

COVID-19 Variant of Concern (VOC) Case Report

August 9, 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 5, 2021, B.1.617.2 (Delta) represented approximately 73% of sequenced samples in New Mexico. Sequenced specimens reported from July 12 to August 9, 2021 are incomplete but do show a rising trend in Delta and could represent as much as 83-100% 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 of COVID-19 VOCs, including B.1.617.2 (Delta), and are the recommended measure to slow the emergence of new variants.

Cumulative number of Specimens Sequenced and Matched to Case Investigations

Lineage	Sequenced Cases	Matched Cases*	Percent Matched
B.1.1.7 (Alpha)	1721	1352	79%
B.1.351 (Beta)	3	0	0%
P.1 (Gamma)	83	72	87%
B.1.617.2 (Delta)	392	351	90%
AY.1 (Delta)	3	3	100%
AY.2 (Delta)	1	1	100%
AY.3 (Delta)	22	18	82%
Other lineage	4595	3858	84%
Total	6820	5655	83%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 125 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

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.

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	-Dominant strain in NM but proportionally declining from 82% the week of 5/24/21 to 18% of samples collected the week of 7/05/21.
B.1.351 (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, and AY.3 (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 73% on 7/05/21, but incomplete data show a rising trend. -Proportion of deaths among cases caused by this variant have decreased from 4% to 2%.
P.1 (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 4% of cases 7/05/21. -Currently has the highest proportion of hospitalizations (29%); oversampling of severe cases may skew these results.

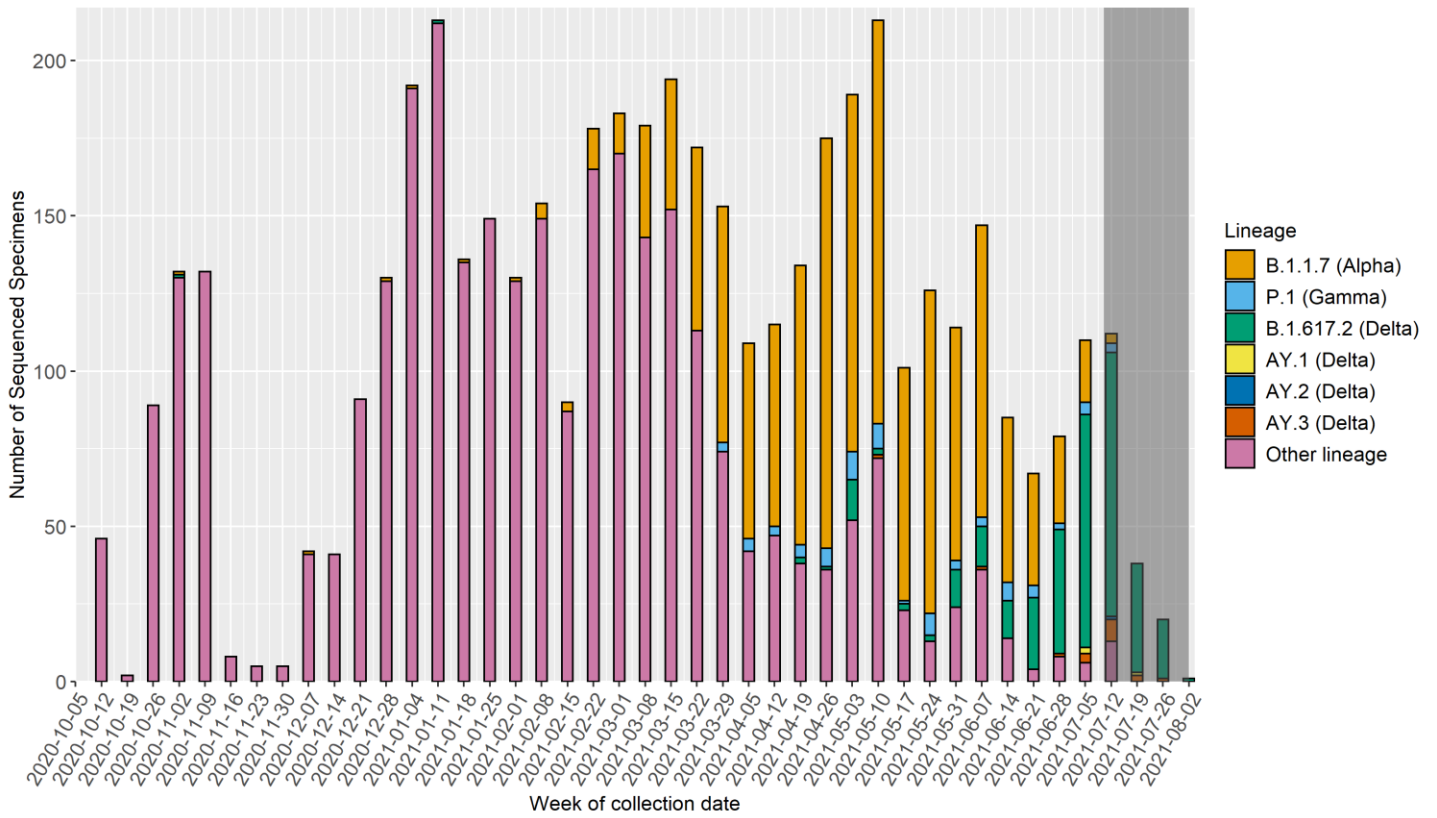
Cumulative number of VOC cases, hospitalizations and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
B.1.1.7 (Alpha)	1341	141	11%	16	1%	78
P.1 (Gamma)**	70	20	29%	2	3%	2
B.1.617.2 (Delta)	362	44	12%	8	2%	89
Other lineage	3757	205	5%	66	2%	40

