COVID-19 Variant of Concern (VOC) 2021 Annual Report

January 1, 2021-December 31, 2021

COVID-19 Genomic Surveillance

Monitoring COVID-19 variants is an important part of epidemiologic surveillance to track the impact 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 standard diagnostic tests do not test for specific variant strains and must be sent to a laboratory for sequencing. Genetic sequencing requires coordinated effort and time and there is a lag time from specimen collection to reporting of approximately 3-4 weeks. This lag time means that results cannot be interpreted and acted upon immediately to influence public health policies.

In this report you will find information about variants of concern circulating in New Mexico in 2021 including the number of specimens sequenced, the associated health outcomes, information about symptoms and underlying conditions, variant distribution by county, race and ethnicity, and age group. Data presented in this report are not representative of all COVID-19 cases because at-risk populations were oversampled, like hospitalized patients, residents in congregate settings such as long-term care facilities and correctional facilities, and reinfection cases. In 2021 in New Mexico, the Alpha variant (B.1.1.7) was dominant (greater than 50% of sequenced specimens) from the week of March 29th, 2021 to June 21, 2021; Delta (B.1.617.2 and all AY sublineages) was dominant June 28th, 2021 to December 20th, 2021, and Omicron (B.1.1.529 and all BA sublineages) was dominant December 27th, 2021 through the end of the year, and continues to remain dominant in 2023 and 2024. In 2021, Delta was the most sequenced variant of concern in circulation (15,271), followed by Alpha (1,830). Although less Alpha variants were sequenced, the proportion of hospitalizations was slightly higher (9%) than Delta (8%), but deaths were highest among Delta variants sequenced (3%). In late 2020, the first COVID-19 vaccines became available. Vaccine administration first began at the end of 2020 and New Mexican residents were 70% vaccinated by July 2021. The first vaccine booster doses became available in September of 2021.

Over the course of 2021 in NM, a total of 20,583 sequenced specimens were reported to NMDOH Epidemiology and Response Division (ERD). Of those, the Variant Investigation Team was able to match 18,216 (88%) specimens to their associated patient profile including social characteristics and health outcomes of interest, when reported. The total NM sequences for 2021 reported on GISAID[1] is 22,776 of which, 90% were reported to NMDOH. The following variants are included in the 2021 report: Alpha (1,830; 9%), Delta (15,271; 74%), Omicron (580; 3%), Beta (10; 0%), Gamma (108; 1%), Epsilon (468; 2%), Eta (4; 0%), Iota (194; 1%), Kappa (2; 0%), Zeta (2; 0%), and Mu (35; 0%). Any lineages that did not demonstrate concerning characteristics and were not designated a VBM, VOI, or VOC are included in the report as "other lineage" (2,089; 10%).[2]

[1]Global Initiative on Sharing Influenza Data (GISAID) is a global repository for infectious disease sequencing results such as influenza, COVID-19, and Mpox (gisaid.org).

[2]The total sequenced specimens are all sequencing results reported to NMDOH in 2021 and may include out of state residents.

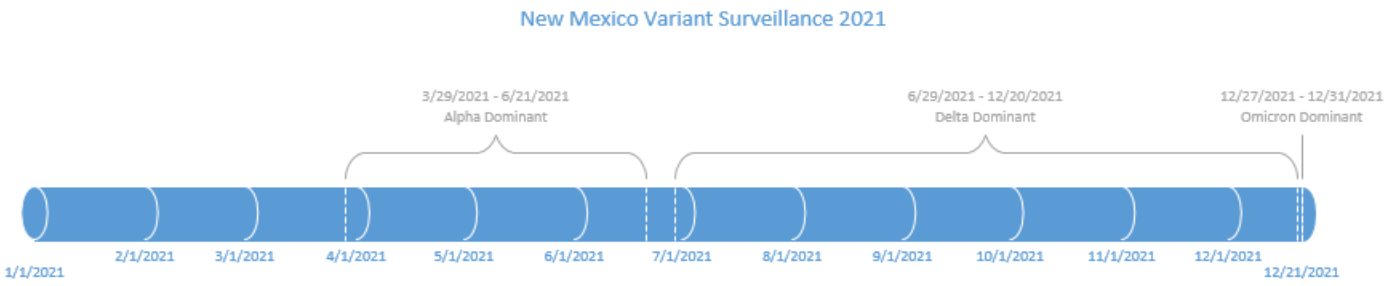


Figure 1: Timeline of CDC Variants of Concern Dominance Periods in New Mexico (2021)

