

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

August 15, 2022

## 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 one VOC currently in the US, Omicron. All other VOCs and VOIs are now classified as VBMs due to their low prevalence including Delta, Alpha, Beta, Gamma, Epsilon, Eta, Iota, Kappa, Zeta, and Mu. CDC designated Omicron a VOC on November 30, 2021. To date, 9983 confirmed cases of Omicron have been sequenced in NM. Since the week of January 24, 2022, Omicron represented approximately 100% of sequenced samples in New Mexico. Sequenced specimens reported from June 18 to August 15, 2022 are incomplete but indicate a continued predominance of Omicron. CDC Nowcast predictive modeling forecasts Omicron to represent approximately 100% of US positive cases the week of August 13, 2022, and that BA.4 and BA.5 sublineages could represent approximately 95% of cases.<sup>4</sup> CDC currently classifies 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.

## NM COVID-19 Variant Epidemiologic Interpretation

CDC VARIANTS OF CONCERN (VOC)			
Name	First Identified	Attributes <sup>1</sup>	New Mexico <sup>2</sup>
<b>Omicron (B.1.1.529 and BA 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 66% of cases. -9983 confirmed cases of Omicron have been sequenced in NM.

## CDC VARIANTS BEING MONITORED (VBM)

Name <sup>3</sup>	First Identified	Attributes <sup>1</sup>	New Mexico <sup>2</sup>
<b>Delta (B.1.617.2 and AY 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 the week of 6/28/21 (56%) to 12/20/21 (72%). -The first Delta was sequenced the week of 4/19/21 and has not been observed in NM since 2/21/22
<b>Alpha (B.1.1.7 and Q lineages)</b>	United Kingdom	-50% more transmissible -Potential to cause more severe cases and deaths	-Alpha remained the dominant variant from the week of 3/29/21 (50%) to 6/21/21 (51%). -The first Alpha was sequenced the week of 12/28/20 and 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 9% 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.
<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 27% 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 7/19/21; Iota peaked at 14% 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 5/3/21 and has not been observed since 9/27/21; 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
BA.1 (Omicron)	7006	6458	92%
BA.2 (Omicron)	2093	2009	96%
BA.4 (Omicron)	182	175	96%
BA.5 (Omicron)	702	681	97%
B.1.617.2 (Delta)	15654	14301	91%
B.1.1.7 (Alpha)	1863	1616	87%
B.1.351 (Beta)	10	5	50%
P.1 (Gamma)	108	94	87%
B.1.427/B.1.429 (Epsilon)	526	441	84%
B.1.525 (Eta)	5	5	100%
B.1.526 (Iota)	200	175	88%
B.1.617.1 (Kappa)	2	2	100%
P.2 (Zeta)	3	2	67%
B.1.621/B.1.621.1 (Mu)	35	32	91%
Other lineage	4034	3262	81%
<b>Total</b>	<b>32423</b>	<b>29258</b>	<b>90%</b>

\*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 281 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.