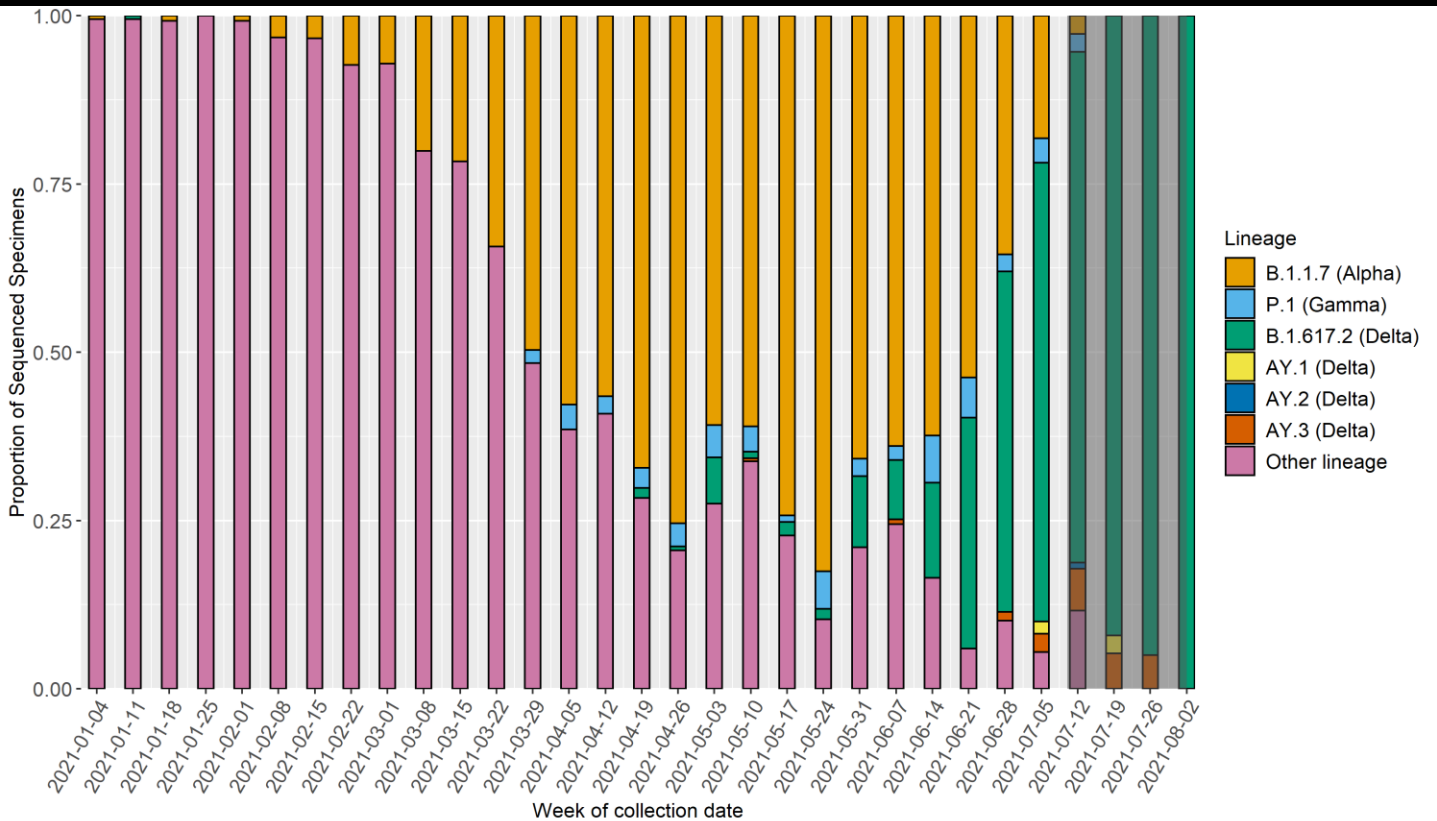
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥ 14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. Because samples collected from VBT cases are more frequently sequenced compared to samples from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

