

# COVID-19 Variant of Concern (VOC) Case Report

June 28, 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 Summary

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 group 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. To date there are no variants that have demonstrated the ability to evade vaccine or natural 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.

As of June 28, 2021, CDC has identified six VOCs in the US. In New Mexico, all six SARS-CoV-2 VOCs have been detected: 1) B.1.1.7 (Alpha), 2) B.1.351 (Beta), 3) B.1.427 (Epsilon), 4) B.1.429 (Epsilon), 5) B.1.617.2 (Delta), and 6) P.1 (Gamma). While B.1.617.2 (Delta) currently represents a relatively small proportion of sequenced samples in New Mexico, observations from other countries and model projections predict that the proportion will continue to grow and will likely become the dominant variant in the US and New Mexico. 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>B.1.1.7</b> (Alpha)	1208	860	71%
<b>B.1.351</b> (Beta)	3	0	0%
<b>B.1.427</b> (Epsilon)	140	109	78%
<b>B.1.429</b> (Epsilon)	297	196	66%
<b>P.1</b> (Gamma)	45	42	93%
<b>B.1.617.2</b> (Delta)	33	30	91%
<b>Other lineage</b>	3788	2950	78%
<b>Total</b>	5514	4187	76%

\*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 71 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 <sup>1</sup>	New Mexico <sup>2</sup>
B.1.1.7/Alpha	United Kingdom	-50% more transmissible -Potential to cause more severe cases and deaths	-Dominant strain in NM at 77% of samples collected the week of 5/24/21
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.1.427/Epsilon	California	-20% more transmissible -Slightly reduces effectiveness of antibody treatments -Reduced response of natural and vaccine immunity	-Peaked in proportion the week of 3/22/21 at 17%, but has not been collected in NM since the week of 5/3/21
B.1.429/Epsilon	California	-20% more transmissible -Reduced effectiveness of some antibody treatments -Reduced response of natural and vaccine immunity	-Peaked in proportion the week of 2/15/21 at 22 but has not been collected in NM since the week of 5/17/21
B.1.617.2/Delta	India	-Increased transmissibility -May reduce effectiveness of antibody treatments -May reduce natural and vaccine immunity	-Has been fluctuating between 1% and 8% since the week 4/19/21 with no clear increasing trend. -Proportion of deaths among cases caused by this variant have decreased from 6% to 3%.
P.1/Gamma	Japan/Brazil	-Reduced effectiveness of some antibody treatments -Reduced response of natural and vaccine immunity	-Has been fluctuating between 1% and 6% since the week of 3/29/21 -Currently has the highest proportion of hospitalizations (31%) and deaths (5%); oversampling of severe cases may skew these results.