NM COVID-19 Variant Epidemiologic Interpretation

CDC VARIANTS OF CONCERN (VOC)
New Mexico 2021

Name[1, 2]	New Mexico Observations
Alpha (B.1.1.7 and Q lineages)	-Alpha was the dominant variant 3/29/21 to 6/21/21, and peaked at 80% of the sequenced specimens the week of 5/24/21 -A total of 1,830 sequenced specimens were reported: 9% of all sequenced specimens in 2021
Delta (B.1.617.2 and AY sublineages)	-Delta was the dominant variant 6/28/21 to 12/20/21, and was 100% from 8/16/21 to 11/29/21 -A total of 15,271 sequenced specimens were reported: 74% of all sequenced specimens in 2021
Omicron (B.1.1.529 and BA sublineages)	-Omicron was first sequenced in New Mexico 12/6/21 and became the dominant variant the week of 12/27/21. Omicron continues to be the dominant variant in circulation in 2024. -A total of 580 sequenced specimens were reported: 3% of all sequenced specimens in 2021
Gamma (P.1 and descendent lineages)	-Gamma circulated in New Mexico from 3/22/21 to 8/9/21, and peaked at 9% of specimens the week of 6/21/21 -A total of 108 sequenced specimens were reported: 1% of all sequenced specimens in 2021
Epsilon (B.1.427, and B.1.429)	-Epsilon circulated in New Mexico from 1/1/21 to 6/7/21, and peaked at 26% of the sequenced specimens the week of 2/15/21 -A total of 468 sequenced specimens were reported: 2% of all sequenced specimens in 2021
Iota (B.1.526)	-Iota circulated in New Mexico from 2/8/21 to 7/19/21, and peaked at 14% of the sequenced specimens the week of 5/10/21 -A total of 194 sequenced specimens were reported: 1% of all sequenced specimens in 2021

[1] Variants of concern are only included in this table if they reached a threshold of 1% of total sequenced cases reported in 2021 in New Mexico.
[2] https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-info.html

Number of specimens sequenced and matched to case investigations			
Lineage	**Sequenced Specimens**	**Matched Cases[1]**	**Percent Matched**
B.1.1.7 (Alpha)	1830	1359	74%
B.1.617.2 (Delta)	15271	14048	92%
BA.1.1.529 & BA sublineages (Omicron)	580	548	94%
B.1.427/B.1.429 (Epsilon)	468	370	79%
B.1.526 (Iota)	194	144	74%
P.1 (Gamma)	108	83	77%
B.1.621/B.1.621.1 (Mu)	35	32	91%
B.1.525 (Eta)	4	4	100%
B.1.351 (Beta)	10	5	50%
B.1.617.1 (Kappa)	2	2	100%
P.2 (Zeta)	2	1	50%
Other lineage	2089	1620	78%
Total	20593	18216	88%