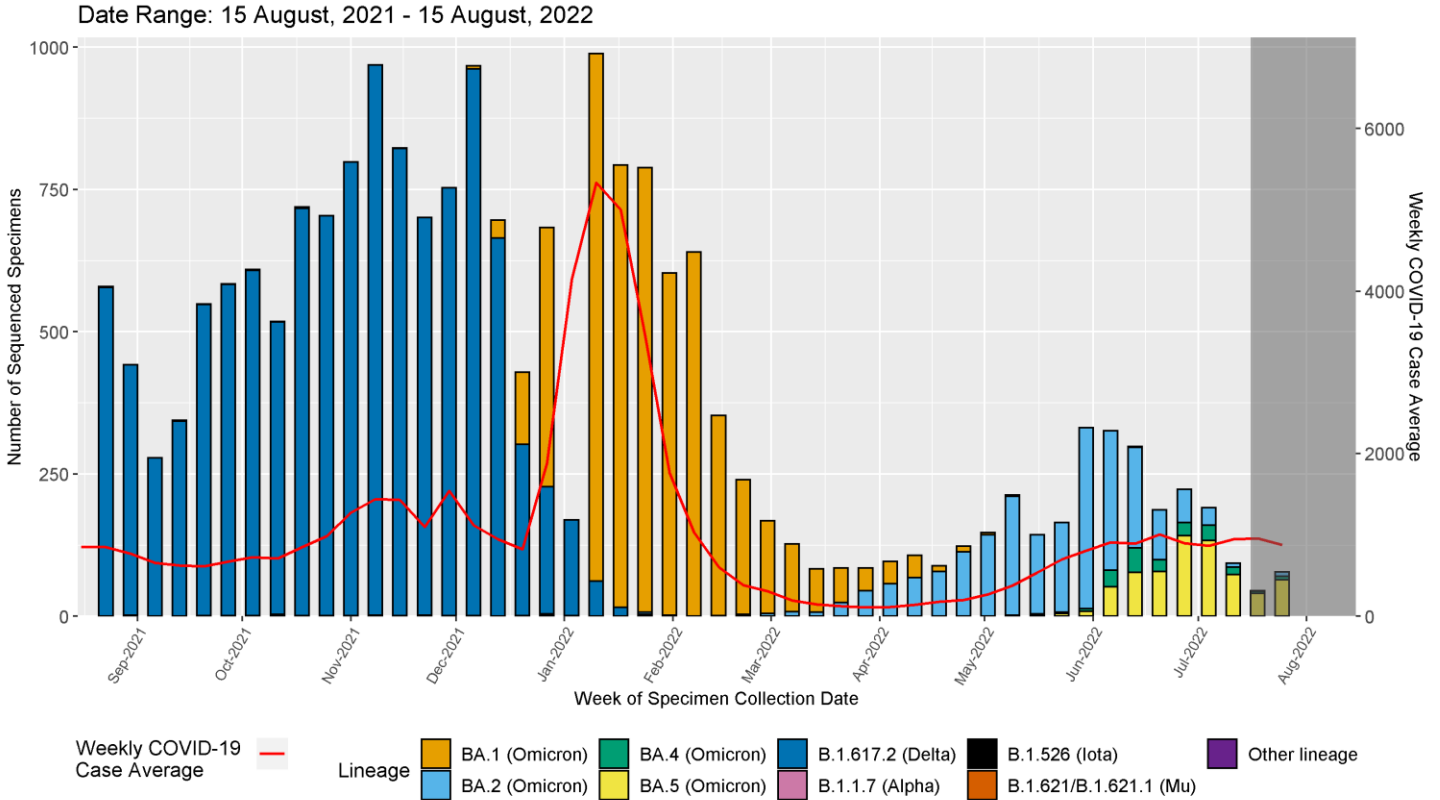
## Health outcomes of cumulative matched specimens

Lineage	Total Matched Cases	Number Hospitalized (%)	Number Died (%)	Number Vaccine Breakthrough (%)*
BA.1 (Omicron)	6423	271 (4%)	57 (1%)	3623 (56%)
BA.2 (Omicron)	1996	129 (6%)	12 (1%)	1478 (74%)
BA.4 (Omicron)	175	8 (5%)	0 (0%)	125 (71%)
BA.5 (Omicron)	677	16 (2%)	0 (0%)	500 (74%)
B.1.617.2 (Delta)	14200	1245 (9%)	443 (3%)	4406 (31%)
B.1.1.7 (Alpha)	1598	152 (10%)	20 (1%)	96 (6%)
B.1.351 (Beta)	5	0 (0%)	0 (0%)	0 (0%)
P.1 (Gamma)	92	22 (24%)	2 (2%)	4 (4%)
B.1.427/B.1.429 (Epsilon)	430	9 (2%)	2 (0%)	9 (2%)
B.1.525 (Eta)	5	0 (0%)	0 (0%)	0 (0%)
B.1.526 (Iota)	173	5 (3%)	1 (1%)	8 (5%)
B.1.617.1 (Kappa)	2	0 (0%)	0 (0%)	0 (0%)
P.2 (Zeta)	2	0 (0%)	0 (0%)	0 (0%)
B.1.621/B.1.621.1 (Mu)	32	1 (3%)	0 (0%)	5 (16%)
Other lineage	3167	196 (6%)	65 (2%)	26 (1%)

