

COVID-19 Variant of Concern (VOC) Case Report

April 11, 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, 4701 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 March 14-April 11, 2022 are incomplete but indicate a continued predominance of Omicron. CDC Nowcast predictive modeling forecasts Omicron to represent approximately 100% of US positive cases the week of April 9, 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 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 75% 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 61% of cases. -To date, 4701 confirmed cases of Omicron have been sequenced in NM.

CDC VARIANTS BEING MONITORED (VBM)			
Name³	First Identified	Attributes¹	New Mexico²
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 5/24/21 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>

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

³All 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.1.1.529 (Omicron)	4701	4392	93%
B.1.617.2 (Delta)	12735	11154	88%
B.1.1.7 (Alpha)	1834	1546	84%
B.1.351 (Beta)	8	3	38%
P.1 (Gamma)	109	95	87%
B.1.427/B.1.429 (Epsilon)	518	427	82%
B.1.525 (Eta)	4	3	75%
B.1.526 (Iota)	191	165	86%
B.1.617.1 (Kappa)	2	2	100%
P.2 (Zeta)	3	2	67%
B.1.621/B.1.621.1 (Mu)	36	30	83%
Other lineage	4016	3223	80%
Total	24157	21042	87%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 252 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.

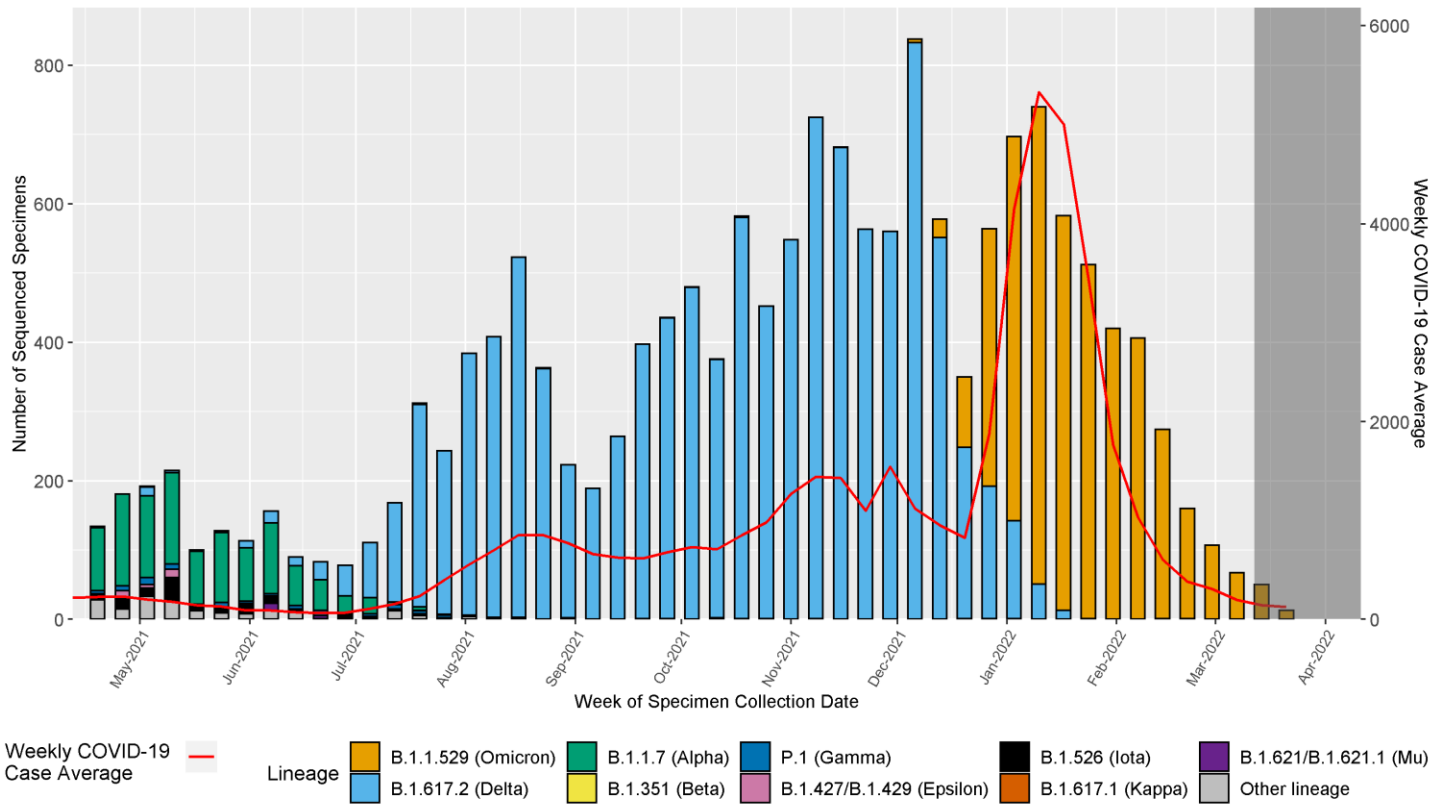
Cumulative number of variant cases, hospitalizations, and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
Omicron	4361	163	4%	37	1%	2529
Delta	11059	1116	10%	372	3%	3729
Alpha	1528	149	10%	19	1%	96
Beta	3	0	0%	0	0%	0
Gamma	93	22	24%	2	2%	4
Epsilon	416	9	2%	2	0%	8
Eta	3	0	0%	0	0%	0
Iota	163	5	3%	1	1%	8
Kappa	2	0	0%	0	0%	0
Zeta	2	0	0%	0	0%	0
Mu	30	1	3%	0	0%	4
Other lineage	3130	198	6%	65	2%	22