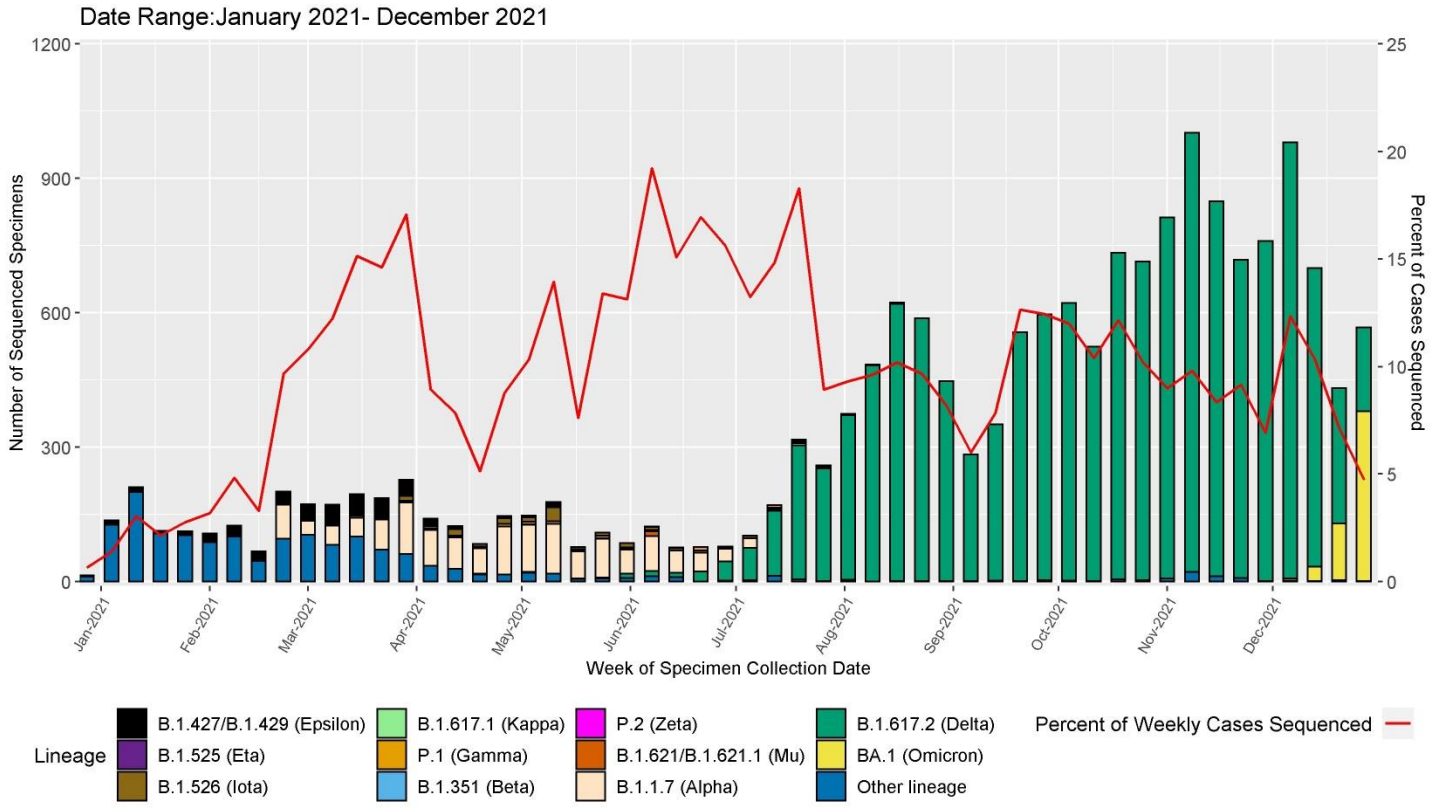
[1]Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 165 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico. These have been removed from the subsequent tables and figures.

Health outcomes of matched New Mexico resident cases				
Lineage	Matched Cases[1]	Number Hospitalized (%)	Number Died (%)	Number COVID Reinfections[2] (%)
B.1.1.7 (Alpha)	1344	120 (9%)	15 (1%)	86 (6%)
B.1.617.2 (Delta)	13958	1207 (9%)	424 (3%)	4368 (31%)
BA.1.1.529 & BA sublineages (Omicron)	543	10 (2%)	4 (1%)	325 (60%)
B.1.427/B.1.429 (Epsilon)	359	6 (2%)	2 (1%)	8 (2%)
B.1.526 (Iota)	142	5 (4%)	1 (1%)	7 (5%)
P.1 (Gamma)	82	20 (24%)	2 (2%)	4 (5%)
B.1.621/B.1.621.1 (Mu)	32	1 (3%)	0 (0%)	5 (16%)
B.1.525 (Eta)	4	0 (0%)	0 (0%)	0 (0%)
B.1.351 (Beta)	5	0 (0%)	0 (0%)	0 (0%)
B.1.617.1 (Kappa)	2	0 (0%)	0 (0%)	0 (0%)
P.2 (Zeta)	1	0 (0%)	0 (0%)	0 (0%)
Other lineage	1579	64 (4%)	17 (1%)	48 (3%)