<sup>1</sup><https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html>

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

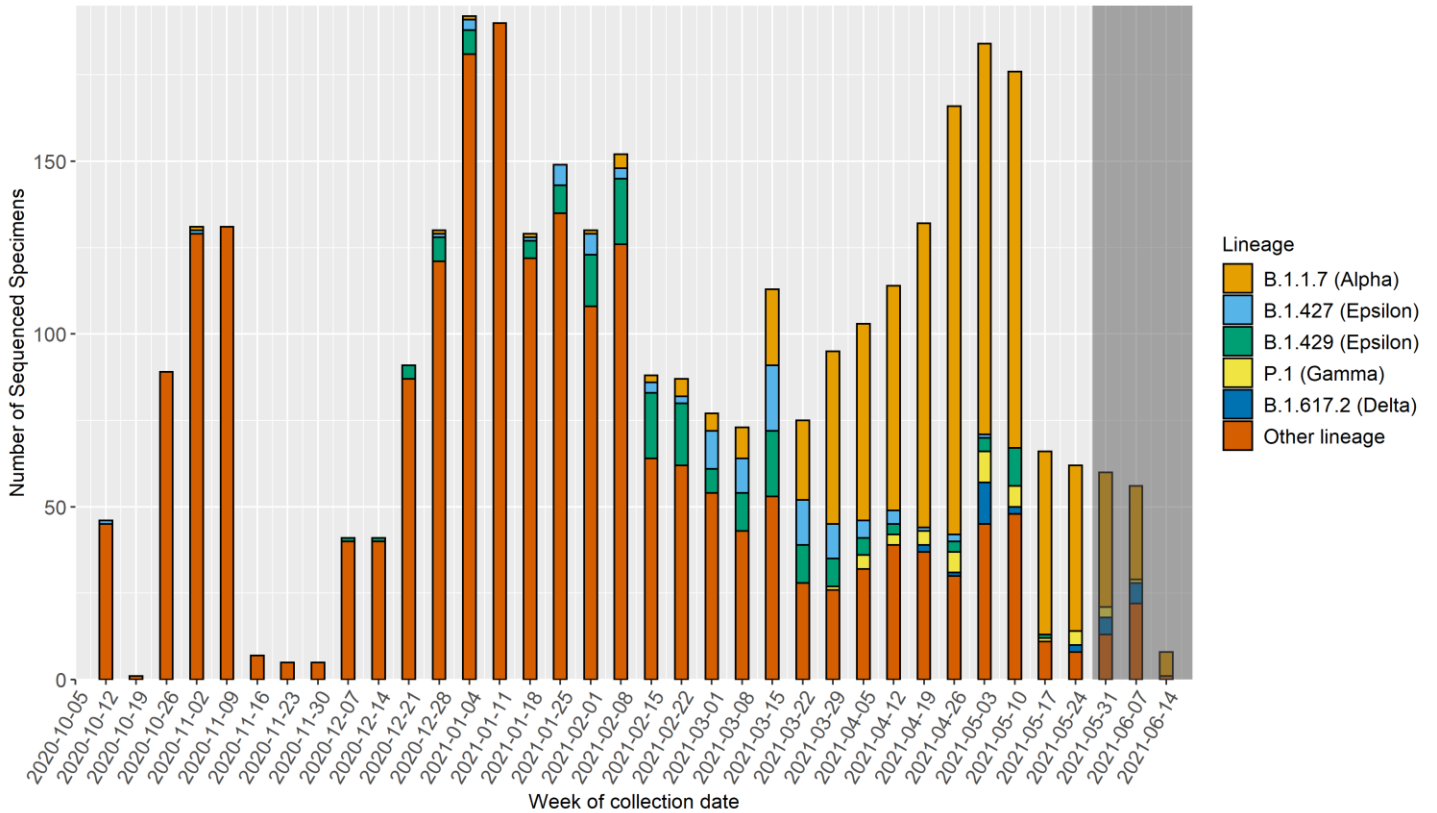
## Cumulative number of VOC cases, hospitalizations and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died
<b>B.1.1.7</b> (Alpha)	857	76	9%	7	1%
<b>B.1.427</b> (Epsilon)	107	3	3%	0	0%
<b>B.1.429</b> (Epsilon)	196	3	2%	1	1%
<b>P.1</b> (Gamma)	42	13	31%	2	5%
<b>B.1.617.2</b> (Delta)	30	1	3%	1	3%
<b>Other lineage</b>	2884	170	6%	58	2%

