COVID-19 Variant of Concern (VOC) Case Report February 21, 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, 2623 confirmed cases of Omicron have been sequenced in NM. Omicron represented approximately 100% of sequenced samples in New Mexico in the week of January 17, 2021. Sequenced specimens reported from January 24-February 21, 2022 are incomplete but indicate a predominance of Omicron compared to other variants. CDC Nowcast predictive modeling forecasts Omicron to represent approximately 100% of US positive cases the week of February 19, 2022.⁴ 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 ¹	New Mexico ²					
Delta	India	-Increased transmissibility	-Delta remained the dominant					
(B.1.617.2 and AY		-May reduce effectiveness of	variant from 6/28/21 to					
sublineages)	sublineages) antibody treatments 12/20/21 and represented 6							
		-May cause more severe illness in	of sequences reported on					
		unvaccinated persons	12/20/21.					
		-May reduce natural and vaccine	-Proportion of deaths is					
immunity currently 3%.								
Omicron	Omicron South Africa -May increase transmissibility -Omicron became the							
(B.1.1.529 and BA		-May reduce effectiveness of	dominant variant 12/27/21					
sublineages)	sublineages) antibody treatments representing 67% of cases.							
		-May reduce natural and vaccine	-To date, 2623 confirmed cases					
		immunity	of Omicron have been					
	, sequenced in NM.							

CDC VARIANTS BEING MONITORED (VBM)

Name ³	First Identified	Attributes ¹	New Mexico ²
Alpha (B.1.1.7 and Q lineages)	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.
Beta (B.1.351 and descendent lineages)	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.
Gamma (P.1 and descendent lineages)	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.
Epsilon (B.1.427, and B.1.429)	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.
lota (B.1.526)	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; lota peaked at 15% of sequenced NM specimens the week of 5/10/21
Mu (B.1.621, and B.1.621.1)	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.

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

 $^2 \rm NM$ interpretations based on data collected >4 weeks ago to allow for lag in genomic sequencing.

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

⁴CDC COVID Data Tracker

Cumulative number of Specimens Sequenced and Matched to Case Investigations

Lineage	Sequenced Cases	Matched Cases*	Percent Matched
B.1.617.2 (Delta)	11924	10505	88%
B.1.1.529 (Omicron)	2623	2496	95%
B.1.1.7 (Alpha)	1835	1538	84%
B.1.351 (Beta)	8	3	38%
P.1 (Gamma)	109	94	86%
B.1.427/B.1.429 (Epsilon)	521	430	83%
B.1.525 (Eta)	4	4	100%
B.1.526 (lota)	191	163	85%
B.1.617.1 (Kappa)	2	2	100%
P.2 (Zeta)	3	2	67%
B.1.621/B.1.621.1 (Mu)	38	30	79%
Other lineage	4522	3223	71%
Total	21780	18490	85%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 222 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*	
Delta	10416	956	9%	280	3%	3469	
Omicron	2484	29	1%	1	0%	1465	
Alpha	1525	151	10%	18	1%	96	
Beta	3	0	0%	0	0%	0	
Gamma	92	21	23%	2	2%	3	
Epsilon	419	9	2%	2	0%	8	
Eta	4	0	0%	0	0%	0	
lota	161	5	3%	1	1%	8	
Карра	2	0	0%	0	0%	0	
Zeta	2	0	0%	0	0%	0	
Mu	30	2	7%	0	0%	4	
Other lineage	3130	206	7%	65	2%	24	

*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*





Cumulative proportion of variant cases by Age Group B.1.617.2 (Delta) B.1.1.529 (Omicron) B.1.1.7 (Alpha) Other lineage 40.0% 30.0% Percent of Specimens 10.0% 0.0% 35 to 64 + 50 1>+ 35 to 64 + 50 1>+ 18 to 34 + 0⁴ 18 to 34 + 35 to 64 + 5001>+ 0 to 4 + 5to 1>+ 0 to 4+ 0 to 4 t 18 to 34 + 18 to 34 + 35 to 64 + . S . S o5, 65, Age Group