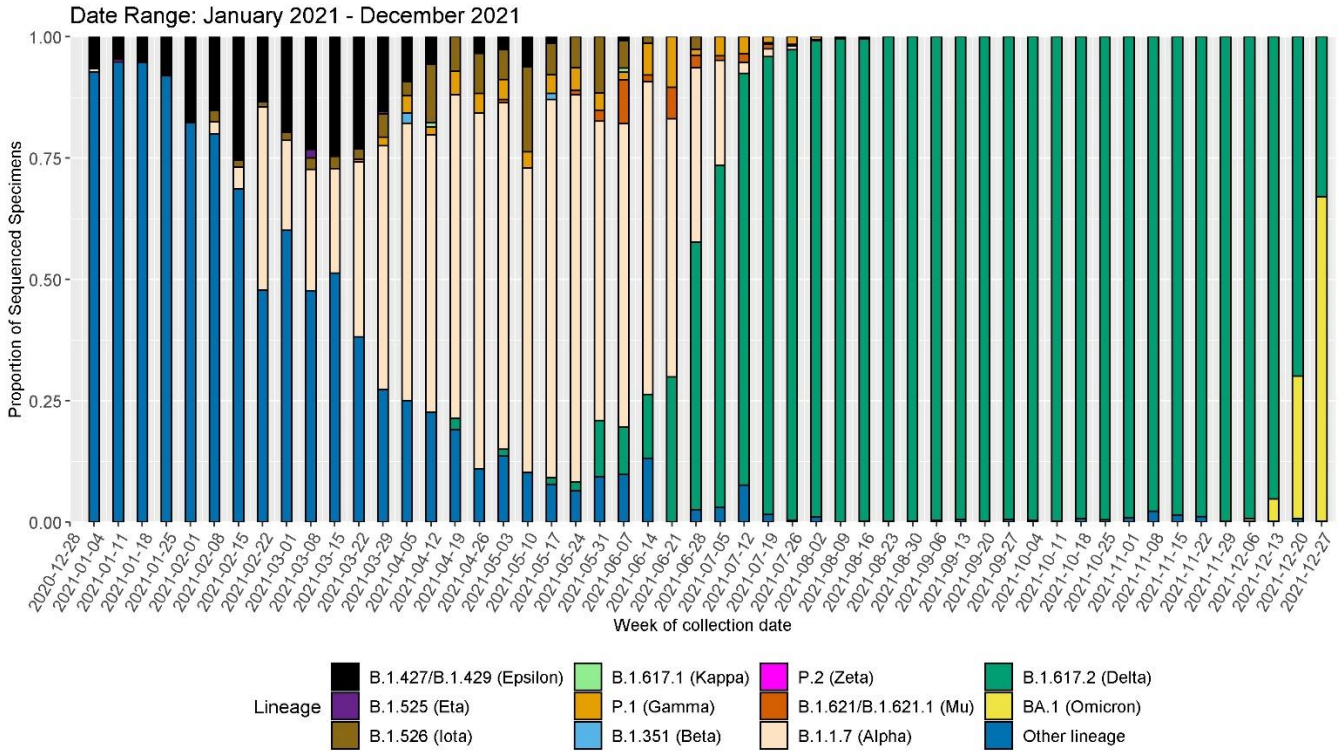
[1]Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table excludes 165 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico and are removed from subsequent tables and figures.

[2]A COVID Reinfection is defined by a laboratory confirmed positive case occurring in the same patient >90 days from a prior infection.