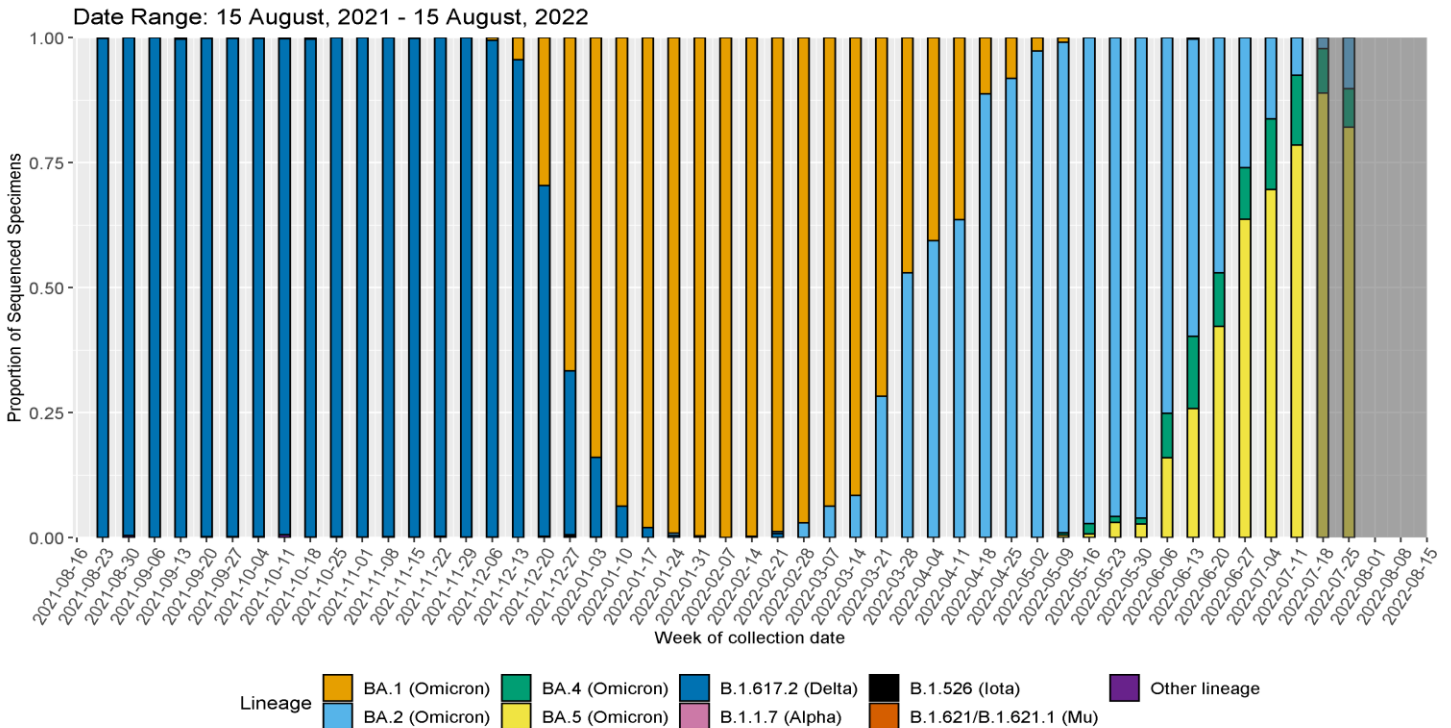
\*A vaccine breakthrough (VBT) case is defined as a person who tests positive  $\geq 14$  days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. *Because samples collected from VBT cases are more frequently sequenced compared to samples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



