COVID-19 Variant of Concern (VOC) Case Report

August 23, 2021

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, and Gravity 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 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 to identify whether they are a VOC 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 has identified four VOCs in the US. In New Mexico, all four SARS-CoV-2 VOCs have been detected: 1) B.1.1.7 (Alpha), 2) B.1.351 (Beta), 3) B.1.617.2 (Delta), and 4) P.1 (Gamma). The week of July 19, 2021, B.1.617.2 (Delta) represented approximately 90% of sequenced samples in New Mexico. Sequenced specimens reported from July 26 to August 2, 2021 are incomplete but do show a rising trend in Delta and could represent as much as 96-100% of cases. On July 6, 2021, the CDC announced that sublineage variants AY.1, AY.2, and AY.3 will be reported in combination with B.1.617.2 (Delta). Studies indicate that vaccines authorized for use in the US are effective at preventing transmission, severe illness, and death caused by a VOC, including B.1.617.2 (Delta), and are the recommended measure to slow the emergence of new variants. Beginning Friday August 20, 2021, NMDOH reinstated wearing masks in all indoor public settings to slow the spread of the highly transmissible Delta variant.

Cumulative number of Specimens Sequenced and Matched to Case Investigations

Lineage	Sequenced Cases	Matched Cases*	Percent Matched
B.1.1.7 (Alpha)	1816	1433	79%
B.1.351 (Beta)	6	2	33%
P.1 (Gamma)	97	84	87%
B.1.617.2 (Delta)	894	758	85%
AY.1 (Delta)	3	3	100%
AY.2 (Delta)	3	2	67%
AY.3 (Delta)	56	45	80%
Other lineage	4705	3960	84%
Total	7580	6287	83%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 134 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

NM COVID-19 VOC Epidemiologic Interpretation

Name	First Identified	Attributes[1]	New Mexico[2]
B.1.1.7 (Alpha)	United Kingdom	-50% more transmissible -Potential to cause more severe cases and deaths	-Alpha has proportionally declined from 82% the week of 5/24/21 to 2% of samples collected the week of 7/19/21.
B.1.351, B.1.351.2, and B.1.351.3 (Beta)	South Africa	-50% more transmissible -Reduced effectiveness of antibody treatments -Reduced response of natural and vaccine induced immunity	- Least reported VOC in NM.
B.1.617.2, AY.1, AY.2, AY.3, AY.4, AY.5, AY.6, AY.7, AY.8, AY.9, AY.10, AY.11, AY.12 (Delta)	India	-Increased transmissibility -May reduce effectiveness of antibody treatments -May cause more severe illness in unvaccinated persons -May reduce natural and vaccine immunity	-Of total specimens sequenced, Delta increased from 10% on 6/7/21 to 90% on 7/19/21, but incomplete data indicate a rising trend. -Proportion of deaths among cases caused by this variant have decreased from 4% to 2%.
P.1, P.1.1, and P.1.2 (Gamma)	Japan/Brazil	-Reduced effectiveness of some antibody treatments -Reduced response of natural and vaccine immunity	-Has varied between 1% and 7% since the week of 3/29/21, and represented 1% of cases 7/19/21. -Currently has the highest proportion of hospitalizations (24%); oversampling of severe cases may skew these results.

[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.