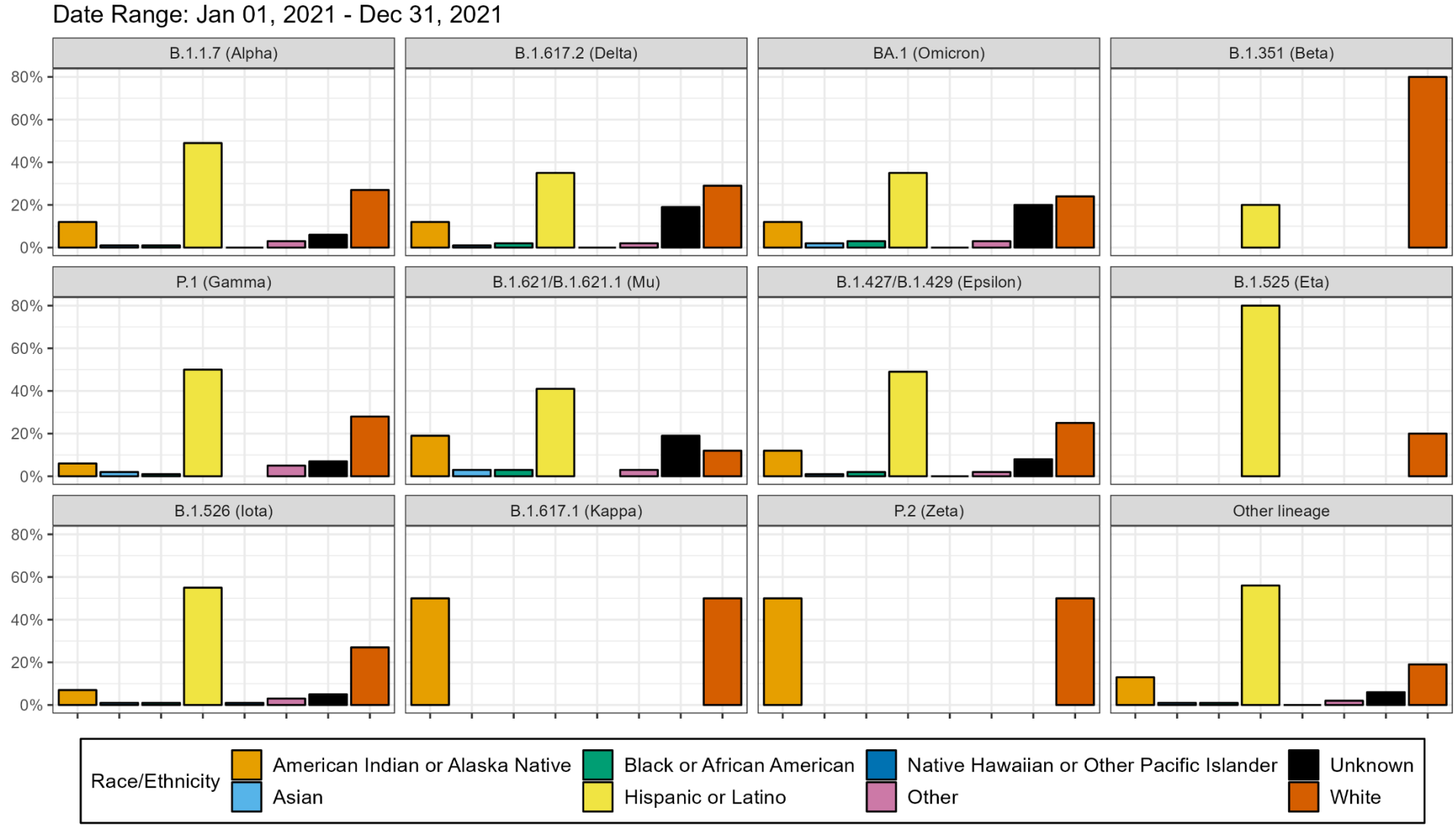
Identified SARS-CoV-2 lineages by week



Proportion of identified SARS-CoV-2 lineages by week

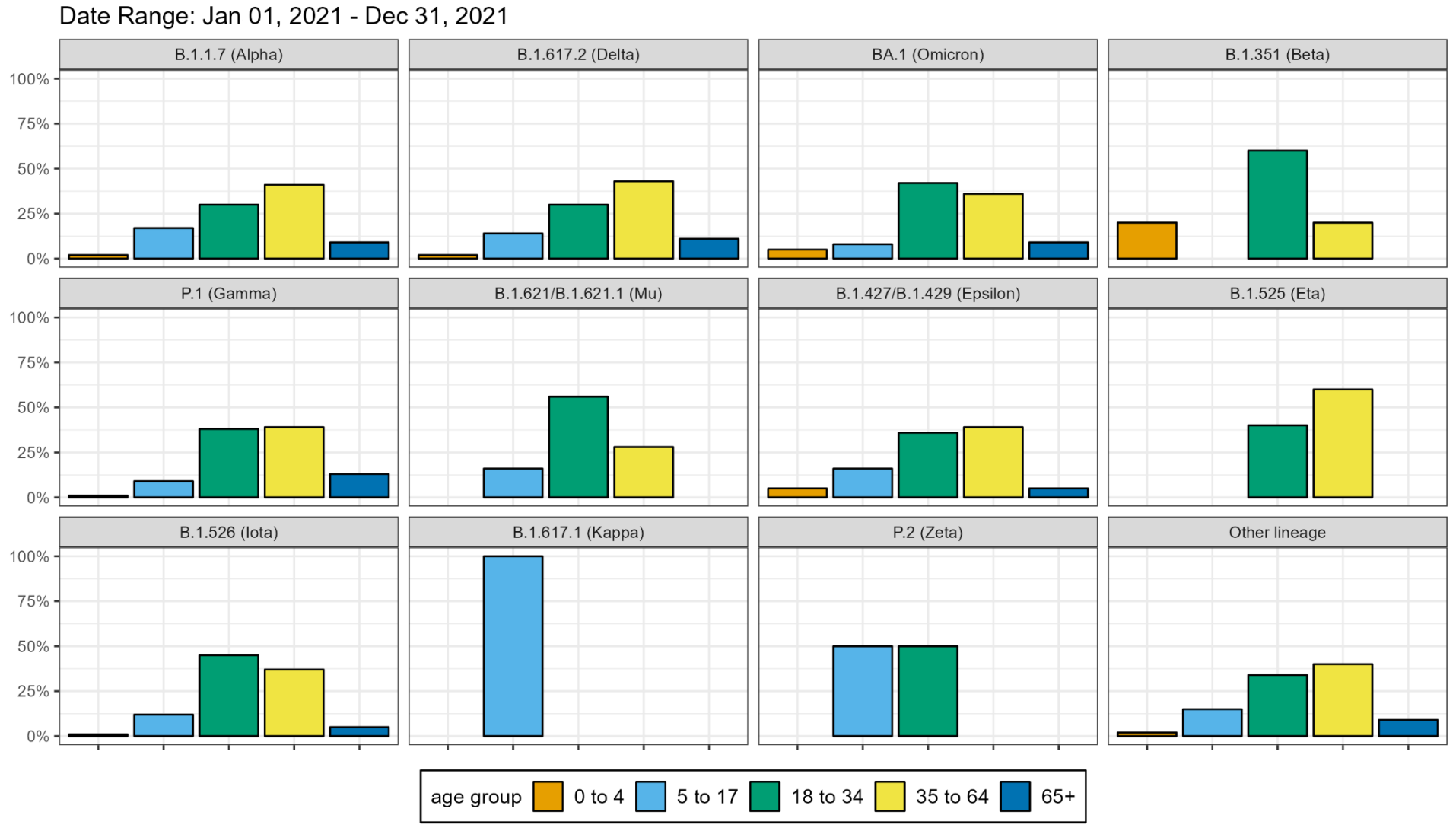


Cumulative percentage of sequenced specimens by variant and race/ethnicity[1]



[1]Sampling was consistent, but not random, so the absolute percentage of cases by race/ethnicity and age group do not reflect the distribution of all cases when a variant was dominant. However, the changes in the relative distribution can reflect differences in relative risk of infection during times when different variants were dominant. For example, the shift to relatively more cases in the 18-34 year age group during the early Omicron period reasonably reflects a change in exposure and susceptibility for this age group. In variants of concern with small numbers of matched cases, group percentages may not reflect actual differences in risk among racial, ethnic, or age categories.

Cumulative percentage of sequenced specimens by variant and age group[1]



[1]Sampling was consistent, but not random, so the absolute percentage of cases by race/ethnicity and age group do not reflect the distribution of all cases when a variant was dominant. However, the changes in the relative distribution can reflect differences in relative risk of infection during times when different variants were dominant. For example, the shift to relatively more cases in the 18-34 year age group during the early Omicron period reasonably reflects a change in exposure and susceptibility for this age group. In variants of concern with small numbers of matched cases, group percentages may not reflect actual differences in risk among racial, ethnic, or age categories.