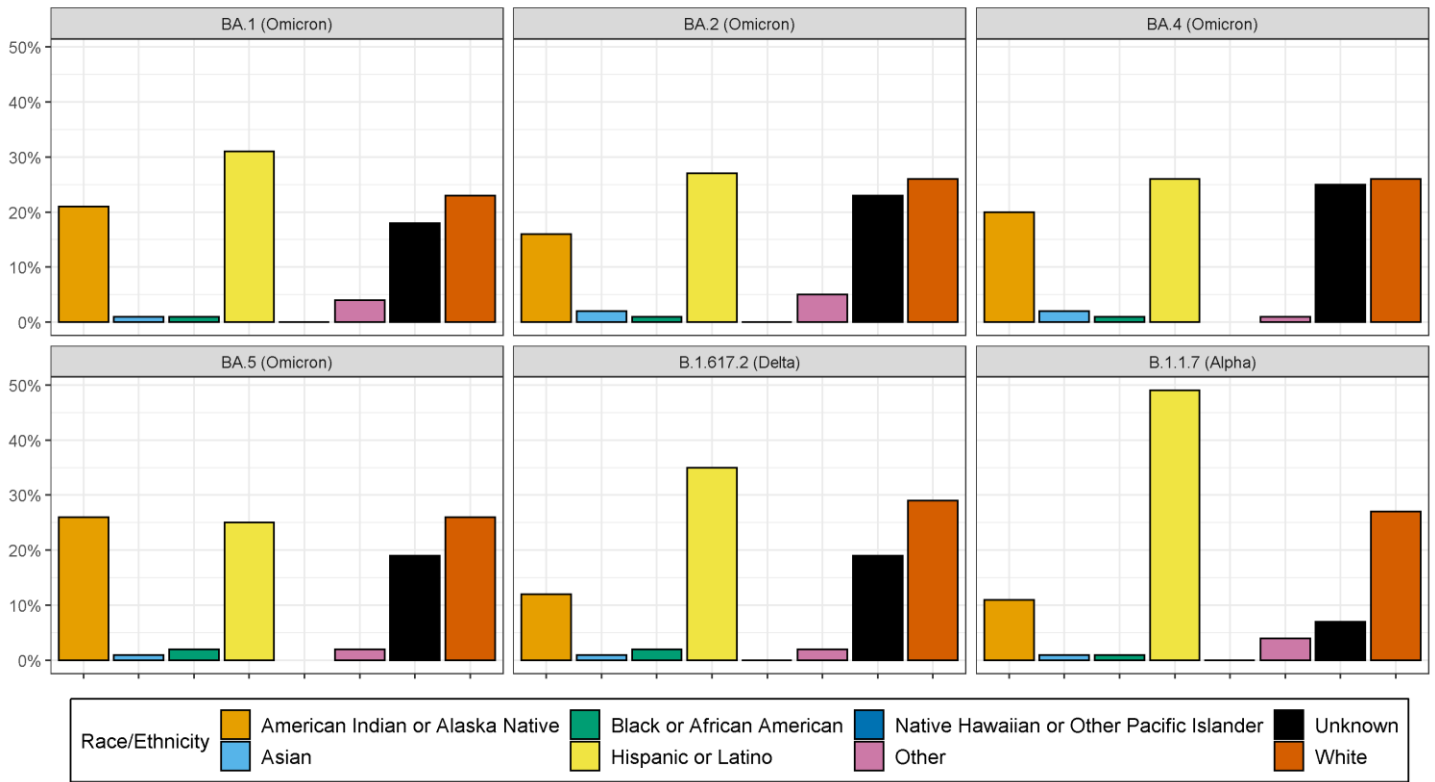
## Proportion of identified SARS-CoV-2 lineages by week\*



\*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.

