

COVID-19 Variant of Concern (VOC) Case Report

October 11, 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

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, Delta. 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. The week of September 6, 2021, B.1.617.2 (Delta) represented approximately 96% of sequenced samples in New Mexico. Sequenced specimens reported from September 13-October 4, 2021 are incomplete but do indicate a continued predominance of Delta. CDC currently classifies all AY sublineage variants in combination with B.1.617.2 (Delta); however, AY.1 and AY.2 are reported separately due to a unique spike protein mutation (K417N). Studies indicate that vaccines authorized for use in the US are effective at preventing transmission, severe illness, and death caused by VOCs, including B.1.617.2 (Delta), and are the recommended measure to slow the emergence of new variants. Beginning August 20, 2021, NMDOH reinstated wearing masks in all indoor public settings to slow the spread of the highly transmissible Delta variant.

NM COVID-19 Variant Epidemiologic Interpretation

CDC VARIANTS OF CONCERN (VOC)			
Name	First Identified	Attributes ¹	New Mexico ²
Delta (B.1.617.2 and AY.1-AY.32)	India	-Increased transmissibility -May reduce effectiveness of antibody treatments -May cause more severe illness in unvaccinated persons -May reduce natural and vaccine immunity	-Since 6/28/21, Delta has remained the dominant VOC, and represented 96% of sequences reported on 9/06/21. -Proportion of deaths among cases caused by this variant have decreased from 4% to 2%.

CDC VARIANTS BEING MONITORED (VBM)			
Name³	First Identified	Attributes¹	New Mexico²
Alpha (B.1.1.7 and Q.1-Q.8)	United Kingdom	-50% more transmissible -Potential to cause more severe cases and deaths	-Alpha has proportionally declined from 81% the week of 5/24/21 to 0% of samples collected the week of 8/23/21. -Has not been observed in NM since 7/19/21.
Beta (B.1.351, B.1.351.2, and B.1.351.3)	South Africa	-50% more transmissible -Reduced effectiveness of antibody treatments -Reduced response of natural and vaccine induced immunity	- Least reported VOC in NM.
Gamma (P.1, P.1.1, and P.1.2)	Japan/Brazil	-Reduced effectiveness of some antibody treatments -Reduced response of natural and vaccine immunity	-Has varied between 0% and 8% since the week of 6/21/21, and represented 0% of sequences reported on 8/23/21. -Currently has the highest proportion of hospitalizations (24%); oversampling of severe cases may skew these results. -Has not been observed in NM since 7/26/21.
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 12/7/20 and has not been observed since 6/7/21; Epsilon peaked at 25% of sequenced NM specimens the week of 3/15/21.
Iota (B.1.526)	U.S.	-Downgraded from a VOI on September 21, 2021	-First case sequenced in NM the week of 2/22/21 and has not been observed since 6/28/21; Iota peaked at 11% of sequenced NM specimens the week of 5/31/21
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 7/26/21; during that time Mu fluctuated between 1-7% of NM cases.

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

²NM 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.

Cumulative number of Specimens Sequenced and Matched to Case Investigations

Lineage	Sequenced Cases	Matched Cases*	Percent Matched
Delta	3887	2549	66%
Alpha	1831	1537	84%
Beta	8	3	38%
Gamma	108	94	87%
Epsilon	517	425	82%
Eta	4	4	100%
Iota	87	73	84%
Kappa	2	2	100%
Zeta	3	2	67%
Mu	37	29	78%
Other lineage	4267	3371	79%
Total	10751	8089	75%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 166 sequences from patients who were tested at New Mexico facilities but reside outside New Mexico. These have been removed from the subsequent tables and figure

