

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

January 31, 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, 1200 confirmed cases of Omicron have been sequenced in NM. Omicron represented approximately 69% of sequenced samples in New Mexico in the week of December 27, 2021. Sequenced specimens reported from January 3-31, 2022 are incomplete but indicate a rising predominance of Omicron compared to other variants. CDC Nowcast predictive modeling forecasts Omicron to represent 99.9% of US positive cases the week of January 29, 2022.<sup>4</sup> 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 <sup>1</sup>	New Mexico <sup>2</sup>
<b>Delta</b> <b>(B.1.617.2 and AY</b> <b>sublineages)</b>	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 69% of sequences reported on 12/20/21. -Proportion of deaths is currently 2%.
<b>Omicron</b> <b>(B.1.1.529 and BA</b> <b>sublineages)</b>	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 69% of cases. -To date, 1200 confirmed cases of Omicron have been sequenced in NM.

<b>CDC VARIANTS BEING MONITORED (VBM)</b>			
<b>Name<sup>3</sup></b>	<b>First Identified</b>	<b>Attributes<sup>1</sup></b>	<b>New Mexico<sup>2</sup></b>
<b>Alpha (B.1.1.7 and Q lineages)</b>	United Kingdom	-50% more transmissible -Potential to cause more severe cases and deaths	-Alpha has proportionally declined from 78% 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.
<b>Beta (B.1.351 and descendent lineages)</b>	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.
<b>Gamma (P.1 and descendent lineages)</b>	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 (23%); oversampling of severe cases may skew these results.
<b>Epsilon (B.1.427, and B.1.429)</b>	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.
<b>Iota (B.1.526)</b>	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
<b>Mu (B.1.621, and B.1.621.1)</b>	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.

<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.

<sup>3</sup>All other VBMs have either not been observed in NM or have had <10 sequenced specimens and are not included in this table.

<sup>4</sup>[CDC COVID Data Tracker](#)

## Cumulative number of Specimens Sequenced and Matched to Case Investigations

Lineage	Sequenced Cases	Matched Cases*	Percent Matched
<b>B.1.617.2 (Delta)</b>	11805	10408	88%
<b>B.1.1.529 (Omicron)</b>	1200	1156	96%
<b>B.1.1.7 (Alpha)</b>	1835	1542	84%
<b>B.1.351 (Beta)</b>	8	3	38%
<b>P.1 (Gamma)</b>	109	94	86%
<b>B.1.427/B.1.429 (Epsilon)</b>	521	431	83%
<b>B.1.525 (Eta)</b>	4	4	100%
<b>B.1.526 (Iota)</b>	191	164	86%
<b>B.1.617.1 (Kappa)</b>	2	2	100%
<b>P.2 (Zeta)</b>	3	2	67%
<b>B.1.621/B.1.621.1 (Mu)</b>	38	30	79%
<b>Other lineage</b>	4504	3226	72%
<b>Total</b>	<b>20220</b>	<b>17062</b>	<b>84%</b>

\*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 219 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.

