COVID-19 Variant of Concern (VOC) Case Report

January 10, 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, 72 confirmed cases of Omicron have been sequenced in NM. Delta represented approximately 100% of sequenced samples in New Mexico in the week of November 29, 2021. Sequenced specimens reported from December 13, 2021 to January 10, 2022 are incomplete but do indicate a predominance of Delta. CDC Nowcast predictive modeling forecasts Omicron to represent 98% of US positive cases the week of January 8, 2022.[4] CDC currently classifies all AY sublineage variants in combination with B.1.617.2 as Delta, and all BA sublineage variants 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. Beginning August 20, 2021, NMDOH reinstated wearing masks in all indoor public settings to slow the spread of emerging variants of COVID-19.

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	-Since 6/28/21, Delta has remained the dominant variant, and represented 100% of sequences reported on 11/29/21. -Proportion of deaths is currently 2%.
Omicron (B.1.1.529 and BA sublineages)	South Africa	-Increased transmissibility -May reduce effectiveness of antibody treatments -May reduce natural and vaccine immunity	-First case observed in NM 12/12/21. - To date, 72 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 79% 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 (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 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)	10999	9727	88%
B.1.1.529 (Omicron)	72	70	97%
B.1.1.7 (Alpha)	1835	1556	85%
B.1.351 (Beta)	8	3	38%
P.1 (Gamma)	109	95	87%
B.1.427/B.1.429 (Epsilon)	521	429	82%
B.1.525 (Eta)	4	4	100%
B.1.526 (Iota)	191	164	86%
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	4475	3233	72%
Total	**18257**	**15315**	**84%**

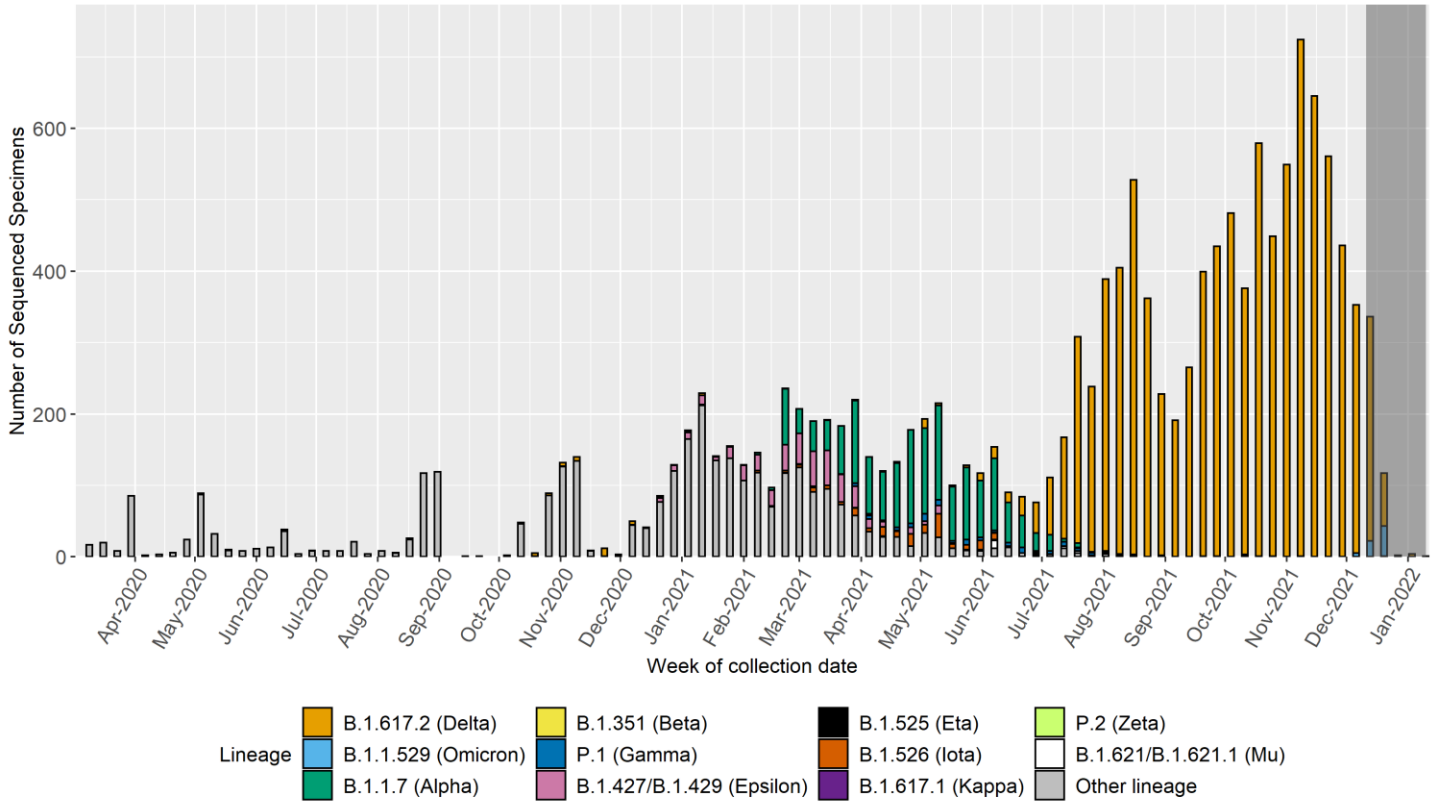
*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 200 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico. These have been removed from the subsequent tables and figures.