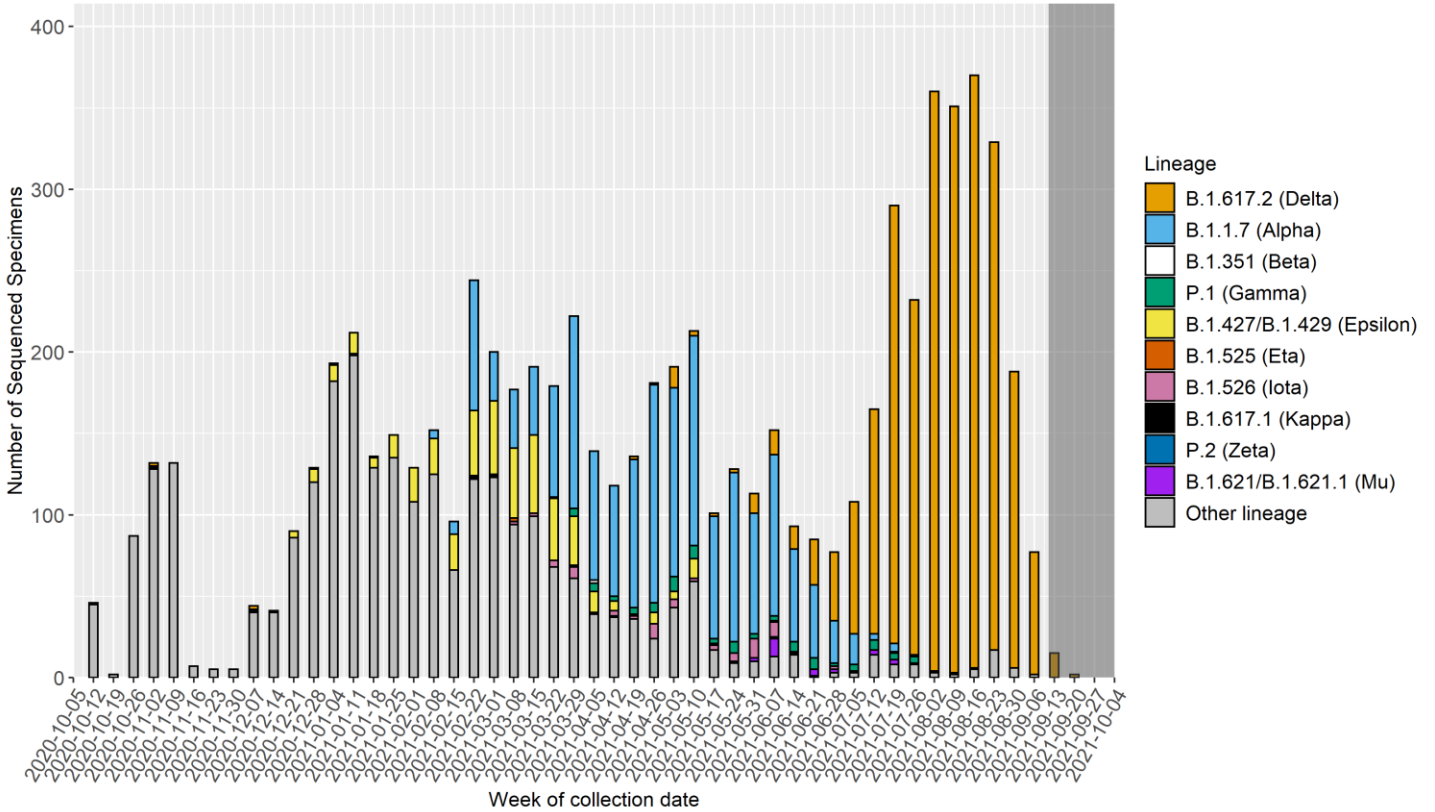
Cumulative number of variant cases, hospitalizations, and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
Delta	2504	274	11%	60	2%	766
Alpha	1521	144	9%	18	1%	89
Beta	3	0	0%	0	0%	0
Gamma	92	21	23%	2	2%	3
Epsilon	414	9	2%	1	0%	8
Eta	4	0	0%	0	0%	0
Iota	71	3	4%	0	0%	4
Kappa	2	0	0%	0	0%	0
Zeta	2	0	0%	0	0%	0
Mu	29	1	3%	0	0%	3
Other lineage	3278	212	6%	66	2%	36