Cumulative number of sequenced specimens by variant and county of residence

County	B.1.1.7 (Alpha)	B.1.617.2 (Delta)	BA.1 (Omicron)	B.1.427/B.1.429 (Epsilon)	B.1.526 (Iota)	P.1 (Gamma)	B.1.621/ B.1.621.1 (Mu)	Other lineage	Total
Bernalillo	337	4658	249	127	41	11	4	450	5885
Chaves	12	336	9	1	1	0	0	8	367
Cibola	13	274	8	29	5	0	3	39	372
Colfax	24	221	10	1	5	0	0	24	285
Curry	16	325	0	1	8	0	0	3	353
Dona Ana	78	903	40	30	2	5	2	251	1312
Eddy	18	373	2	6	3	0	2	22	426
Grant	12	130	24	6	0	2	0	13	187
Guadalupe	1	56	0	4	0	0	0	10	71
Lea	15	226	2	2	0	1	0	14	260
Lincoln	3	116	2	2	0	4	0	34	161
Los Alamos	8	50	1	6	0	0	0	13	78
Luna	13	58	1	1	0	0	0	14	87
McKinley	17	350	14	0	2	0	1	19	403
Otero	27	772	23	15	1	2	0	103	943
Quay	1	73	0	0	0	1	0	0	75
Rio Arriba	88	189	4	2	0	0	0	25	308
Roosevelt	1	76	1	1	3	0	0	3	85
San Juan	303	1642	45	10	3	26	6	97	2134
San Miguel	5	152	6	3	0	0	0	30	196
Sandoval	65	952	39	40	10	6	2	76	1190
Santa Fe	85	721	33	37	3	0	0	173	1052
Sierra	5	122	0	0	0	0	0	1	128
Socorro	8	89	0	2	0	0	0	22	121
Taos	16	235	4	8	0	0	0	11	274
Torrance	15	171	0	8	51	1	0	10	256
Valencia	60	546	22	17	4	4	0	75	728

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

Number (%) of matched and sequenced COVID-19 cases reporting any symptoms by variant					
Lineage	**Total**	**Total Investigated (%)**	**No**	**Yes**	**Percent Symptomatic**
B.1.1.7 (Alpha)	1344	1022 (76%)	95	927	91%
B.1.617.2 (Delta)	13958	5617 (40%)	385	5232	93%
BA.1 (Omicron)	543	100 (18%)	12	88	88%
B.1.427/B.1.429 (Epsilon)	359	304 (85%)	32	272	89%
B.1.526 (Iota)	142	83 (58%)	7	76	92%
P.1 (Gamma)	82	68 (83%)	9	59	87%
B.1.621/B.1.621.1 (Mu)	32	15 (47%)	6	9	60%
B.1.525 (Eta)	4	4 (100%)	1	3	75%
B.1.351 (Beta)	5	3 (60%)	0	3	100%
B.1.617.1 (Kappa)	2	1 (50%)	1	0	0%
Other lineage	1579	1268 (80%)	153	1115	88%

Number (%) of symptomatic cases reported by symptom category and variant

The table below includes data ONLY from symptomatic cases.

Variant	Upper Respiratory (Runny nose, sore throat)	Lower Respiratory (Cough, shortness of breath)	Gastrointestinal (Nausea/Vomiting, abdominal pain, diarrhea)	Systemic (Fever, chills, muscle Aches, headache, fatigue, loss of Appetite)	Loss of Taste and Smell
B.1.1.7 (Alpha)	626 (68%)	703 (76%)	385 (42%)	816 (88%)	347 (37%)
B.1.617.2 (Delta)	3410 (65%)	4121 (79%)	2309 (44%)	4618 (88%)	2517 (48%)
BA.1 (Omicron)	76 (86%)	70 (80%)	36 (41%)	79 (90%)	30 (34%)
B.1.427/B.1.429 (Epsilon)	195 (72%)	186 (68%)	118 (43%)	248 (91%)	140 (51%)
B.1.526 (Iota)	59 (78%)	57 (75%)	44 (58%)	72 (95%)	43 (57%)
P.1 (Gamma)	34 (58%)	50 (85%)	30 (51%)	48 (81%)	18 (31%)
B.1.621/B.1.621.1 (Mu)	7 (78%)	8 (89%)	3 (33%)	8 (89%)	5 (56%)
B.1.525 (Eta)	3 (100%)	3 (100%)	3 (100%)	3 (100%)	3 (100%)
Other lineage	747 (67%)	725 (65%)	424 (38%)	972 (87%)	491 (44%)