Cumulative number of variant cases, hospitalizations, and deaths

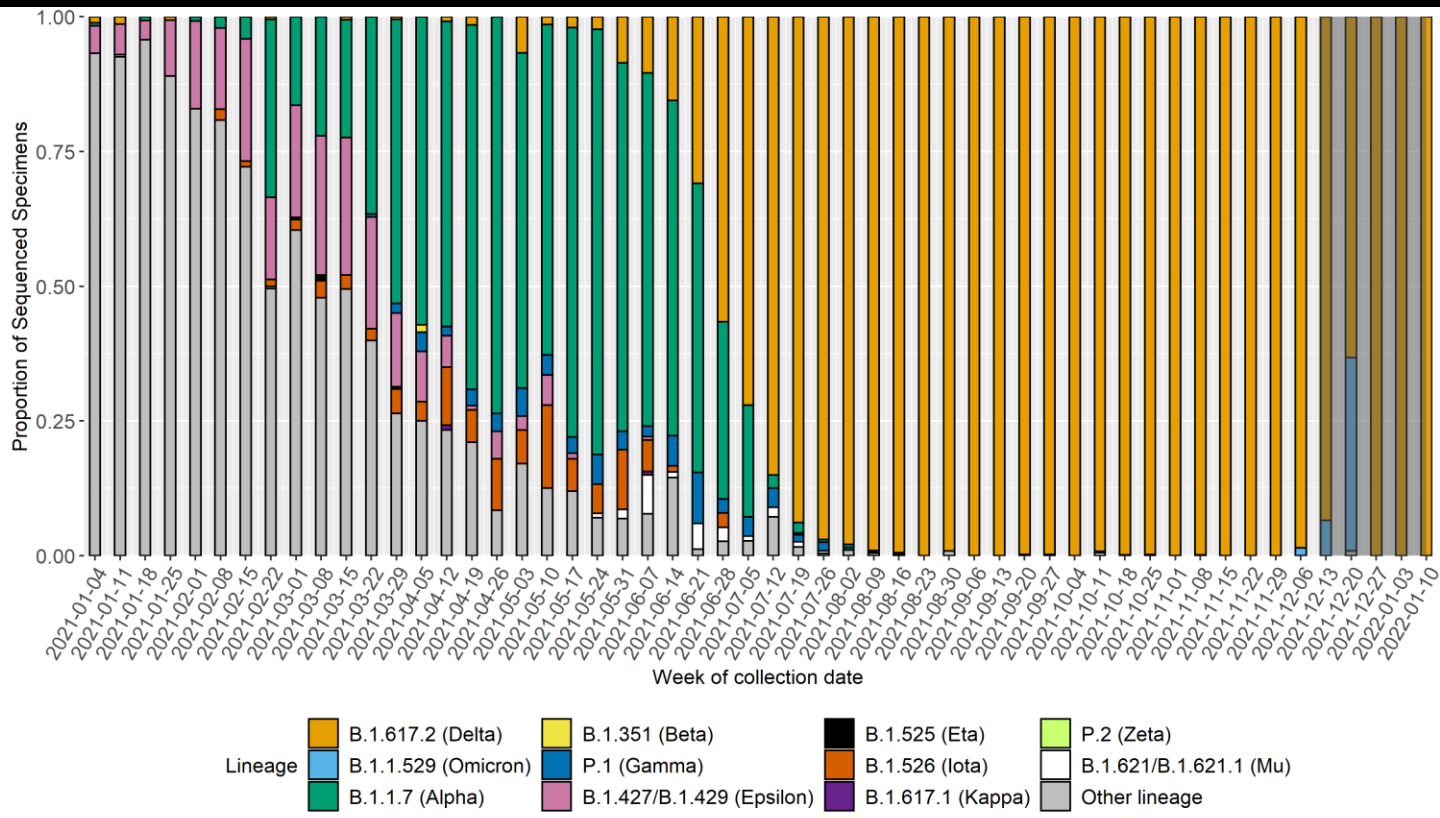
Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
Delta	9653	750	8%	177	2%	3228
Omicron	70	0	0%	0	0%	43
Alpha	1539	157	10%	20	1%	94
Beta	3	0	0%	0	0%	0
Gamma	93	22	24%	2	2%	3
Epsilon	418	9	2%	2	0%	8
Eta	4	0	0%	0	0%	0
Iota	162	5	3%	1	1%	8
Kappa	2	0	0%	0	0%	0
Zeta	2	0	0%	0	0%	0
Mu	30	2	7%	0	0%	4
Other lineage	3139	206	7%	65	2%	23