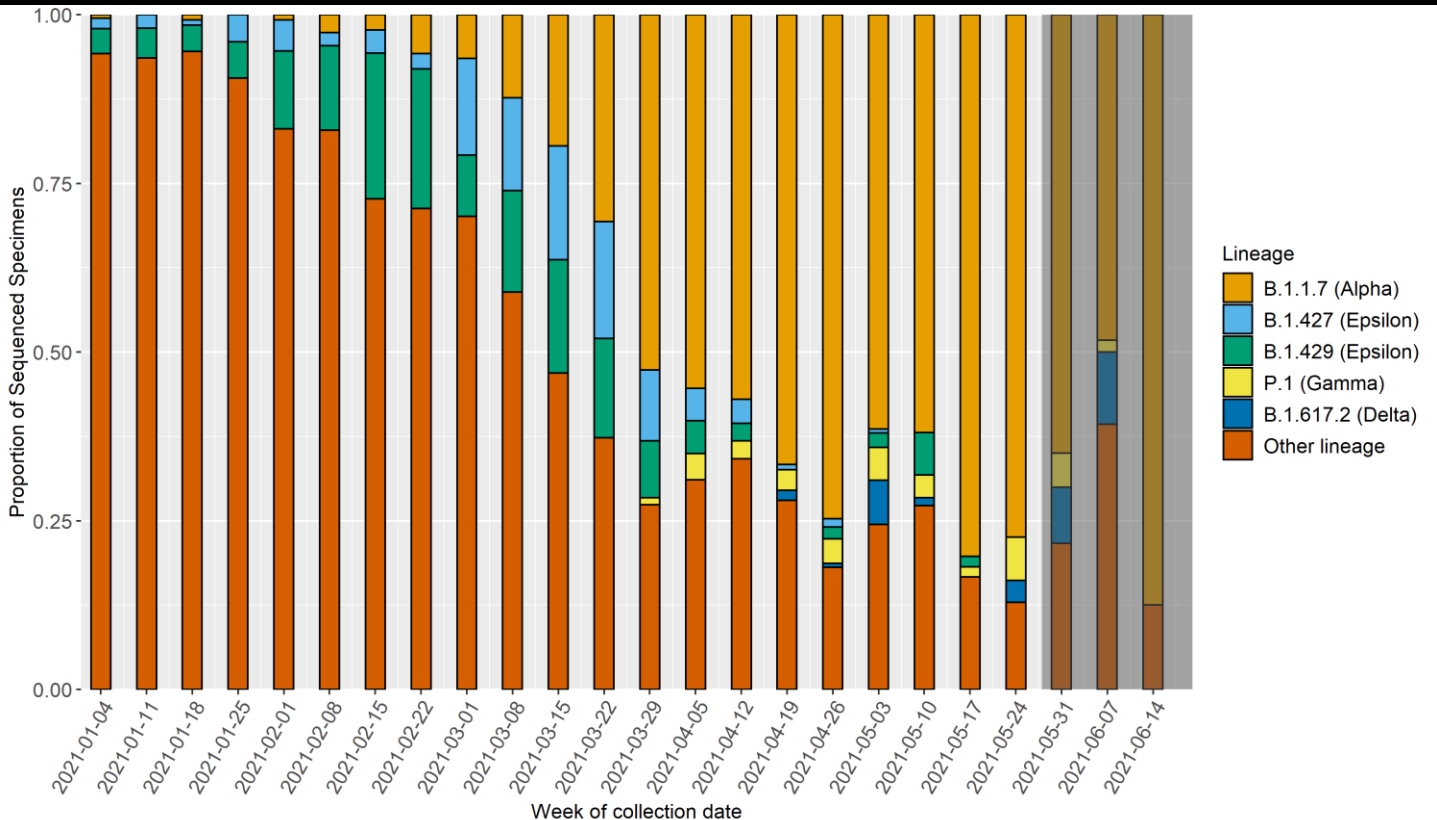
\*The specimen submission process for sequencing is not representative. A large proportion of P.1(Gamma) cases were collected from a single hospital in San Juan County that submitted specimens on hospital admissions, rather than on a representative set of cases in the county. This is likely increasing the apparent severity of this VOC.

## Identified SARS-CoV-2 lineages by week

\*The dark grey shaded region represents the lag period between specimen collection and genomic sequencing results.