Cumulative number of variant cases by county of residence*

	B.1.617.2	B.1.1.529	B.1.1.7	
County	(Delta)	(Omicron)	(Alpha)	Other lineage
Bernalillo	3404	724	443	1048
Chaves	227	15	13	59
Cibola	210	58	13	108
Colfax	136	13	24	26
Curry	124	1	24	29
Dona Ana	750	161	81	425
Eddy	275	11	19	97
Grant	81	36	13	34
Guadalupe	63	12	1	19
Lea	143	8	16	115
Lincoln	47	7	5	57
Los Alamos	44	8	9	24
Luna	42	44	14	20
McKinley	314	226	18	126
Otero	682	137	24	149
Rio Arriba	152	24	92	39
San Juan	1522	620	317	292
San Miguel	107	21	10	55
Sandoval	601	126	73	231
Santa Fe	532	99	97	294
Sierra	104	18	5	5
Socorro	53	3	9	31
Taos	120	9	16	39
Torrance	126	11	16	22
Valencia	429	76	70	118

Counties with less than 50 matched sequenced cases are not included in the table below.

*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.1.617.2 (Delta)	10409	4085(39%)	249	3836	94%	
B.1.1.529 (Omicron)	2484	191(8%)	19	172	90%	
B.1.1.7 (Alpha)	1525	1162(76%)	104	1058	91%	
Other lineage	3597	2787(78%)	392	2395	86%	

Percentage of specific symptoms reported by symptomatic variant cases

The table below includes data ONLY from symptomatic cases.

-	B.1.617.2	B.1.1.529		
Symptom	(Delta)	(Omicron)	B.1.1.7 (Alpha)	Other lineage
Fever (Measured	53% (1989)	44% (74)	47% (484)	43% (1012)
of Subjective)	400/ (1707)		ACO((A77)	440/ (1050)
Chills	40% (1797)	44% (75)	40% (477)	44% (1050)
	55% (2068)	51% (87)	57% (590)	56% (1317)
Muscle Aches	, , , , , , , , , , , , , , , , , , ,	, <i>,</i> ,		. ,
	54% (2059)	68% (116)	53% (550)	53% (1257)
Runny Nose				
	44% (1648)	60% (102)	45% (465)	42% (1000)
Sore Throat	()			
Jore mout	74% (2817)	76% (130)	73% (764)	64% (1511)
Coursh	7470 (2017)	7070 (150)	7370 (704)	04/0 (1011)
Cougn	240((4470)	250((42)	200/ (207)	240((500)
Shortness of	31% (1178)	25% (43)	30% (307)	24% (569)
Breath				
	27% (1024)	21% (36)	27% (280)	23% (536)
Nausea/Vomiting				
	64% (2415)	64% (108)	66% (685)	65% (1538)
Headache				
	14% (540)	11% (19)	16% (162)	14% (328)
Abdominal Pain				
	29% (1108)	20% (34)	29% (297)	26% (622)
Diarrhea				
	67% (2538)	63% (107)	70% (729)	66% (1551)
Fatigue	. ,			
	40% (1494)	31% (53)	40% (415)	36% (849)
Loss of Appetite		01/0 (00)		
Loss of Taste or	48% (1822)	22% (37)	39% (409)	44% (1030)
Smell				

*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.1.617.2 (Delta)	10409	3925 (38%)	2921	1004	26%
B.1.1.529 (Omicron)	2484	174 (7%)	146	28	16%
B.1.1.7 (Alpha)	1525	1156 (76%)	596	560	48%
Other lineage	3597	2701 (75%)	1653	1048	39%

Percentage of specific underlying conditions reported by variant cases

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

	B.1.617.2	B.1.1.529		Other
Symptom	(Delta)	(Omicron)	B.1.1.7 (Alpha)	lineage
Chronic Lung Disease	23% (191)	16% (4)	25% (127)	26% (243)
	5% (38)	4% (1)	3% (17)	4% (38)
Chronic Liver Disease				
	11% (93)	12% (3)	4% (19)	5% (44)
Chronic Renal Disease				
	35% (287)	28% (7)	19% (95)	22% (203)
Diabetes Mellitus				
	36% (298)	32% (8)	32% (162)	28% (264)
Cardiovascular Disease				
	6% (49)	8% (2)	8% (40)	5% (45)
Autoimmune Disease				
	8% (67)	16% (4)	6% (31)	9% (81)
Neurological Disability				
	36% (298)	52% (13)	53% (270)	50% (467)
Current or Former Smoker				

* 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 <u>CDC COVID Data Tracker</u>

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.