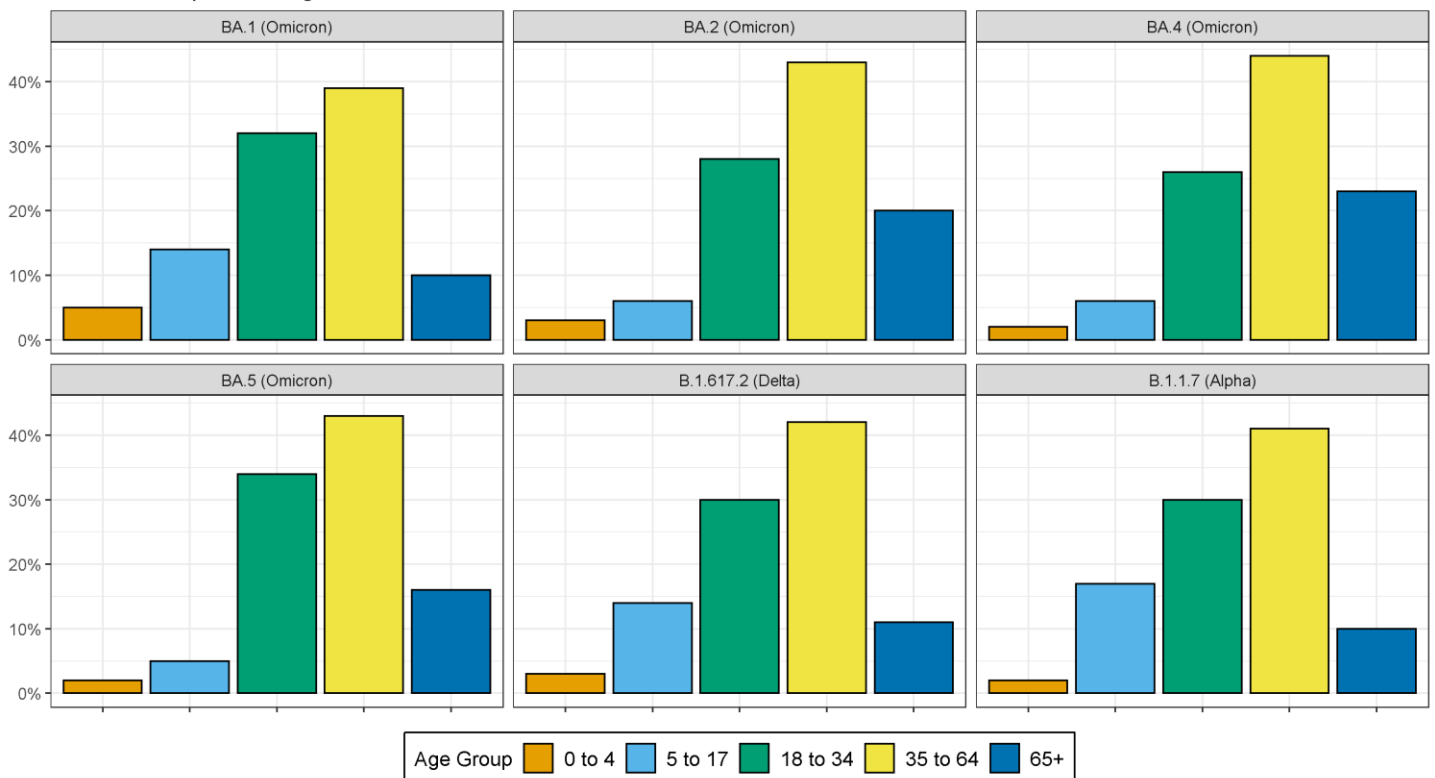
## Cumulative proportion of variant cases by race/ethnicity

Cumulative up to 15 August, 2022



## Cumulative proportion of variant cases by age group

Cumulative up to 15 August, 2022



## Cumulative number of variant cases by county of residence\*

County	BA.1 (Omicron)	BA.2 (Omicron)	BA.4 (Omicron)	BA.5 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
Bernalillo	2436	799	81	268	4792	471
Chaves	57	7	1	8	352	13
Cibola	208	124	10	17	290	14
Colfax	36	3	0	1	206	28
Curry	117	58	0	6	332	30
Dona Ana	300	83	6	32	905	85
Eddy	63	9	0	11	379	21
Grant	82	51	1	3	132	16
Guadalupe	22	0	0	0	67	1
Lea	30	3	0	2	224	17
Lincoln	44	26	1	3	119	6
Los Alamos	30	14	1	3	49	9
Luna	66	11	0	1	59	15
McKinley	340	5	0	9	357	19
Otero	214	30	4	4	773	26
Quay	12	4	0	1	79	4
Rio Arriba	103	75	6	12	194	92
Roosevelt	16	2	0	1	78	1
San Juan	960	191	28	165	1623	325
San Miguel	67	28	0	2	158	10
Sandoval	438	219	13	61	961	77
Santa Fe	353	152	19	41	744	101
Sierra	31	14	0	4	124	5
Socorro	17	8	0	0	92	9
Taos	46	22	1	5	230	17
Torrance	47	9	0	2	173	16
Valencia	247	39	3	9	564	70

\* Counties with less than 50 matched sequenced cases are not included in the table below. Excludes all VBMs other than Alpha and Delta.

## Percentage of variant cases reporting any symptoms

Lineage	Total	Total Investigated (%)	No	Yes	Percent Symptomatic
<b>BA.1 (Omicron)</b>	6423	1852 (29%)	120	1732	94%
<b>BA.2 (Omicron)</b>	1996	568 (28%)	40	528	93%
<b>BA.4 (Omicron)</b>	175	24 (14%)	2	22	92%
<b>BA.5 (Omicron)</b>	677	62 (9%)	4	58	94%
<b>B.1.617.2 (Delta)</b>	14200	5671 (40%)	381	5290	93%
<b>B.1.1.7 (Alpha)</b>	1598	1221 (76%)	115	1106	91%

## Percentage of specific symptoms reported by symptomatic variant cases

The table below includes data ONLY from symptomatic cases.