*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

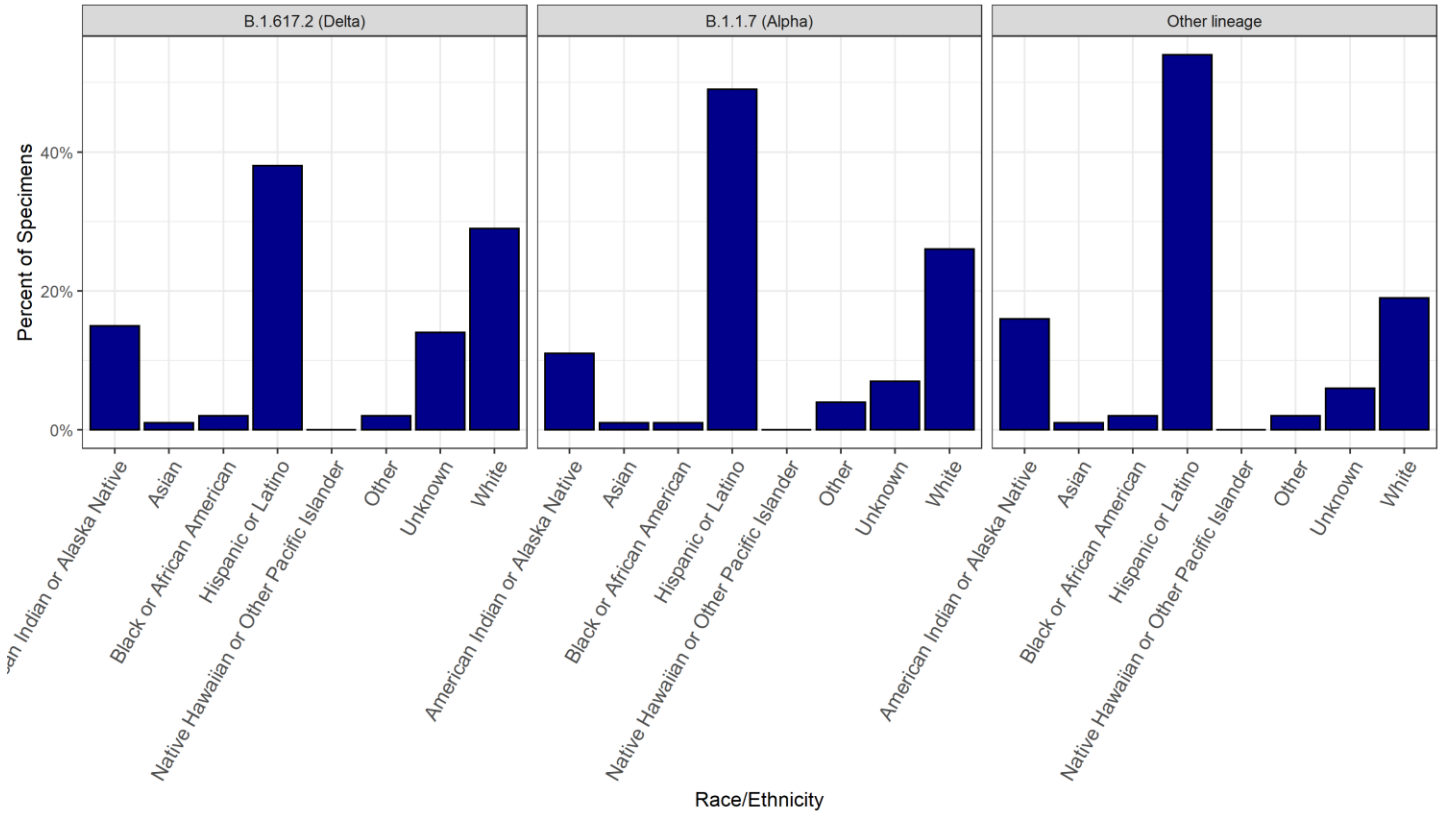


Proportion of identified SARS-CoV-2 lineages by week

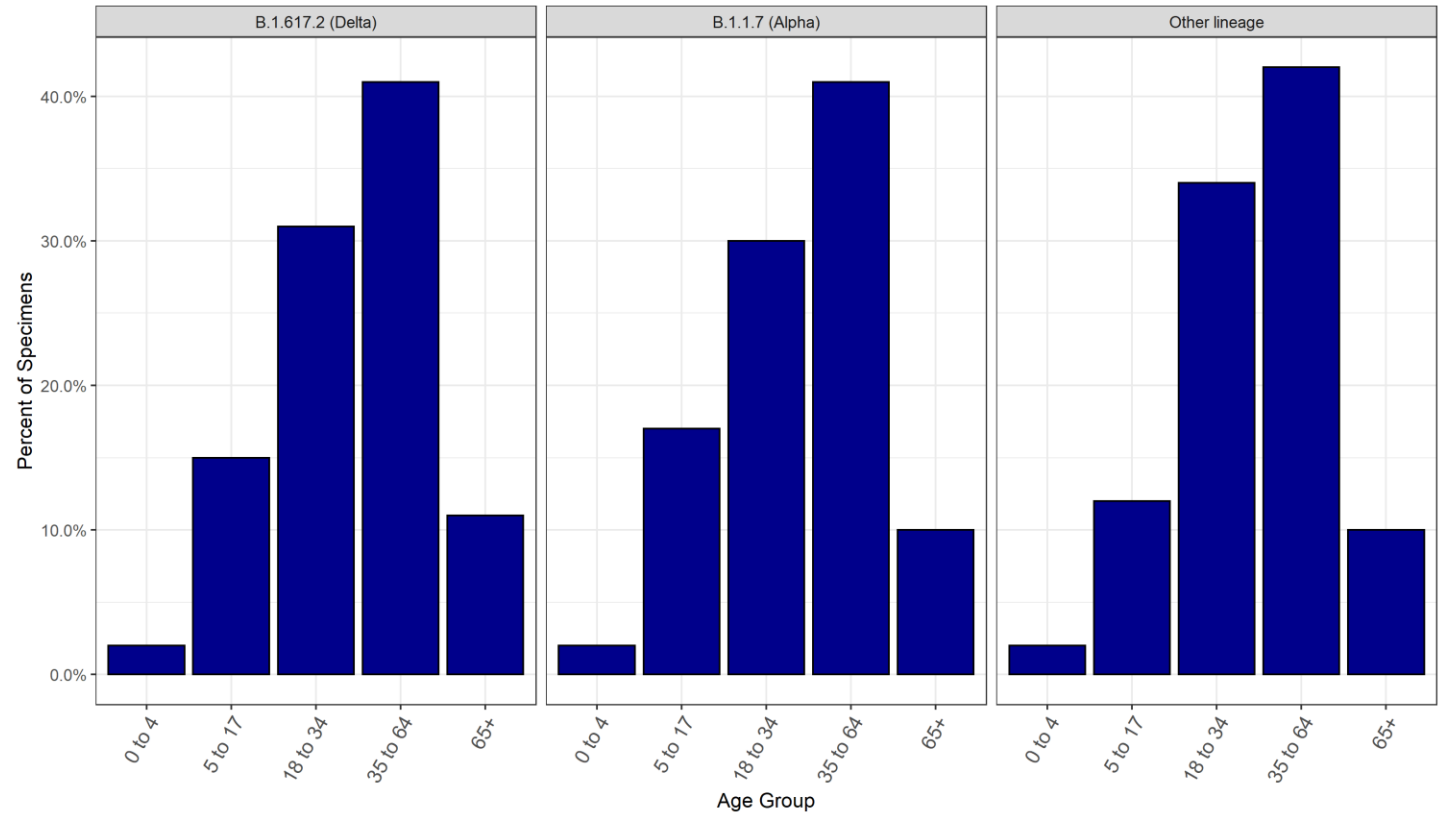


*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

Cumulative proportion of variant cases by Race/Ethnicity



Cumulative proportion of variant cases by Age Group



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

Cumulative number of variant cases by county of residence*

Counties with less than 5 matched sequenced cases are not included in the table below.

County	B.1.617.2 (Delta)	B.1.1.7 (Alpha)	Other lineage	Total
Bernalillo	2971	450	1054	4475
Chaves	203	13	59	275
Cibola	186	13	108	307
Colfax	131	24	26	181
Curry	123	24	28	175
Dona Ana	709	81	423	1213
Eddy	260	19	97	376
Grant	75	13	34	122
Guadalupe	57	1	19	77
Hidalgo	12	0	1	13
Lea	139	16	114	269
Lincoln	46	5	58	109
Los Alamos	42	9	24	75
Luna	40	14	20	74
McKinley	301	19	126	446
Mora	6	0	2	8
Otero	682	24	150	856