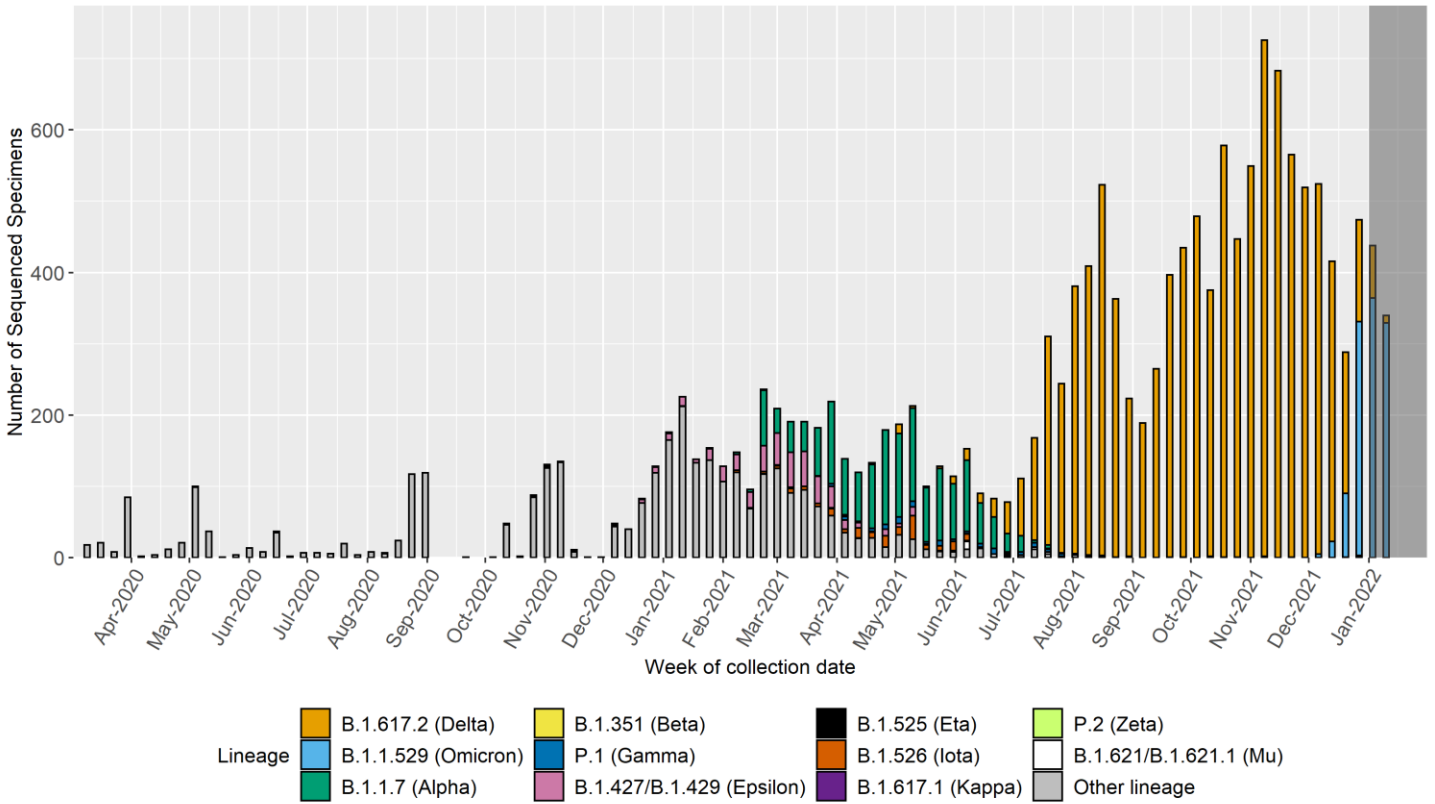
## Cumulative number of variant cases, hospitalizations, and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
<b>Delta</b>	10320	935	9%	243	2%	3407
<b>Omicron</b>	1146	17	1%	0	0%	641
<b>Alpha</b>	1529	152	10%	18	1%	95
<b>Beta</b>	3	0	0%	0	0%	0
<b>Gamma</b>	92	21	23%	2	2%	3
<b>Epsilon</b>	420	9	2%	2	0%	8
<b>Eta</b>	4	0	0%	0	0%	0
<b>Iota</b>	162	5	3%	1	1%	8
<b>Kappa</b>	2	0	0%	0	0%	0
<b>Zeta</b>	2	0	0%	0	0%	0
<b>Mu</b>	30	2	7%	0	0%	4
<b>Other lineage</b>	3133	206	7%	65	2%	23