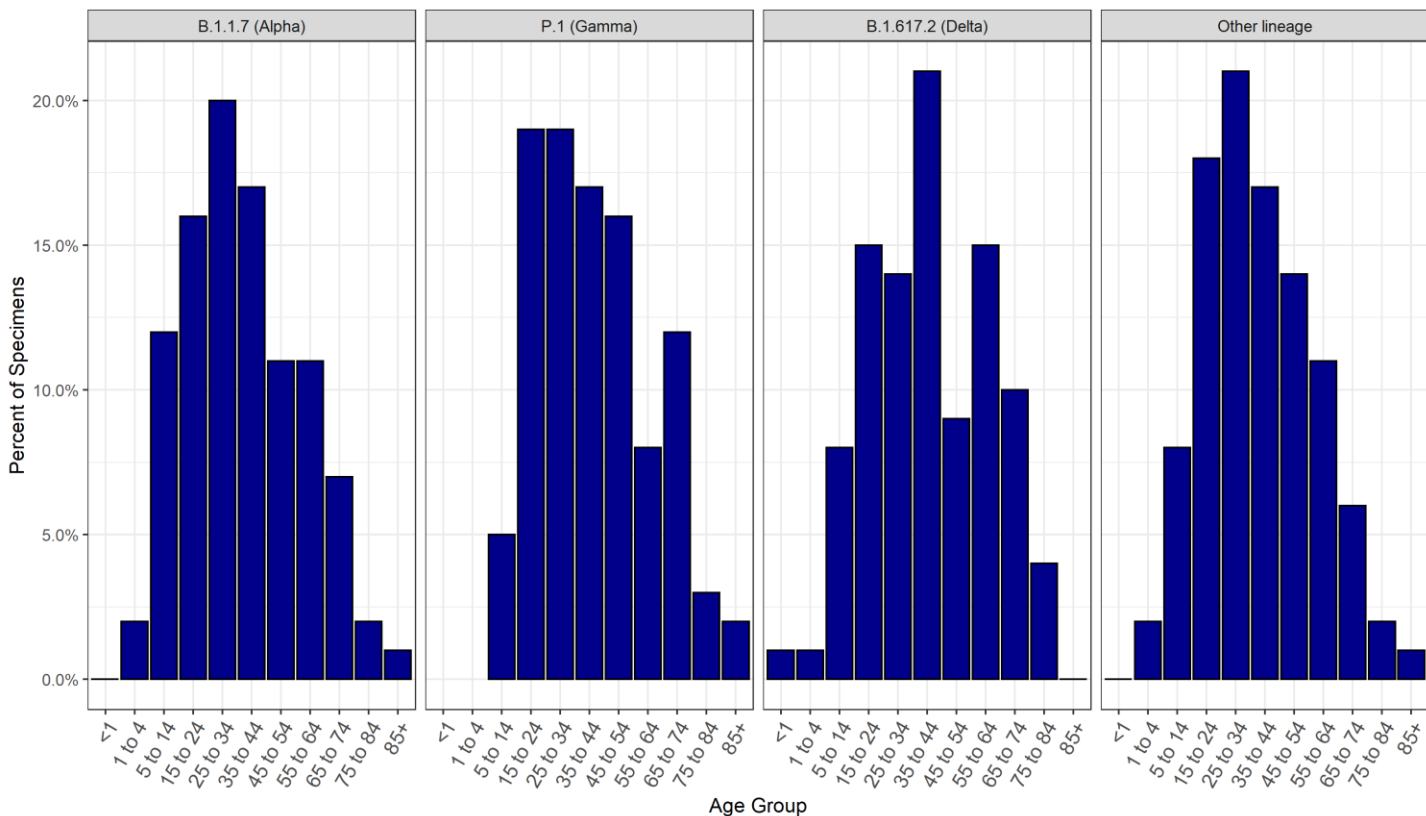


Proportion of identified SARS-CoV-2 lineages by week*

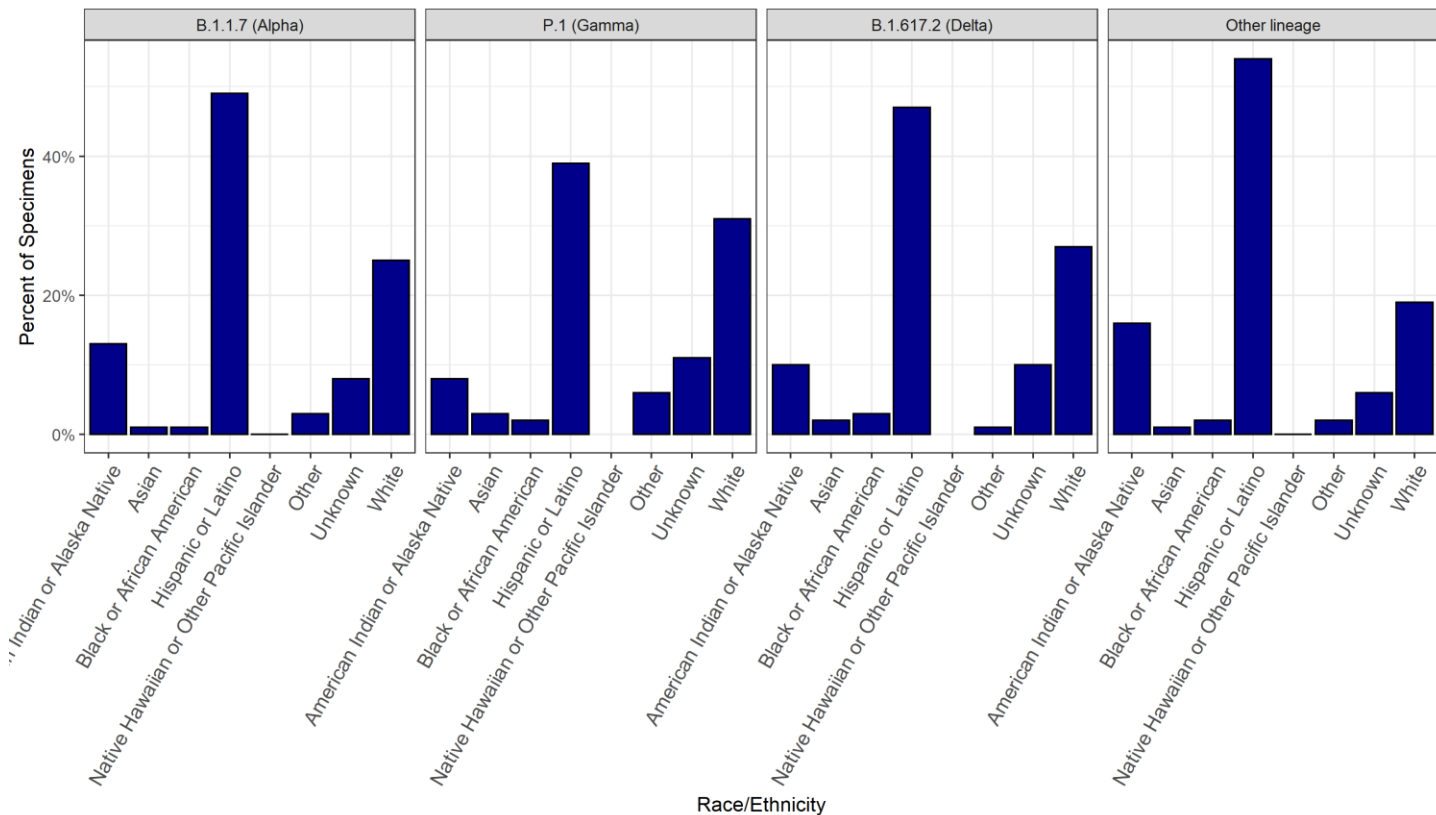


*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

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)	P.1 (Gamma)	B.1.617.2 (Delta)	Other lineage
Bernalillo	355	11	66	1054
Chaves	13	0	1	60
Cibola	12	0	7	136
Colfax	21	0	0	32
Curry	19	0	2	37
Dona Ana	77	5	12	396
Eddy	19	0	5	96
Grant	12	2	0	35
Guadalupe	1	0	20	20
Lea	18	1	1	140
Lincoln	4	2	1	52
Los Alamos	9	0	5	24
Luna	13	0	1	20
McKinley	18	0	5	125
Otero	25	8	8	220
Rio Arriba	78	0	3	41
Roosevelt	0	0	0	12
San Juan	312	28	31	299
San Miguel	6	0	5	55
Sandoval	47	3	6	242
Santa Fe	90	0	13	304
Sierra	5	0	0	5
Socorro	7	0	2	28
Taos	12	0	4	39
Torrance	13	0	0	85
Valencia	55	3	12	127

Percentage of VOC cases reporting any symptoms

