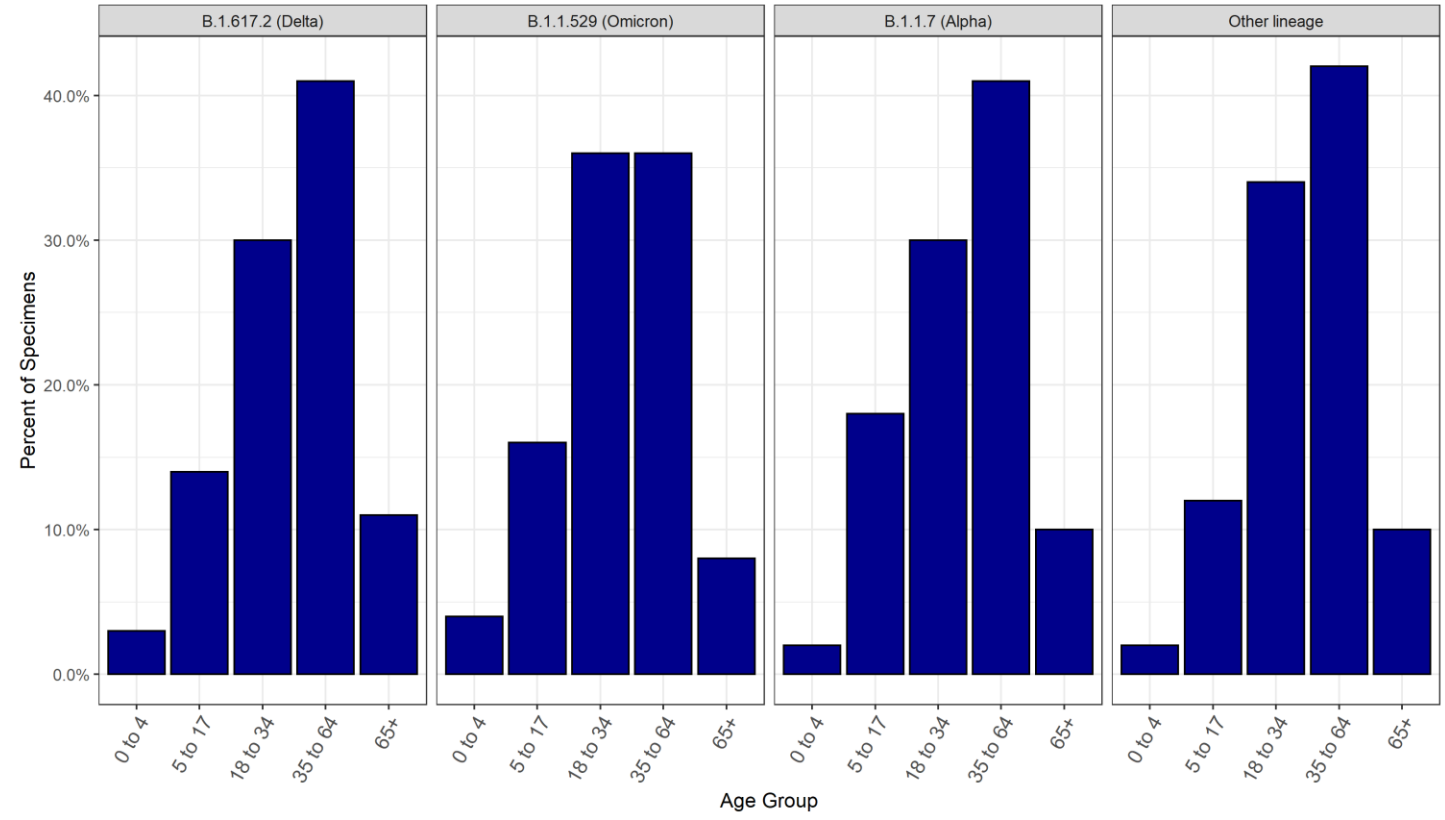


*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

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*

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

County	B.1.617.2 (Delta)	B.1.1.529 (Omicron)	B.1.1.7 (Alpha)	Other lineage
Bernalillo	3380	554	443	1050
Chaves	212	10	13	59
Cibola	209	50	13	108
Colfax	135	12	24	26
Curry	124	1	24	29
Dona Ana	748	120	80	424
Eddy	274	7	19	97
Grant	81	32	13	34
Guadalupe	63	11	1	19
Lea	143	6	16	114
Lincoln	47	6	5	57
Los Alamos	44	7	9	24
Luna	42	31	14	20
McKinley	314	197	18	126
Otero	682	106	24	149
Rio Arriba	152	19	92	39
San Juan	1518	465	317	292
San Miguel	107	19	10	55
Sandoval	596	85	73	231
Santa Fe	531	67	97	292
Sierra	104	16	5	5
Socorro	53	3	9	31
Taos	120	6	16	39
Torrance	126	7	16	22
Valencia	429	50	70	118

*Only VOCs with greater than 100 sequenced specimens in NM are reported and excludes all VBMs other than Alpha.