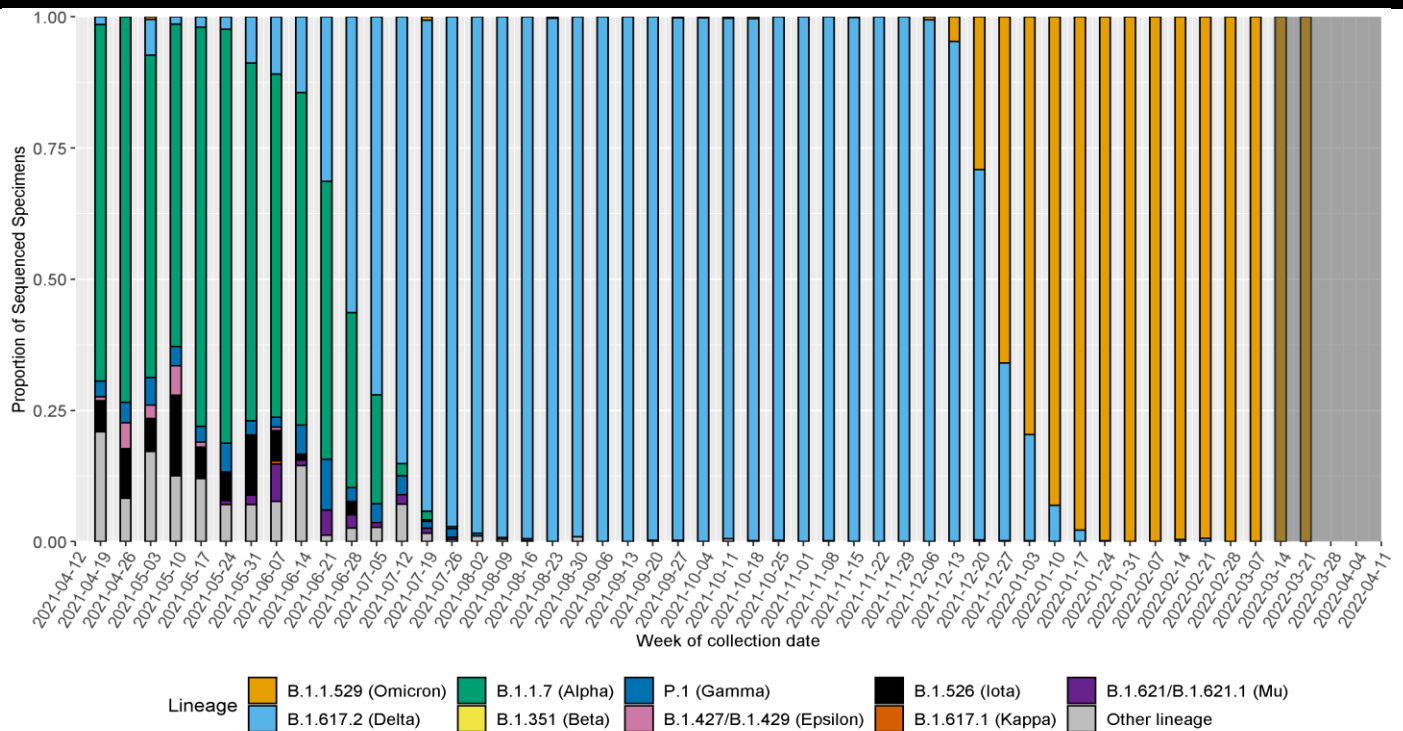
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥ 14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. *Because samples collected from VBT cases are more frequently sequenced compared to samples from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