Quay	27	3	0	30
Rio Arriba	135	92	39	266
Roosevelt	6	0	11	17
San Juan	1481	321	295	2097
San Miguel	104	10	55	169
Sandoval	563	75	232	870
Santa Fe	509	97	294	900
Sierra	101	5	5	111
Socorro	50	9	31	90
Taos	123	16	39	178
Torrance	111	16	22	149
Union	6	1	0	7
Valencia	397	70	118	585

*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)	9646	3882 (40%)	239	3643	94%
B.1.1.7 (Alpha)	1539	1173 (76%)	106	1067	91%
Other lineage	3605	2791 (77%)	394	2397	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.1.1.7 (Alpha)	Other lineage
Fever (Measured or Subjective)	53% (1893)	47% (488)	43% (1012)
Chills	48% (1718)	46% (481)	44% (1051)
Muscle Aches	55% (1996)	57% (596)	56% (1313)
Runny Nose	56% (2004)	53% (552)	53% (1258)
Sore Throat	45% (1609)	45% (469)	42% (1000)
Cough	75% (2689)	73% (771)	64% (1511)
Shortness of Breath	30% (1075)	29% (308)	24% (568)
Nausea/Vomiting	27% (956)	27% (285)	23% (535)
Headache	65% (2339)	66% (692)	65% (1537)
Abdominal Pain	14% (508)	16% (164)	14% (327)
Diarrhea	29% (1054)	29% (299)	26% (621)
Fatigue	67% (2424)	70% (737)	66% (1552)
Loss of Appetite	40% (1422)	40% (420)	36% (848)
Loss of Taste or Smell	49% (1771)	39% (411)	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)	9646	3724 (39%)	2848	876	24%
B.1.1.7 (Alpha)	1539	1167 (76%)	597	570	49%
Other lineage	3605	2705 (75%)	1657	1048	39%

Percentage of specific underlying conditions reported by variant cases

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

Condition	B.1.617.2 (Delta)	B.1.1.7 (Alpha)	Other lineage
Chronic Lung Disease	24% (173)	25% (130)	26% (243)
Chronic Liver Disease	5% (35)	3% (17)	4% (38)
Chronic Renal Disease	12% (83)	4% (20)	5% (44)
Diabetes Mellitus	34% (244)	19% (98)	22% (203)
Cardiovascular Disease	36% (255)	32% (164)	29% (265)
Autoimmune Disease	6% (43)	8% (40)	5% (45)
Neurological Disability	8% (57)	6% (31)	9% (81)
Current or Former Smoker	39% (277)	53% (274)	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.