Percentage of variant cases reporting any symptoms

Lineage	Total	Total Investigated (%)	No	Yes	Symptomatic (%)
B.1.617.2 (Delta)	10354	4066 (39%)	249	3817	94%
B.1.1.529 (Omicron)	1901	142 (8%)	15	127	89%
B.1.1.7 (Alpha)	1524	1162 (76%)	104	1058	91%
Other lineage	3595	2785 (78%)	392	2393	86%

Percentage of specific symptoms reported by symptomatic variant cases

The table below includes data ONLY from symptomatic cases.

Symptom	B.1.617.2 (Delta)	B.1.1.529 (Omicron)	B.1.1.7 (Alpha)	Other lineage
Fever (Measured or Subjective)	53% (1980)	46% (58)	47% (484)	43% (1013)
Chills	48% (1788)	43% (54)	46% (477)	44% (1050)
Muscle Aches	55% (2061)	50% (63)	57% (590)	56% (1315)
Runny Nose	55% (2055)	67% (84)	53% (550)	53% (1258)
Sore Throat	44% (1643)	63% (79)	45% (465)	42% (1001)
Cough	74% (2804)	77% (96)	73% (764)	64% (1510)
Shortness of Breath	31% (1167)	23% (29)	30% (307)	24% (569)
Nausea/Vomiting	27% (1017)	22% (28)	27% (280)	23% (536)
Headache	64% (2406)	64% (80)	66% (685)	65% (1537)
Abdominal Pain	14% (536)	11% (14)	16% (162)	14% (328)
Diarrhea	29% (1101)	20% (25)	29% (297)	26% (622)
Fatigue	67% (2526)	59% (74)	70% (729)	66% (1550)
Loss of Appetite	39% (1483)	27% (34)	40% (415)	36% (849)
Loss of Taste or Smell	48% (1818)	24% (30)	39% (409)	44% (1030)

*Only VOCs with greater than 100 sequenced specimens in NM are reported and excludes all VBMs other than Alpha.

Percentage of variant cases reporting underlying conditions

Lineage	Total	Total Investigated (%)	No	Yes	Underlying Conditions (%)
B.1.617.2 (Delta)	10354	3901 (38%)	2912	989	25%
B.1.1.529 (Omicron)	1901	135 (7%)	119	16	12%
B.1.1.7 (Alpha)	1524	1156 (76%)	596	560	48%
Other lineage	3595	2700 (75%)	1653	1047	39%

Percentage of specific underlying conditions reported by variant cases

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

Symptom	B.1.617.2 (Delta)	B.1.1.529 (Omicron)	B.1.1.7 (Alpha)	Other lineage
Chronic Lung Disease	23% (188)	20% (3)	25% (127)	26% (243)
Chronic Liver Disease	5% (38)	0% (0)	3% (17)	4% (38)
Chronic Renal Disease	11% (92)	7% (1)	4% (19)	5% (44)
Diabetes Mellitus	35% (282)	27% (4)	19% (95)	22% (203)
Cardiovascular Disease	36% (291)	33% (5)	32% (162)	29% (264)
Autoimmune Disease	6% (49)	7% (1)	8% (40)	5% (45)
Neurological Disability	8% (65)	20% (3)	6% (31)	9% (81)
Current or Former Smoker	37% (296)	53% (8)	53% (270)	50% (466)

* Note: One P.1 variant case reported an underlying condition that is not included on the list above.

**Only VOCs with greater than 100 sequenced specimens in NM are reported and excludes all VBMs other than Alpha.

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**
  - New Mexico Department of Health (NMDOH) receives sequencing data for specimens sequenced at the NMDOH Scientific Laboratory Division (SLD), University of New Mexico, Centers for Disease Control and Prevention (CDC), Aegis, LabCorp, Fulgent Genetics, Gravity, and Helix Genetics.
- **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.