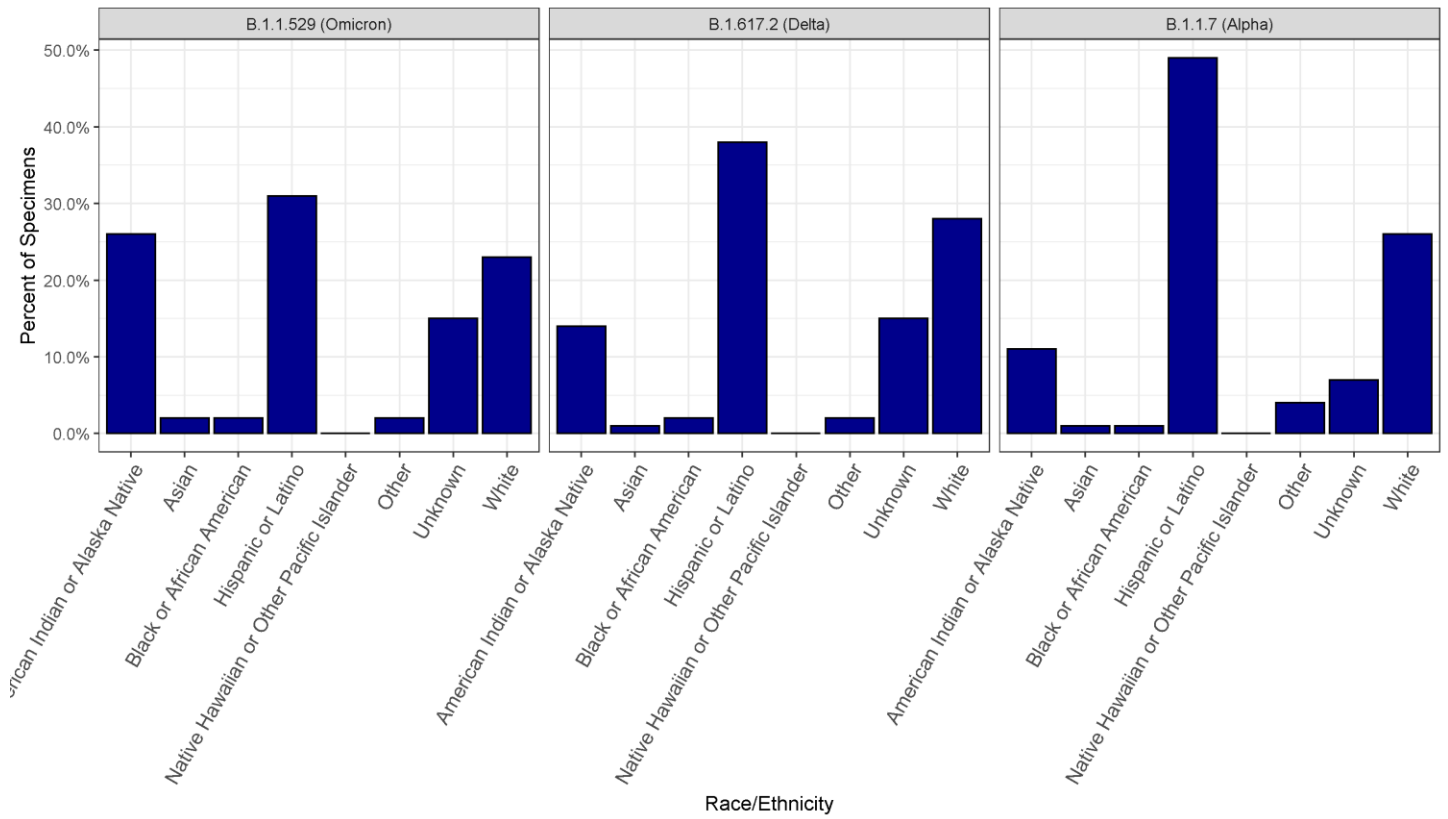


Proportion of identified SARS-CoV-2 lineages by week*

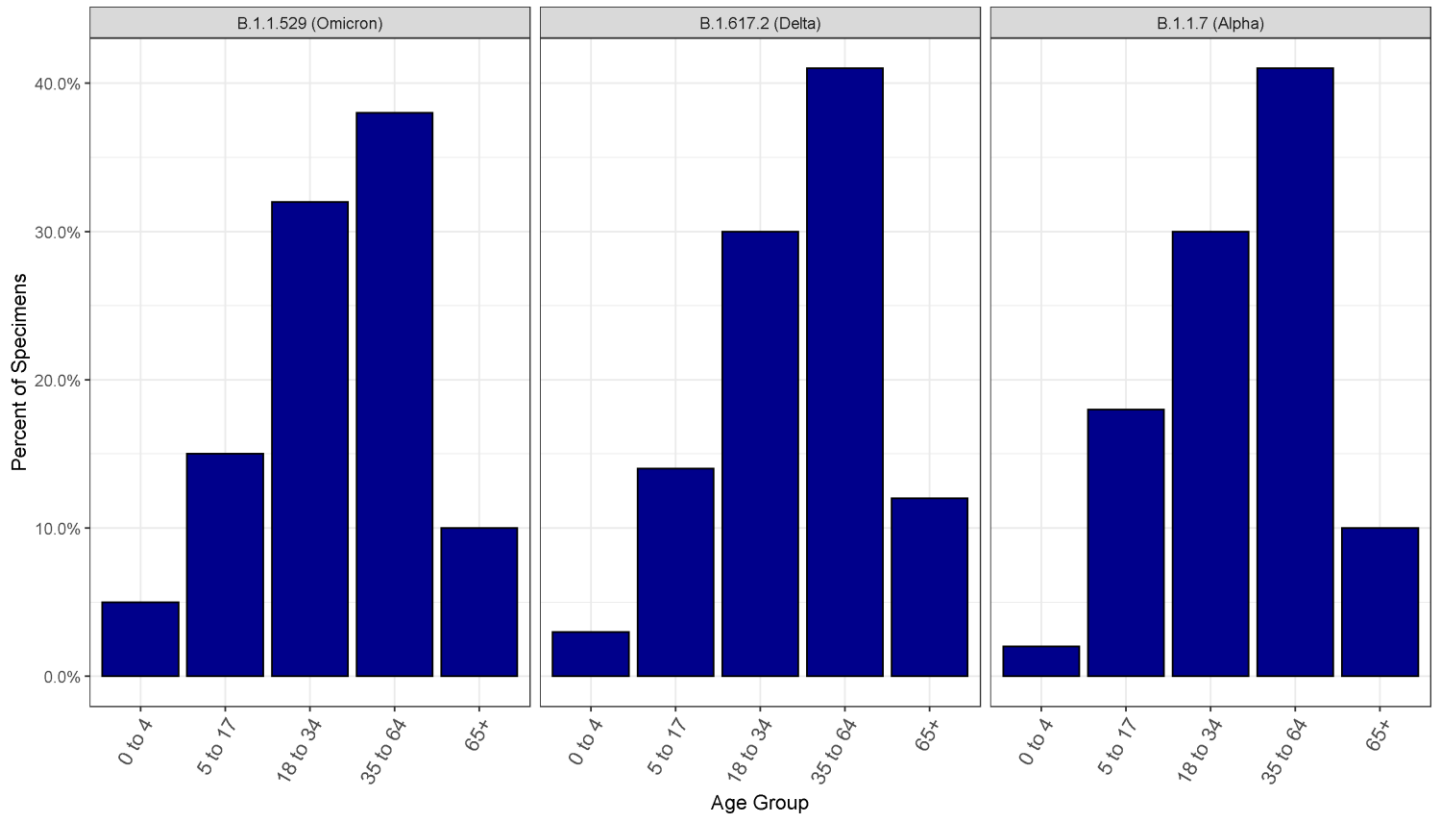


*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

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	B.1.1.529 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Bernalillo	1567	3693	448
Chaves	42	257	13
Cibola	129	214	13
Colfax	19	139	24
Curry	17	151	24
Dona Ana	241	757	80
Eddy	21	293	19
Grant	52	87	13
Guadalupe	20	63	1
Lea	12	145	16
Lincoln	12	71	5
Los Alamos	17	44	9
Luna	53	47	14
McKinley	268	319	18
Otero	186	686	24
Quay	2	66	3
Rio Arriba	51	158	92
San Juan	904	1538	317
San Miguel	43	118	10
Sandoval	241	655	72
Santa Fe	203	566	97
Sierra	23	104	5
Socorro	4	64	9
Taos	21	121	16
Torrance	27	135	16
Valencia	161	457	70

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

Percentage of variant cases reporting any symptoms