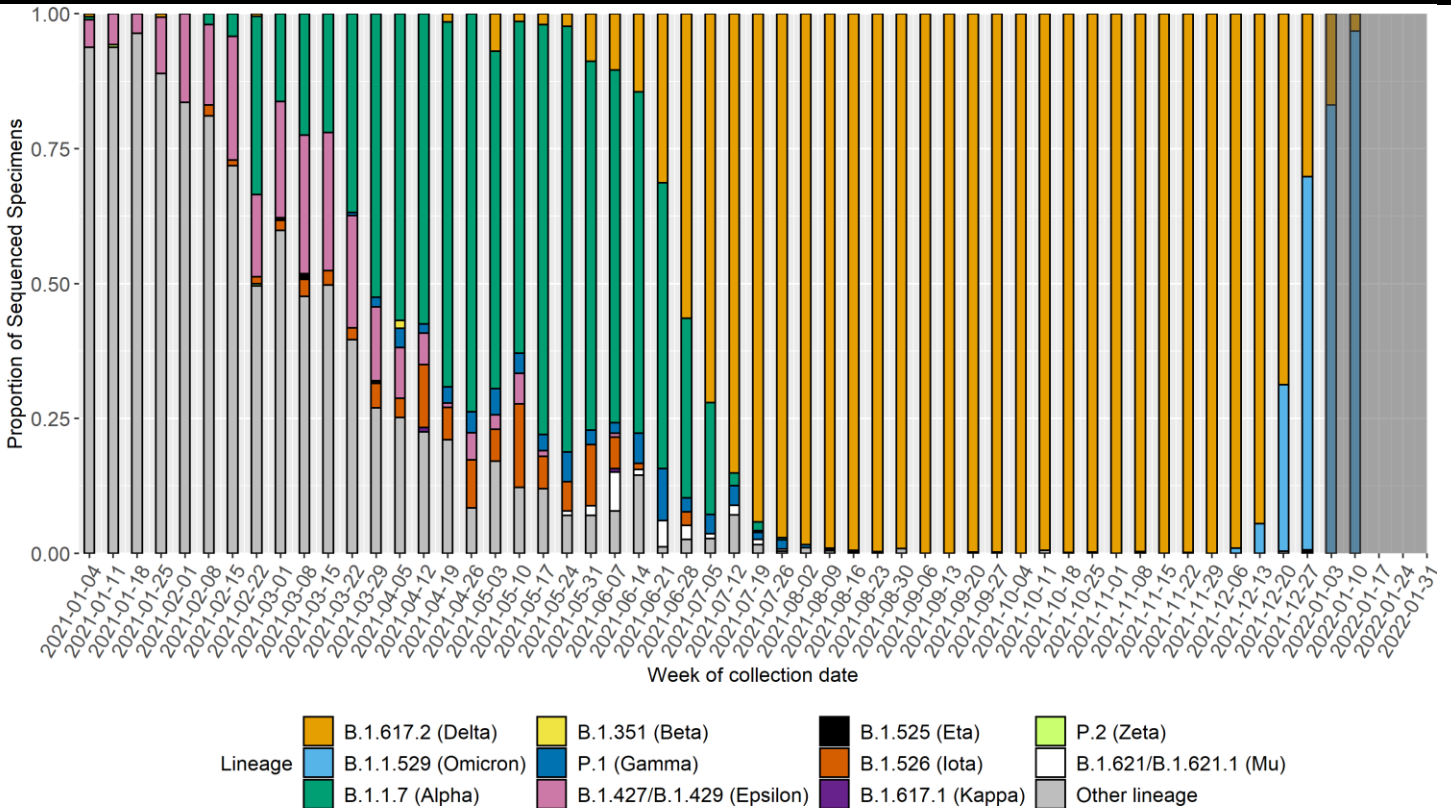
\*A vaccine breakthrough (VBT) case is defined as a person who tests positive  $\geq 14$  days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. *Because samples collected from VBT cases are more frequently sequenced compared to samples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