Lineage	No Symptoms	Unknown Symptoms	Yes Symptoms	Total Cases	Percent Symptomatic
B.1.1.7 (Alpha)	83	256	905	1244	73%
P.1 (Gamma)	7	13	44	64	69%
B.1.617.2 (Delta)	4	46	160	210	76%
Other lineage	426	871	2391	3688	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% (419)	58% (25)	57% (91)	43% (1023)
Chills	47% (413)	72% (31)	52% (83)	45% (1064)
Muscle Aches	57% (509)	63% (27)	65% (104)	56% (1322)
Runny Nose	53% (471)	40% (17)	52% (84)	53% (1258)
Sore Throat	45% (398)	42% (18)	42% (68)	43% (1007)
Cough	74% (660)	84% (36)	73% (117)	64% (1518)
Shortness of Breath	30% (265)	49% (21)	30% (48)	25% (580)
Nausea/Vomiting	28% (246)	44% (19)	34% (55)	23% (550)
Headache	67% (593)	53% (23)	68% (109)	66% (1557)
Abdominal Pain	16% (144)	12% (5)	17% (27)	14% (338)
Diarrhea	29% (258)	33% (14)	36% (57)	27% (634)
Fatigue	70% (626)	81% (35)	72% (115)	66% (1566)
Loss of Appetite	41% (360)	49% (21)	49% (78)	36% (860)
Loss of Taste or Smell	39% (346)	40% (17)	52% (83)	44% (1049)

Percentage of VOC cases reporting underlying conditions

Lineage	No	Unknown	Yes	Total Cases	Percent with underlying conditions
B.1.1.7 (Alpha)	520	278	446	1244	36%
P.1 (Gamma)	23	13	28	64	44%
B.1.617.2 (Delta)	64	49	97	210	46%
Other lineage	1266	1394	1028	3688	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	25% (109)	32% (8)	32% (29)	29% (283)
Chronic Liver Disease	3% (13)	0% (0)	2% (2)	4% (38)
Chronic Renal Disease	4% (19)	8% (2)	9% (8)	4% (41)
Diabetes Mellitus	18% (80)	16% (4)	20% (18)	21% (205)
Cardiovascular Disease	31% (138)	36% (9)	37% (33)	27% (259)
Autoimmune Disease	7% (30)	8% (2)	9% (8)	5% (45)
Neurological Disability	6% (28)	16% (4)	11% (10)	9% (83)
Current or Former Smoker	56% (247)	68% (17)	49% (44)	49% (480)

* 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.