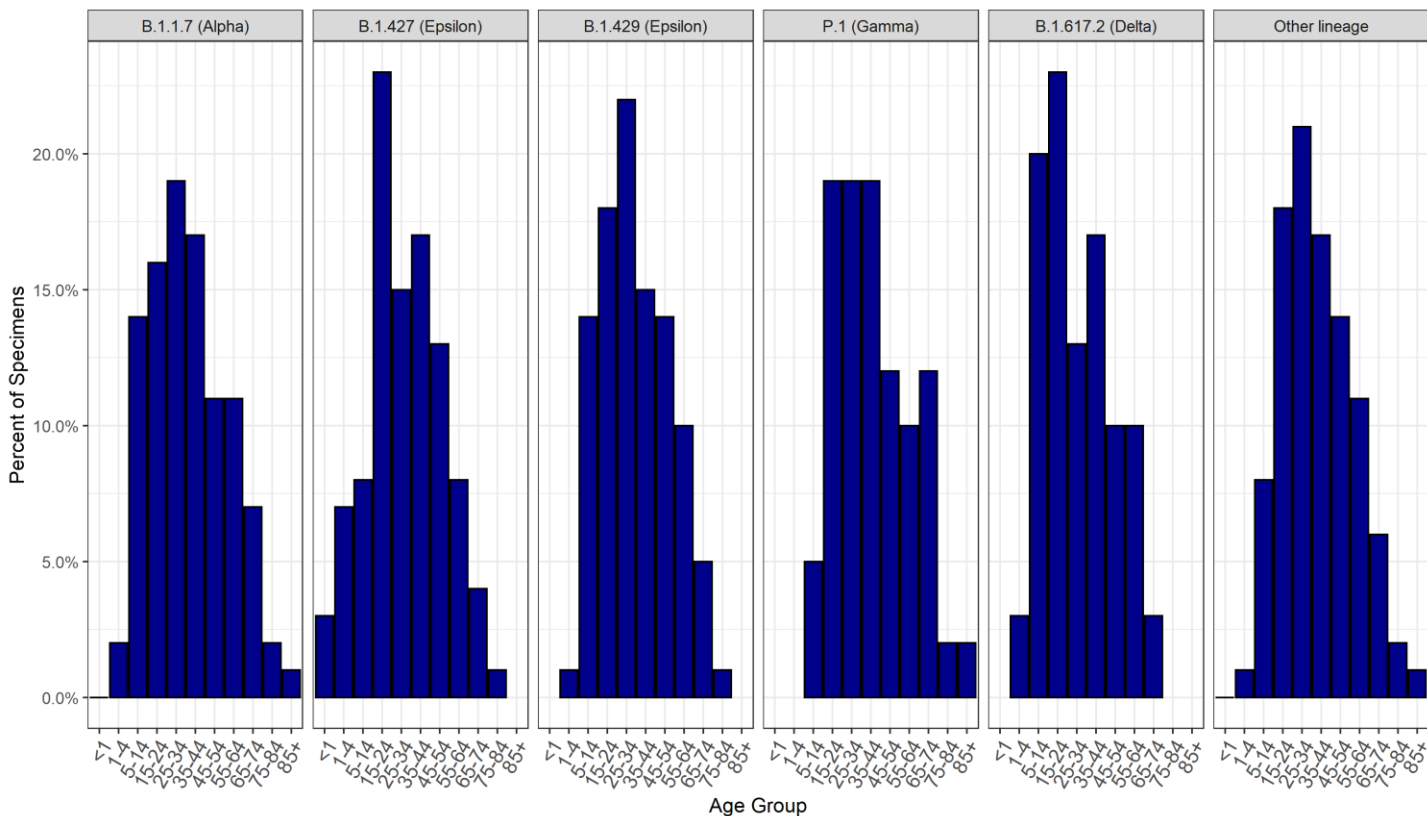


## Proportion of identified SARS-CoV-2 lineages by week

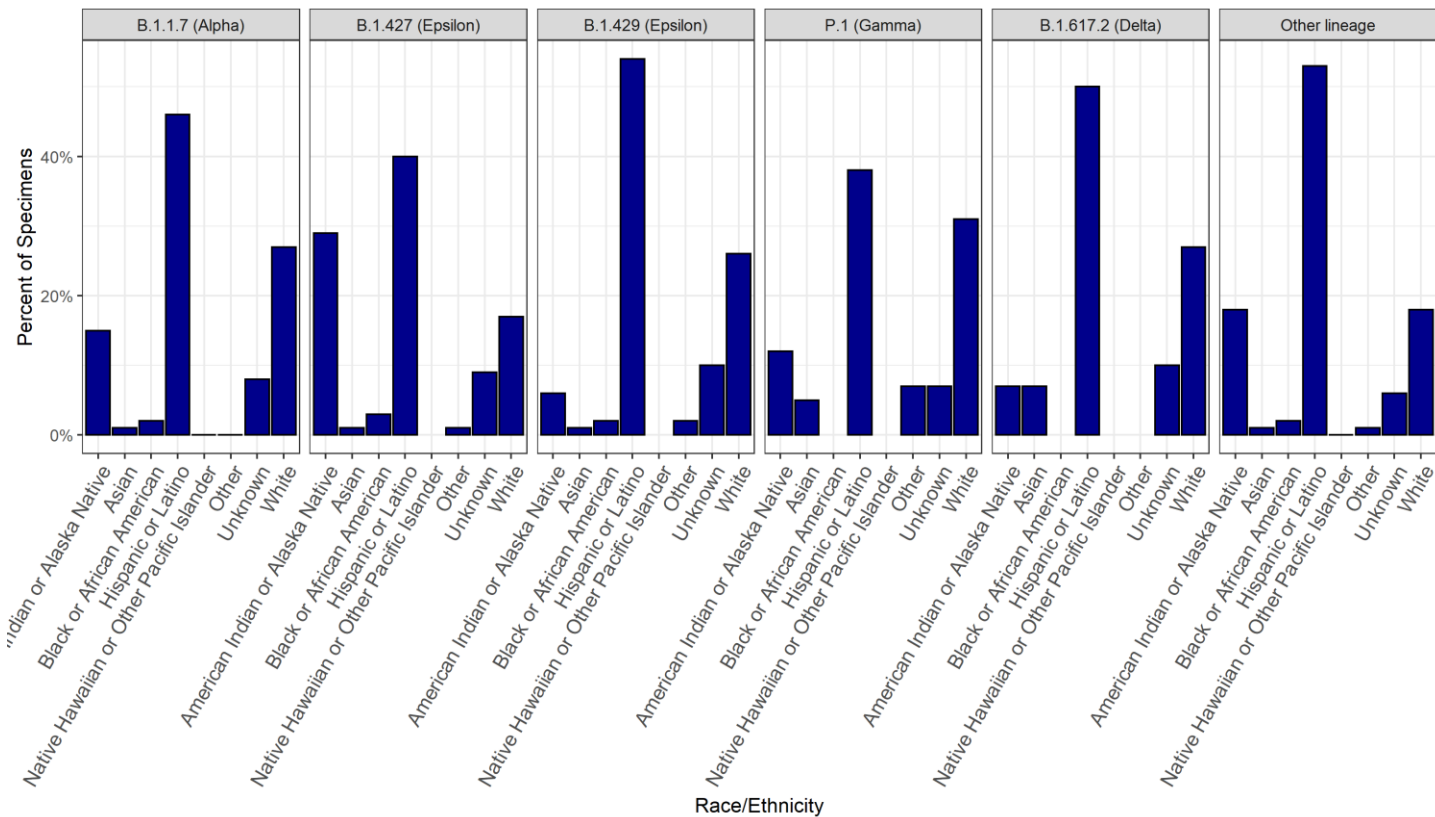


\*The dark grey shaded region represents the lag period between specimen collection and genomic sequencing results

## 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.1.427 (Epsilon)	B.1.429 (Epsilon)	P.1 (Gamma)	B.1.617.2 (Delta)	Non-VOC lineages
Bernalillo	213	36	77	7	1	807
Chaves	11	0	0	0	0	58
Cibola	6	26	4	0	5	98
Colfax	16	0	1	0	0	26
Curry	6	2	0	0	0	28
Dona Ana	53	3	23	1	0	289
Eddy	16	2	1	0	0	80
Grant	10	0	7	0	0	23
Guadalupe	0	0	4	0	13	15
Lea	5	0	0	1	0	99
Lincoln	3	0	0	0	0	30
Los Alamos	8	3	1	0	2	15
Luna	9	0	0	0	0	13
McKinley	14	0	2	0	0	121
Otero	24	0	14	3	0	182
Rio Arriba	40	1	1	0	0	33
Roosevelt	0	0	0	0	0	11
San Juan	275	6	6	28	7	274
San Miguel	3	1	1	0	1	46
Sandoval	29	7	7	2	0	168
Santa Fe	55	8	29	0	0	257
Sierra	3	0	0	0	0	4
Socorro	2	2	0	0	0	25
Taos	10	1	6	0	0	29
Torrance	8	6	1	0	0	71
Valencia	35	3	11	0	1	78