Symptom	BA.1 (Omicron)	BA.2 (Omicron)	BA.4 (Omicron)	BA.5 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
<b>Upper Respiratory</b> (Runny nose, sore throat)	1462 (84%)	430 (81%)	14 (64%)	44 (76%)	3471 (66%)	742 (67%)
<b>Lower Respiratory</b> (Cough, shortness of breath)	1423 (82%)	446 (84%)	16 (73%)	48 (83%)	4172 (79%)	840 (76%)
<b>Gastrointestinal</b> (Nausea/vomiting, abdominal pain, diarrhea)	714 (41%)	201 (38%)	11 (50%)	32 (55%)	2346 (44%)	474 (43%)
<b>Systemic</b> (Fever, chills, muscle aches, headache, fatigue, loss of appetite)	1567 (90%)	468 (89%)	20 (91%)	51 (88%)	4699 (89%)	975 (88%)
<b>Loss of Taste and Smell</b>	379 (22%)	101 (19%)	6 (27%)	11 (19%)	2558 (48%)	426 (39%)

\* Excludes all VBMs other than Alpha and Delta.

## Percentage of variant cases reporting underlying conditions

Lineage	Total	Total Investigated (%)	No	Yes	Percent Underlying Conditions
<b>BA.1 (Omicron)</b>	5603	1038 (19%)	601	437	42%
<b>BA.2 (Omicron)</b>	1995	556 (28%)	155	401	72%
<b>BA.4 (Omicron)</b>	175	24 (14%)	7	17	71%
<b>BA.5 (Omicron)</b>	677	54 (8%)	22	32	59%
<b>B.1.617.2 (Delta)</b>	14154	5496 (39%)	4204	1292	24%
<b>B.1.1.7 (Alpha)</b>	1597	1215 (76%)	625	590	49%

## Percentage of specific underlying conditions reported by variant cases

Data below includes ONLY cases who report having a preexisting condition.

Symptom	BA.1 (Omicron)	BA.2 (Omicron)	BA.4 (Omicron)	BA.5 (Omicron)	B.1.617.2 (Delta)	B.1.1.7 (Alpha)
<b>Chronic Lung Disease</b>	109 (29%)	99 (30%)	3 (20%)	6 (22%)	246 (23%)	136 (26%)
<b>Chronic Liver Disease</b>	15 (4%)	15 (4%)	1 (7%)	1 (4%)	53 (5%)	18 (3%)
<b>Chronic Renal Disease</b>	42 (11%)	36 (11%)	2 (13%)	3 (11%)	126 (12%)	21 (4%)
<b>Diabetes Mellitus</b>	111 (29%)	86 (26%)	6 (40%)	9 (33%)	397 (38%)	95 (18%)
<b>Cardiovascular Disease</b>	150 (39%)	133 (40%)	4 (27%)	7 (26%)	384 (37%)	171 (32%)
<b>Autoimmune Disease</b>	12 (3%)	9 (3%)	1 (7%)	1 (4%)	60 (6%)	41 (8%)
<b>Neurological Disability</b>	45 (12%)	32 (10%)	3 (20%)	1 (4%)	80 (8%)	31 (6%)
<b>Current or Former Smoker</b>	162 (43%)	156 (47%)	7 (47%)	13 (48%)	358 (34%)	285 (54%)

\* Excludes all VBMs other than Alpha and Delta.

\*\*Beginning January 2022, case investigation interviews conducted via webform survey no longer collected underlying conditions, and have been excluded from the underlying conditions tables.



## 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**
  - Cases reported here include cases with specimens sequenced at the Scientific Laboratory Division (SLD), the University of New Mexico, and the following partnering labs with the Centers for Disease Control and Prevention (CDC): Aegis Sciences Corporation, Fulgent Genetics, Gravity Diagnostics, Helix/Illumina, LabCorp, Quest Diagnostics, and Infinity BiologiX (Sampled).
- **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.