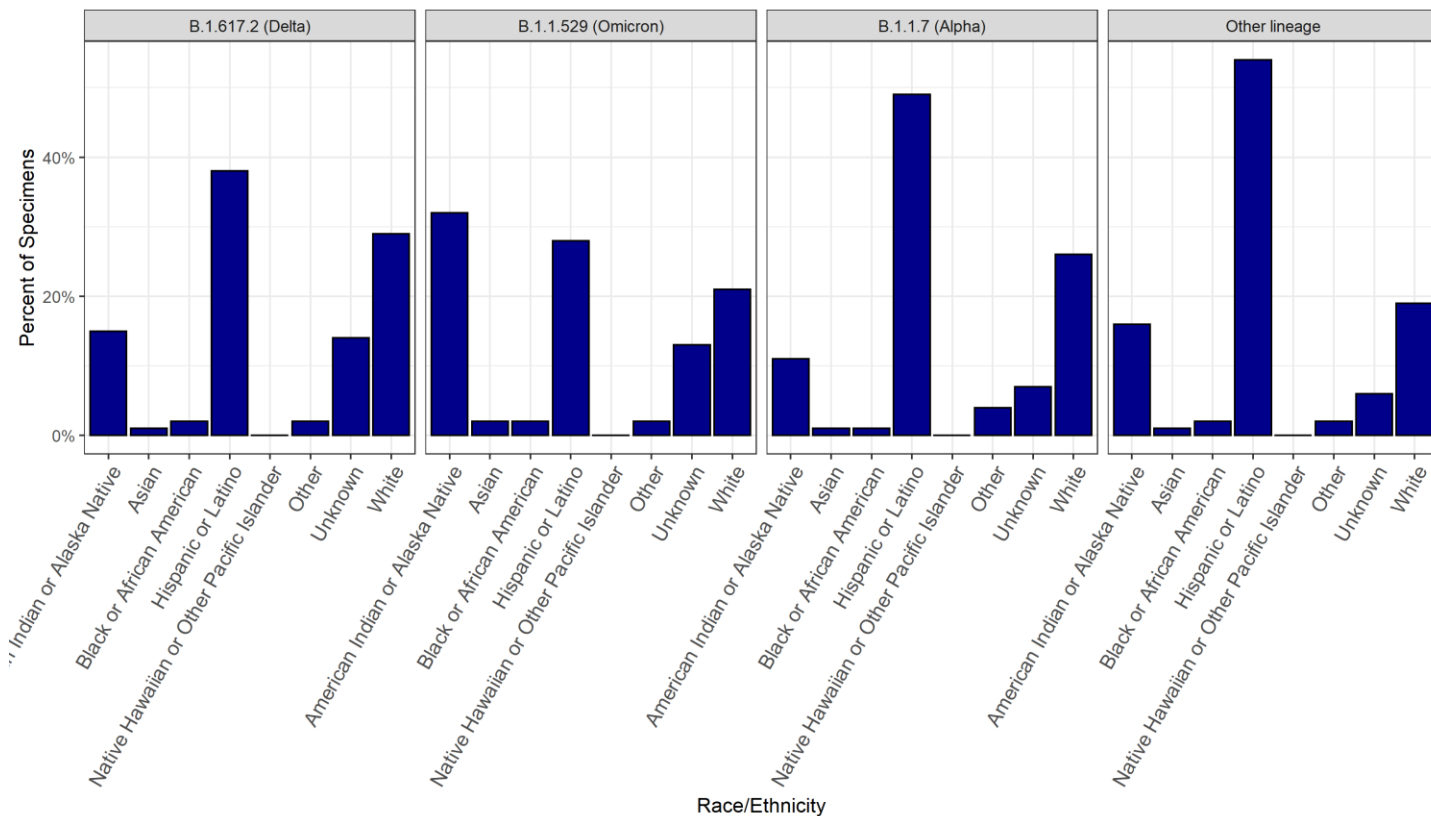


## Proportion of identified SARS-CoV-2 lineages by week

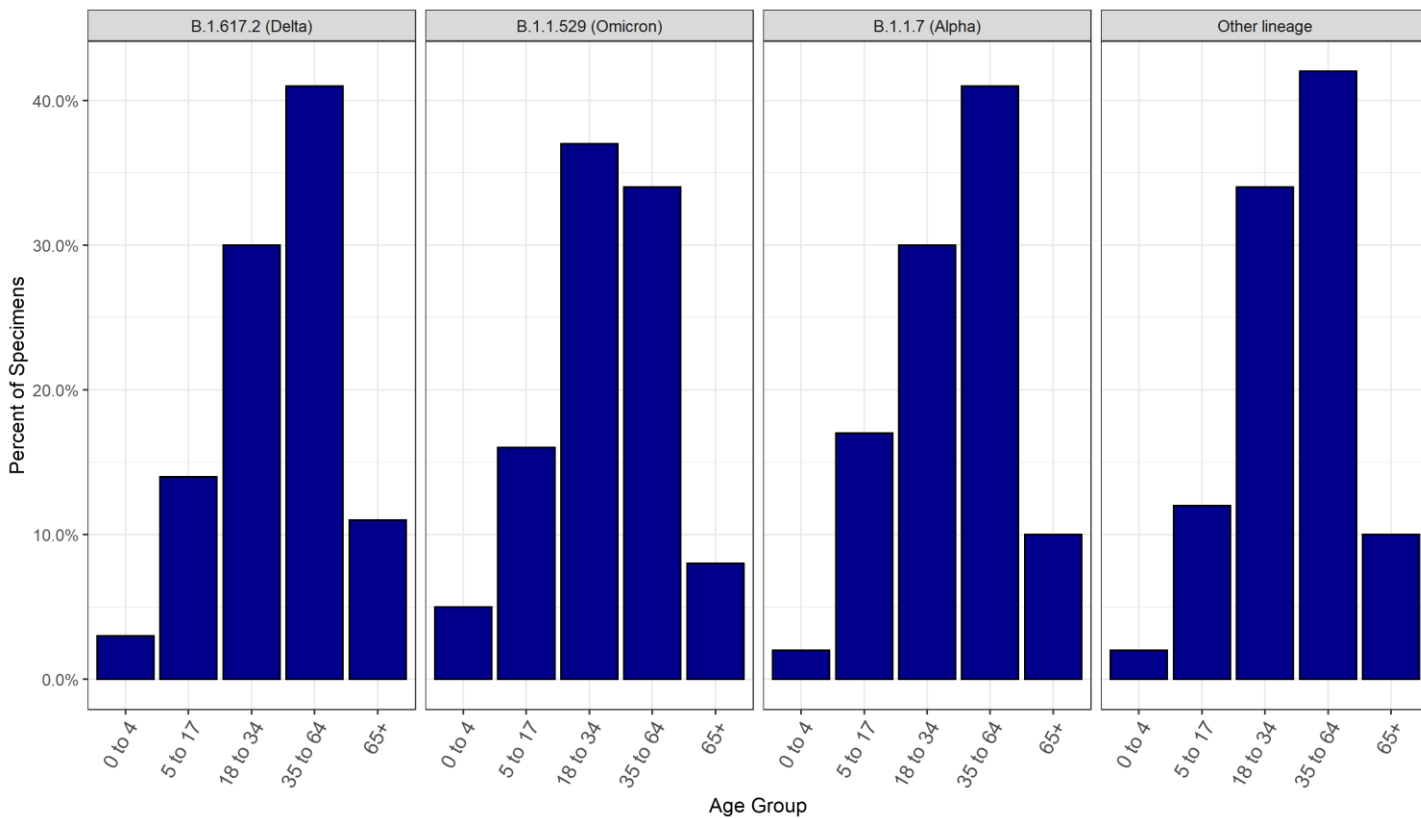


\*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

## 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.1.1.529 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)	Other lineage
<b>Bernalillo</b>	390	3369	444	1052
<b>Chaves</b>	7	212	13	59
<b>Cibola</b>	36	203	13	108
<b>Colfax</b>	3	132	24	26
<b>Curry</b>	0	124	24	29
<b>Dona Ana</b>	71	747	82	425
<b>Eddy</b>	2	274	19	97
<b>Grant</b>	22	81	13	34
<b>Guadalupe</b>	3	62	1	19
<b>Lea</b>	1	143	16	115
<b>Lincoln</b>	3	47	5	57
<b>Los Alamos</b>	5	44	9	24
<b>Luna</b>	12	42	15	20
<b>McKinley</b>	78	315	19	126
<b>Otero</b>	47	683	24	149
<b>Rio Arriba</b>	9	149	92	39
<b>San Juan</b>	296	1518	317	292
<b>San Miguel</b>	8	105	10	55
<b>Sandoval</b>	56	588	73	231
<b>Santa Fe</b>	43	527	97	294
<b>Sierra</b>	7	104	5	5
<b>Socorro</b>	3	53	9	31
<b>Taos</b>	4	120	16	39
<b>Torrance</b>	0	123	16	22
<b>Valencia</b>	32	429	70	118