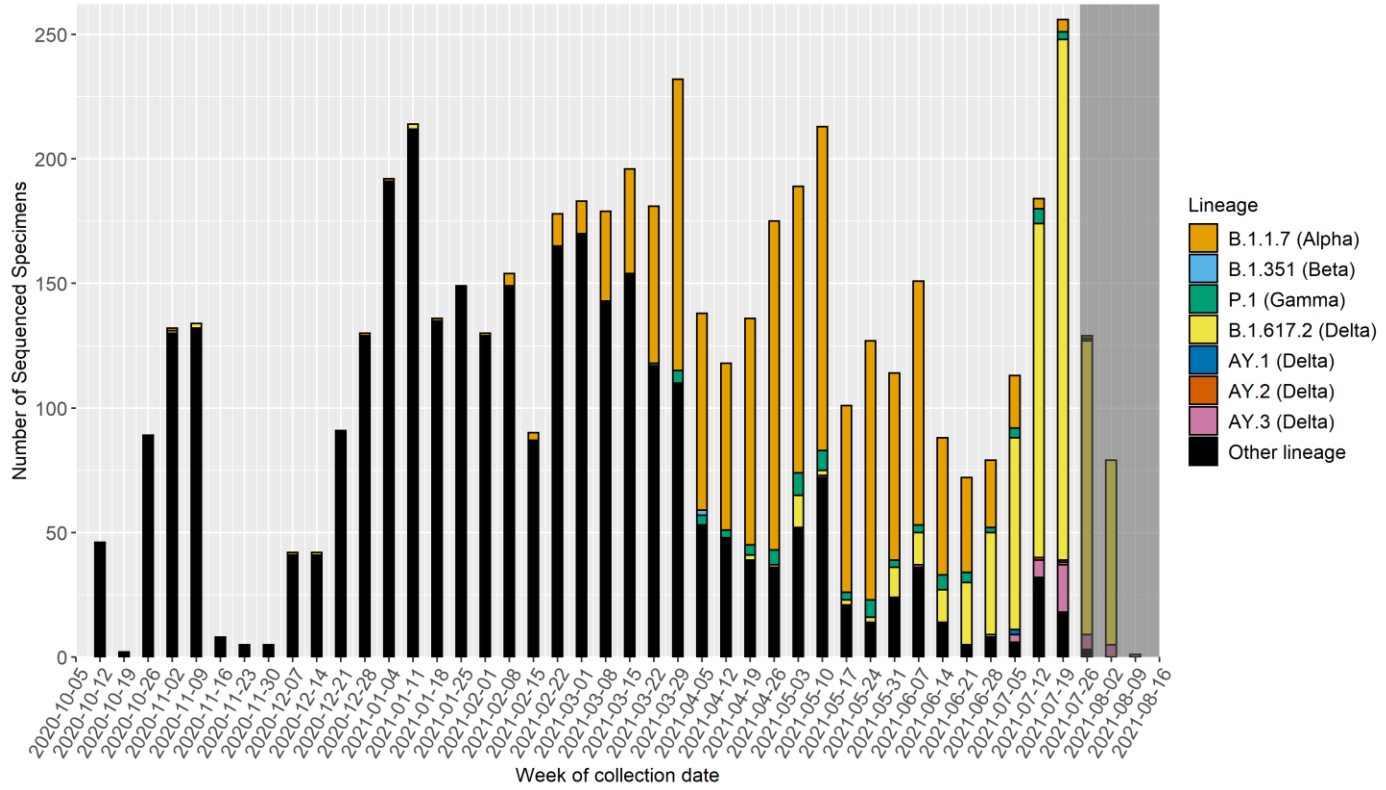
Cumulative number of VOC cases, hospitalizations and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
B.1.1.7 (Alpha)	1421	147	10%	17	1%	84
B.1.351 (Beta)	2	0	0%	0	0%	0
P.1 (Gamma)**	82	20	24%	2	2%	3
B.1.617.2 (Delta)	796	79	10%	15	2%	224
Other lineage	3852	213	6%	66	2%	56