Lineage	Total	Total Investigated (%)	No	Yes	Symptomatic (%)
B.1.1.529 (Omicron)	4361	647 (15%)	58	589	91%
B.1.617.2 (Delta)	11059	4338 (39%)	264	4074	94%
B.1.1.7 (Alpha)	1528	1165 (76%)	105	1060	91%

Percentage of specific symptoms reported by symptomatic variant cases

The table below includes data ONLY from symptomatic cases.

Symptom	B.1.1.529 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Upper Respiratory (Runny nose, sore throat)	73% (762)	54% (3896)	51% (1014)
Lower Respiratory (Cough, shortness of breath)	56% (605)	56% (4283)	52% (1070)
Gastrointestinal (Nausea/Vomiting, abdominal pain, diarrhea)	21% (326)	26% (2835)	25% (740)
Systemic (Fever, chills, muscle Aches, headache, fatigue, loss of Appetite)	57% (1747)	60% (12995)	56% (3382)
Loss of Taste and Smell	24% (117)	55% (1902)	41% (408)

* Excludes all VBMs other than Alpha.

Percentage of variant cases reporting underlying conditions

Lineage	Total	Total Investigated (%)	No	Yes	Underlying Conditions (%)
B.1.1.529 (Omicron)	4361	641 (15%)	410	231	36%
B.1.617.2 (Delta)	11059	4202 (38%)	3065	1137	27%
B.1.1.7 (Alpha)	1528	1159 (76%)	594	565	49%

Percentage of specific underlying conditions reported by variant cases

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

Symptom	B.1.1.529 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Chronic Lung Disease	35% (48)	38% (215)	26% (127)
Chronic Liver Disease	7% (9)	9% (46)	4% (17)
Chronic Renal Disease	11% (15)	21% (115)	4% (20)
Diabetes Mellitus	33% (51)	50% (336)	19% (96)
Cardiovascular Disease	42% (66)	54% (346)	34% (164)
Autoimmune Disease	13% (4)	12% (55)	8% (40)
Neurological Disability	18% (24)	14% (72)	6% (31)
Current or Former Smoker	83% (85)	53% (322)	57% (272)

* 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.