## Percentage of VOC cases reporting any symptoms

Lineage	No Symptoms	Unknown Symptoms	Yes Symptoms	Total Cases	Percent Symptomatic
<b>B.1.1.7 (Alpha)</b>	52	172	633	857	74%
<b>B.1.427 (Epsilon)</b>	9	36	62	107	58%
<b>B.1.429 (Epsilon)</b>	14	25	157	196	80%
<b>P.1 (Gamma)</b>	4	8	30	42	71%
<b>B.1.617.2 (Delta)</b>	1	5	24	30	80%
<b>Other lineage</b>	318	731	1835	2884	64%

## Percentage of specific symptoms reported by symptomatic VOC cases

The table below includes data ONLY from symptomatic cases

Symptom	B.1.1.7 (n)	B.1.427 (n)	B.1.429 (n)	P.1 (n)	B.1.617.2 (n)	Non-VOC (n)
<b>Fever (Measured or Subjective)</b>	48% (298)	47% (29)	47% (73)	55% (16)	54% (13)	44% (796)
<b>Chills</b>	47% (295)	55% (34)	46% (71)	79% (23)	42% (10)	44% (802)
<b>Muscle Aches</b>	57% (355)	61% (38)	62% (97)	69% (20)	67% (16)	55% (999)
<b>Runny Nose</b>	56% (350)	65% (40)	62% (97)	41% (12)	38% (9)	53% (950)
<b>Sore Throat</b>	46% (289)	48% (30)	46% (72)	41% (12)	38% (9)	42% (757)
<b>Cough</b>	74% (462)	74% (46)	63% (98)	83% (24)	54% (13)	64% (1162)
<b>Shortness of Breath</b>	30% (187)	34% (21)	17% (27)	48% (14)	12% (3)	25% (458)
<b>Nausea/Vomiting</b>	28% (172)	26% (16)	24% (37)	41% (12)	8% (2)	23% (413)
<b>Headache</b>	66% (413)	58% (36)	72% (113)	59% (17)	58% (14)	65% (1167)
<b>Abdominal Pain</b>	16% (100)	15% (9)	13% (21)	10% (3)	25% (6)	14% (262)
<b>Diarrhea</b>	29% (181)	24% (15)	27% (42)	28% (8)	25% (6)	27% (482)
<b>Fatigue</b>	71% (439)	73% (45)	67% (105)	86% (25)	58% (14)	65% (1181)
<b>Loss of Appetite</b>	39% (241)	37% (23)	35% (55)	41% (12)	38% (9)	37% (669)
<b>Loss of Taste or Smell</b>	38% (234)	40% (25)	56% (88)	41% (12)	29% (7)	44% (792)

## Percentage of VOC cases reporting underlying conditions

Lineage	No	Unknown	Yes	Total Cases	Percent with underlying conditions
<b>B.1.1.7</b> (Alpha)	375	187	295	857	34%
<b>B.1.427</b> (Epsilon)	39	45	23	107	22%
<b>B.1.429</b> (Epsilon)	91	50	55	196	28%
<b>P.1</b> (Gamma)	15	8	19	42	45%
<b>B.1.617.2</b> (Delta)	11	6	13	30	43%
<b>Other lineage</b>	932	1177	775	2884	27%

## 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 (n)	B.1.427 (n)	B.1.429 (n)	P.1 (n)	B.1.617.2 (n)	Non-VOC (n)
<b>Chronic Lung Disease</b>	25% (73)	36% (8)	15% (8)	24% (4)	17% (2)	27% (199)
<b>Chronic Liver Disease</b>	3% (8)	0% (0)	0% (0)	0% (0)	0% (0)	4% (33)
<b>Chronic Renal Disease</b>	3% (9)	9% (2)	2% (1)	12% (2)	8% (1)	4% (31)
<b>Diabetes Mellitus</b>	19% (54)	5% (1)	17% (9)	24% (4)	8% (1)	23% (170)
<b>Cardiovascular Disease</b>	32% (94)	23% (5)	19% (10)	35% (6)	25% (3)	27% (199)
<b>Autoimmune Disease</b>	6% (17)	14% (3)	4% (2)	12% (2)	0% (0)	4% (32)
<b>Neurological Disability</b>	7% (20)	18% (4)	2% (1)	18% (3)	0% (0)	10% (70)
<b>Current or Former Smoker</b>	56% (162)	32% (7)	70% (37)	65% (11)	50% (6)	48% (351)

\* 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.