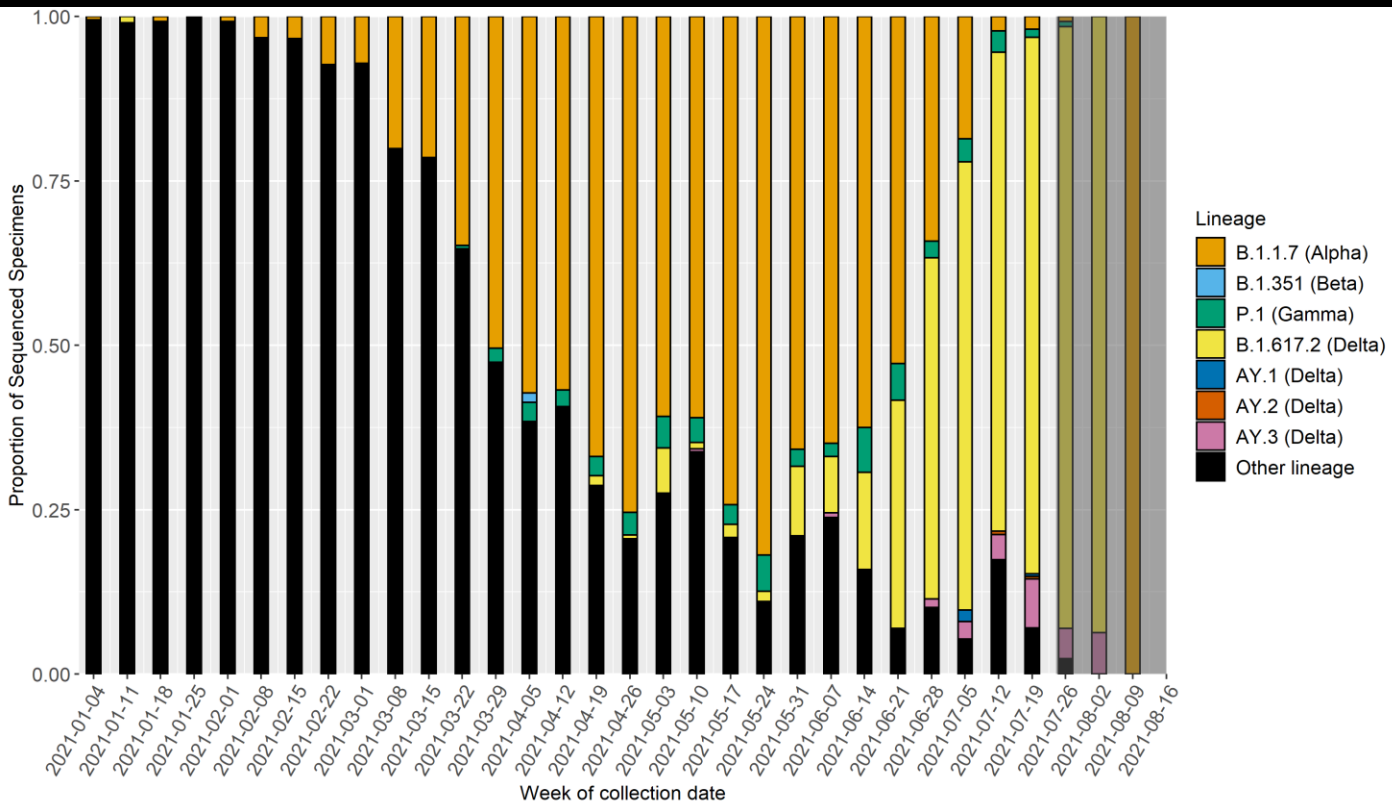
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. Because samples collected from VBT cases are more frequently sequenced compared to samples from other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