Number (%) of matched and sequenced specimens by any underlying condition and variant					
Lineage	Total	Total Investigated (%)	No	Yes	Percent Underlying Conditions (%)
B.1.1.7 (Alpha)	1344	1015 (76%)	534	481	47%
B.1.617.2 (Delta)	13958	5485 (39%)	4255	1230	22%
BA.1 (Omicron)	543	97 (18%)	91	6	6%
B.1.427/B.1.429 (Epsilon)	359	304 (85%)	196	108	36%
B.1.526 (Iota)	142	83 (58%)	43	40	48%
P.1 (Gamma)	82	67 (82%)	34	33	49%
B.1.621/B.1.621.1 (Mu)	32	10 (31%)	4	6	60%
B.1.525 (Eta)	4	4 (100%)	4	0	0%
B.1.617.1 (Kappa)	2	1 (50%)	1	0	0%
P.2 (Zeta)	1	0 (0%)	0	0	0%
Other lineage	1579	1258 (80%)	816	442	35%

Number (%) of sequenced specimens for cases reporting underlying conditions by specific condition and variant

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

Variant	Chronic Lung Disease	Chronic Liver Disease	Chronic Renal Disease	Diabetes Mellitus	Cardiovascular Disease	Autoimmune Disease	Neurological Disability	Current or Former Smoker
B.1.1.7 (Alpha)	110 (25%)	15 (3%)	17 (4%)	77 (17%)	143 (32%)	33 (7%)	28 (6%)	238 (53%)
B.1.617.2 (Delta)	234 (23%)	51 (5%)	118 (12%)	381 (38%)	358 (36%)	56 (6%)	72 (7%)	340 (34%)
BA.1 (Omicron)	1 (20%)	1 (20%)	0 (0%)	1 (20%)	1 (20%)	1 (20%)	1 (20%)	3 (60%)
B.1.427/B.1.429 (Epsilon)	25 (24%)	0 (0%)	4 (4%)	13 (12%))	22 (21%)	5 (5%)	7 (7%)	67 (63%)
B.1.526 (Iota)	11 (28%)	0 (0%)	0 (0%)	4 (10%)	8 (21%)	1 (3%)	1 (3%)	22 (56%)
P.1 (Gamma)	8 (28%)	0 (0%)	2 (7%)	4 (14%)	9 (31%)	2 (7%)	4 (14%)	21 (72%)
B.1.621/B.1.621.1 (Mu)	1 (20%)	0 (0%)	1 (20%)	1 (20%)	1 (20%)	1 (20%)	0 (0%)	3 (60%)
B.1.351 (Beta)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	0 (0%)	0 (0%)
Other lineage	118 (26%)	19 (4%)	18 (4%)	93 (20%)	151 (33%)	22 (5%)	31 (7%)	240 (52%)

Data Sources

- **COVID-19 data**
- **New Mexico Electronic Disease Surveillance System (NMEDSS)**, *Infectious Disease Epidemiology Bureau, Epidemiology and Response Division, New Mexico Department of Health*. Disease incidence data (counts) are derived from reports of notifiable infectious diseases. NMEDSS includes hospitalization counts for those reported with COVID-19. 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 from lack of awareness about reporting requirements or lack of compliance with those requirements. Not all cases of infectious diseases are detected for various reasons including lack of access to health care services and lack of laboratory testing. Specific and standardized national case definitions are used to classify disease reports by case status.
- **New Mexico Statewide Immunization Information System (NMSIIS)** is the immunization registry for the New Mexico Department of Health which includes patient and vaccination data submitted by healthcare providers, hospitals, schools and other vaccinating partners following administration of approved vaccines.
- **Salesforce/MTX COVID-19 Case Investigation Platform,** many case investigation were conducted on the Salesforce Software Platform to capture symptoms and underlying conditions. Not all cases were investigated. The Contact Tracing and Case Investigation Unit (CTCI) was operating at peak capacity from November 2019 to December 2020. Over the course of 2021 the program gradually pared down. In October 2022, the program was terminated. Therefore, reporting of symptoms and underlying conditions is not complete and may not reflect the experience of all cases.

- **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 laboratories 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: Variants of the Virus | CDC.
- **CDC COVID Data Tracker** CDC COVID Data Tracker.

Data Notes

The data presented here on the New Mexico Department of Health (NMDOH) dashboard may differ from data on Centers for Disease Control and Prevention (CDC) sites. This likely represents differing levels of data completeness. Data presented by the state are likely to be more complete.

Race/Ethnicity are reported as a single value. If a case is identified as Hispanic then the single category value is Hispanic. If a case is not identified as Hispanic, then the case is categorized by the reported race category.