\*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>B.1.1.529 (Omicron)</b>	1146	113 (10%)	12	101	89%
<b>B.1.617.2 (Delta)</b>	10313	4060 (39%)	248	3812	94%
<b>B.1.1.7 (Alpha)</b>	1529	1163 (76%)	104	1059	91%
<b>Other lineage</b>	3601	2790 (78%)	392	2398	86%

## 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)	Other lineage
<b>Fever (Measured or Subjective)</b>	47% (47)	53% (1980)	46% (484)	43% (1013)
<b>Chills</b>	43% (43)	48% (1789)	46% (477)	44% (1050)
<b>Muscle Aches</b>	50% (50)	55% (2062)	57% (590)	56% (1318)
<b>Runny Nose</b>	69% (69)	55% (2054)	53% (550)	53% (1260)
<b>Sore Throat</b>	64% (64)	44% (1643)	45% (465)	42% (1002)
<b>Cough</b>	77% (77)	74% (2800)	73% (765)	64% (1513)
<b>Shortness of Breath</b>	24% (24)	31% (1166)	30% (308)	24% (569)
<b>Nausea/Vomiting</b>	22% (22)	27% (1017)	27% (280)	23% (536)
<b>Headache</b>	62% (62)	64% (2406)	66% (685)	65% (1539)
<b>Abdominal Pain</b>	12% (12)	14% (536)	16% (162)	14% (328)
<b>Diarrhea</b>	21% (21)	29% (1101)	29% (297)	26% (622)
<b>Fatigue</b>	62% (62)	67% (2526)	70% (730)	66% (1553)