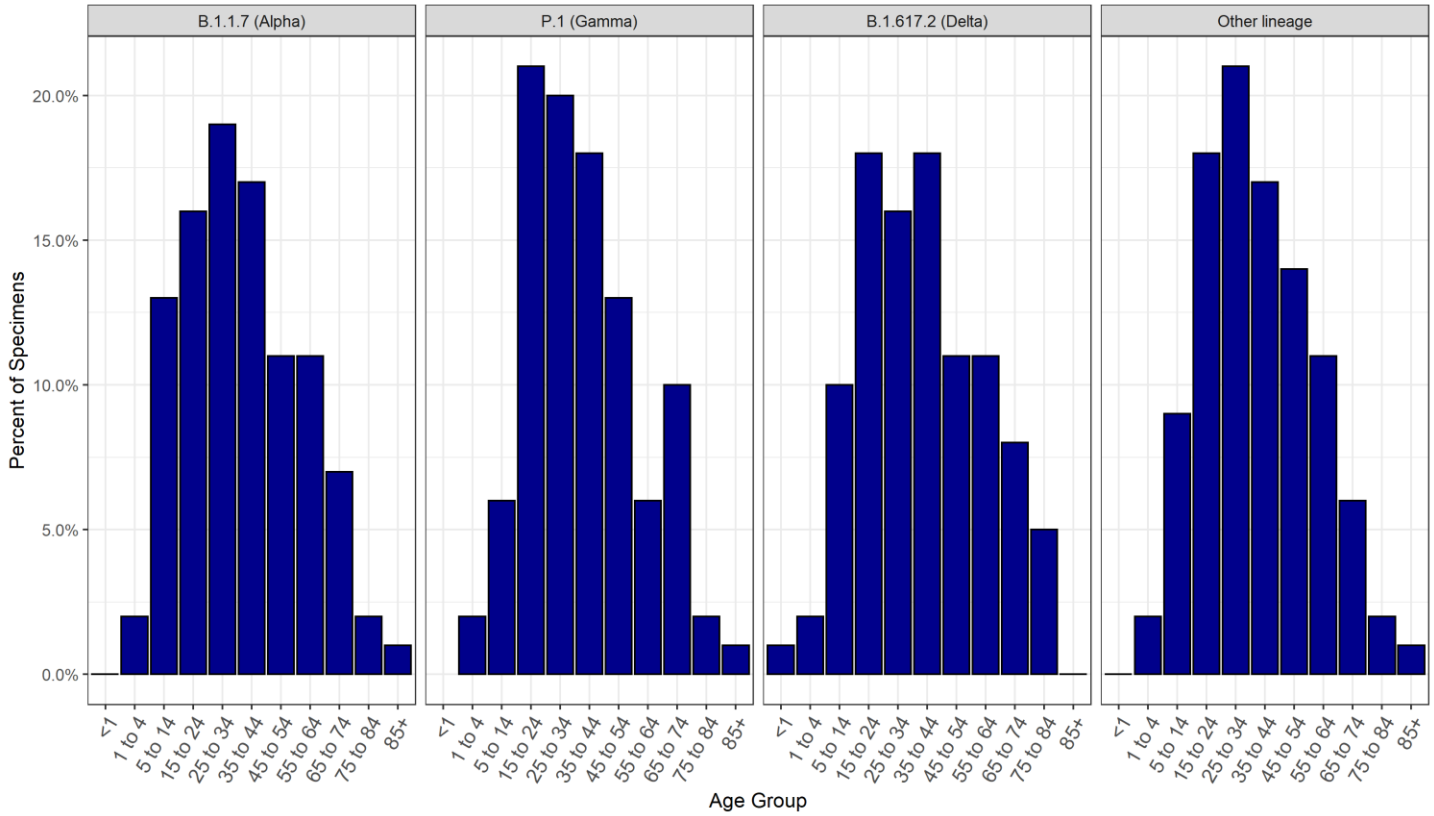


Proportion of identified SARS-CoV-2 lineages by week*

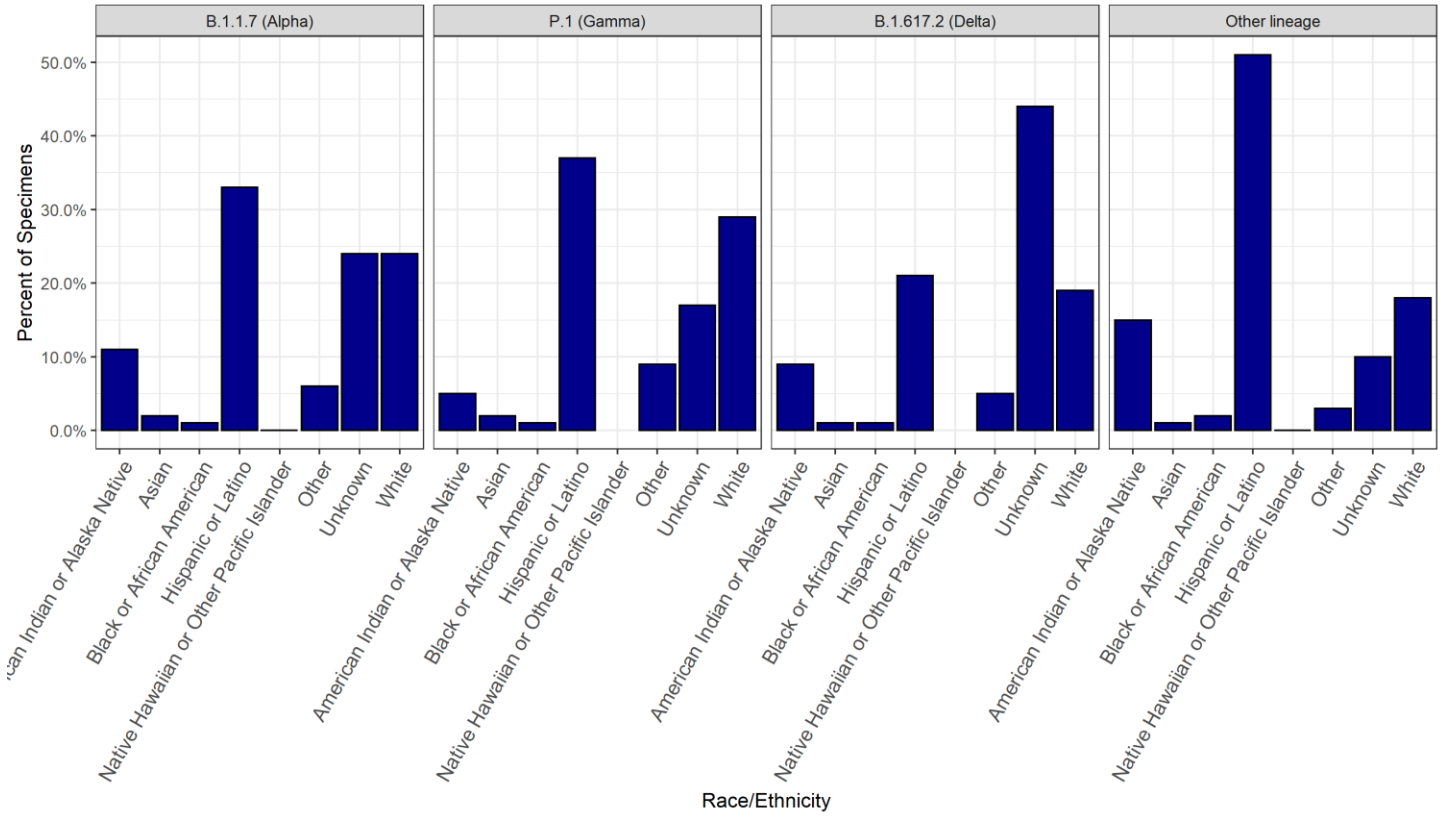


*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

Cumulative proportion of VOC cases by age group



Cumulative proportion of VOC cases by race/ethnicity



Cumulative number of VOC cases by county of residence

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

County	B.1.1.7 (Alpha)	B.1.351 (Beta)	P.1 (Gamma)	B.1.617.2 (Delta)	Other lineage
Bernalillo	435	2	16	295	1116
Chaves	13	0	0	13	62
Cibola	13	0	0	13	136
Colfax	23	0	0	6	32
Curry	24	0	0	13	38
Dona Ana	88	0	6	37	424
Eddy	19	0	0	45	103
Grant	13	0	2	7	35
Guadalupe	1	0	0	21	20
Lea	21	0	1	7	143
Lincoln	5	0	2	2	57
Los Alamos	9	0	0	8	24
Luna	14	0	0	5	22
McKinley	18	0	0	18	125
Otero	26	0	16	44	235
Quay	3	0	1	3	1
Rio Arriba	92	0	0	8	42
Roosevelt	0	0	0	0	12
San Juan	320	0	28	77	306
San Miguel	10	0	0	13	57
Sandoval	70	0	6	41	255
Santa Fe	94	0	0	55	308
Sierra	5	0	0	0	5
Socorro	8	0	0	8	30
Taos	14	0	0	10	39
Torrance	15	0	0	2	86
Valencia	67	0	3	42	136

Percentage of VOC cases reporting any symptoms

Lineage	No Symptoms	Unknown Symptoms	Yes Symptoms	Total Cases	Percent Symptomatic