<b>Loss of Appetite</b>	29% (29)	39% (1483)	40% (415)	36% (850)
<b>Loss of Taste or Smell</b>	24% (24)	48% (1818)	39% (409)	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>B.1.1.529 (Omicron)</b>	1146	9%	95	10	10%
<b>B.1.617.2 (Delta)</b>	10313	38%	2908	981	25%
<b>B.1.1.7 (Alpha)</b>	1529	76%	596	561	49%
<b>Other lineage</b>	3601	75%	1656	1048	39%

## 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)	Other lineage
<b>Chronic Lung Disease</b>	20% (2)	24% (189)	25% (127)	26% (243)
<b>Chronic Liver Disease</b>	0% (0)	5% (38)	3% (17)	4% (38)
<b>Chronic Renal Disease</b>	0% (0)	12% (92)	4% (19)	5% (44)
<b>Diabetes Mellitus</b>	20% (2)	35% (278)	19% (95)	22% (203)
<b>Cardiovascular Disease</b>	30% (3)	36% (286)	32% (163)	28% (264)
<b>Autoimmune Disease</b>	10% (1)	6% (49)	8% (40)	5% (45)
<b>Neurological Disability</b>	0% (0)	8% (65)	6% (31)	9% (81)
<b>Current or Former Smoker</b>	50% (5)	37% (295)	54% (271)	50% (467)

\* 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 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.