B.1.1.7 (Alpha)	102	287	1032	1421	73%
B.1.351 (Beta)	0	1	1	2	50%
P.1 (Gamma)	9	13	60	82	73%
B.1.617.2 (Delta)	20	201	575	796	72%
Other lineage	442	899	2511	3852	65%

Percentage of specific symptoms reported by symptomatic VOC cases

The table below includes data ONLY from symptomatic cases

Symptom	B.1.1.7 (Alpha)	P.1 (Gamma)	B.1.617.2 (Delta)	Other lineage
Fever (Measured or Subjective)	47% (477)	51% (30)	56% (322)	43% (1069)
Chills	47% (473)	59% (35)	49% (277)	45% (1111)
Muscle Aches	57% (582)	53% (31)	60% (345)	56% (1378)
Runny Nose	53% (534)	46% (27)	56% (318)	53% (1323)
Sore Throat	45% (460)	46% (27)	50% (283)	43% (1057)
Cough	75% (755)	83% (49)	77% (439)	64% (1593)
Shortness of Breath	30% (299)	41% (24)	24% (136)	24% (606)
Nausea/Vomiting	27% (278)	36% (21)	27% (152)	23% (574)
Headache	66% (670)	51% (30)	66% (377)	65% (1618)
Abdominal Pain	16% (160)	12% (7)	15% (88)	14% (349)
Diarrhea	29% (294)	24% (14)	29% (165)	27% (663)
Fatigue	71% (715)	71% (42)	70% (401)	66% (1645)
Loss of Appetite	41% (412)	39% (23)	40% (226)	36% (904)
Loss of Taste or Smell	39% (392)	34% (20)	48% (272)	44% (1089)

Percentage of VOC cases reporting underlying conditions

Lineage	No	Unknown	Yes	Total Cases	Percent with underlying conditions
B.1.1.7 (Alpha)	600	312	509	1421	36%
B.1.351 (Beta)	1	1	0	2	0%
P.1 (Gamma)	37	13	32	82	39%
B.1.617.2 (Delta)	273	245	278	796	35%
Other lineage	1347	1422	1083	3852	28%

Percentage of specific underlying conditions reported by VOC cases

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

Condition	B.1.1.7 (Alpha)	P.1 (Gamma)	B.1.617.2 (Delta)	Other lineage
Chronic Lung Disease	26% (131)	28% (8)	26% (70)	29% (294)
Chronic Liver Disease	3% (14)	0% (0)	3% (7)	4% (40)
Chronic Renal Disease	4% (19)	7% (2)	6% (17)	4% (43)
Diabetes Mellitus	19% (93)	14% (4)	20% (54)	21% (211)
Cardiovascular Disease	32% (160)	31% (9)	36% (97)	27% (278)
Autoimmune Disease	8% (38)	7% (2)	7% (19)	5% (47)
Neurological Disability	6% (29)	14% (4)	7% (20)	8% (84)
Current or Former Smoker	55% (276)	72% (21)	51% (137)	49% (505)

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

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, and Gravity 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.

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.