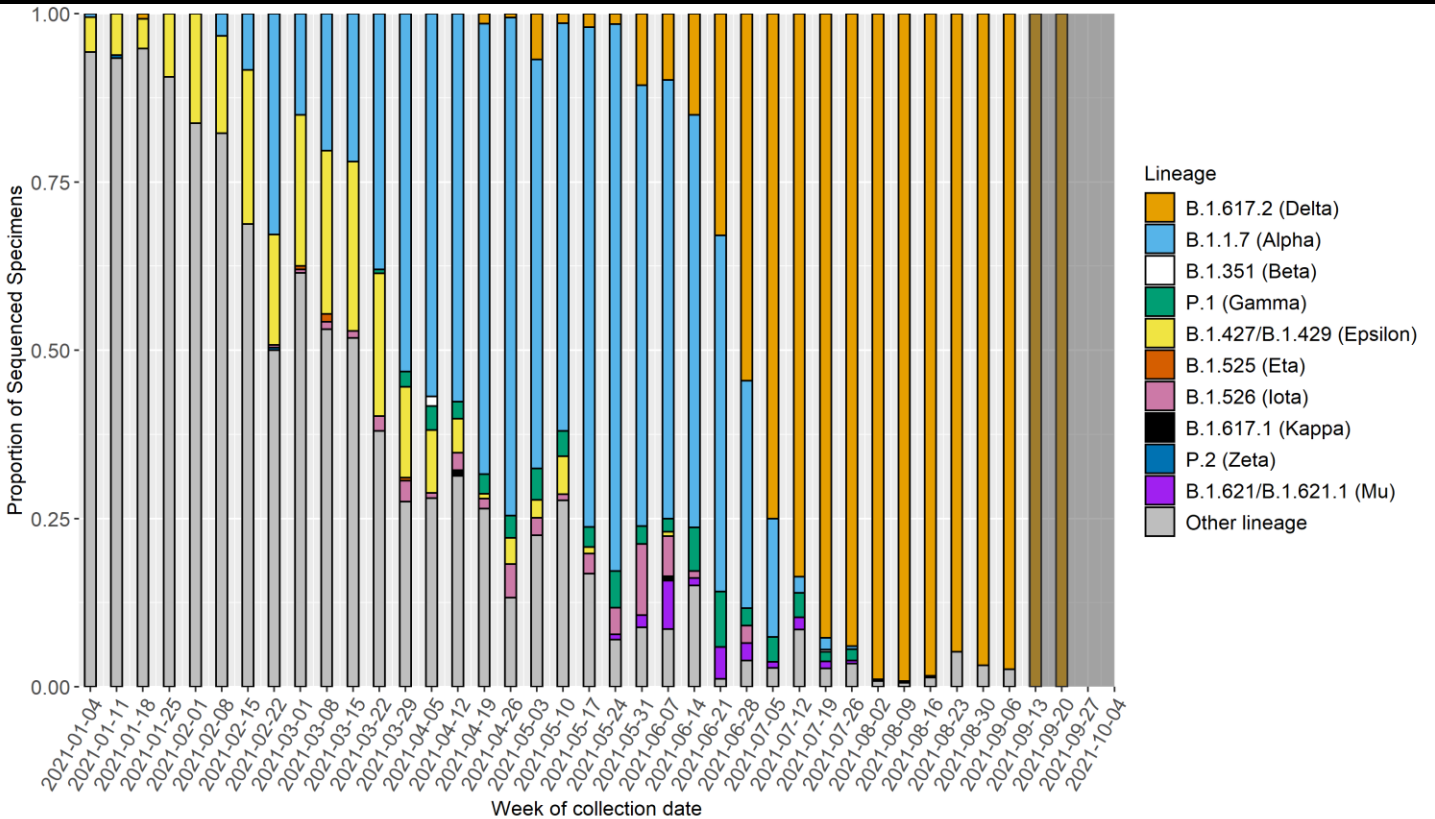
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥ 14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. Because samples collected from VBT cases are more frequently sequenced compared to samples from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

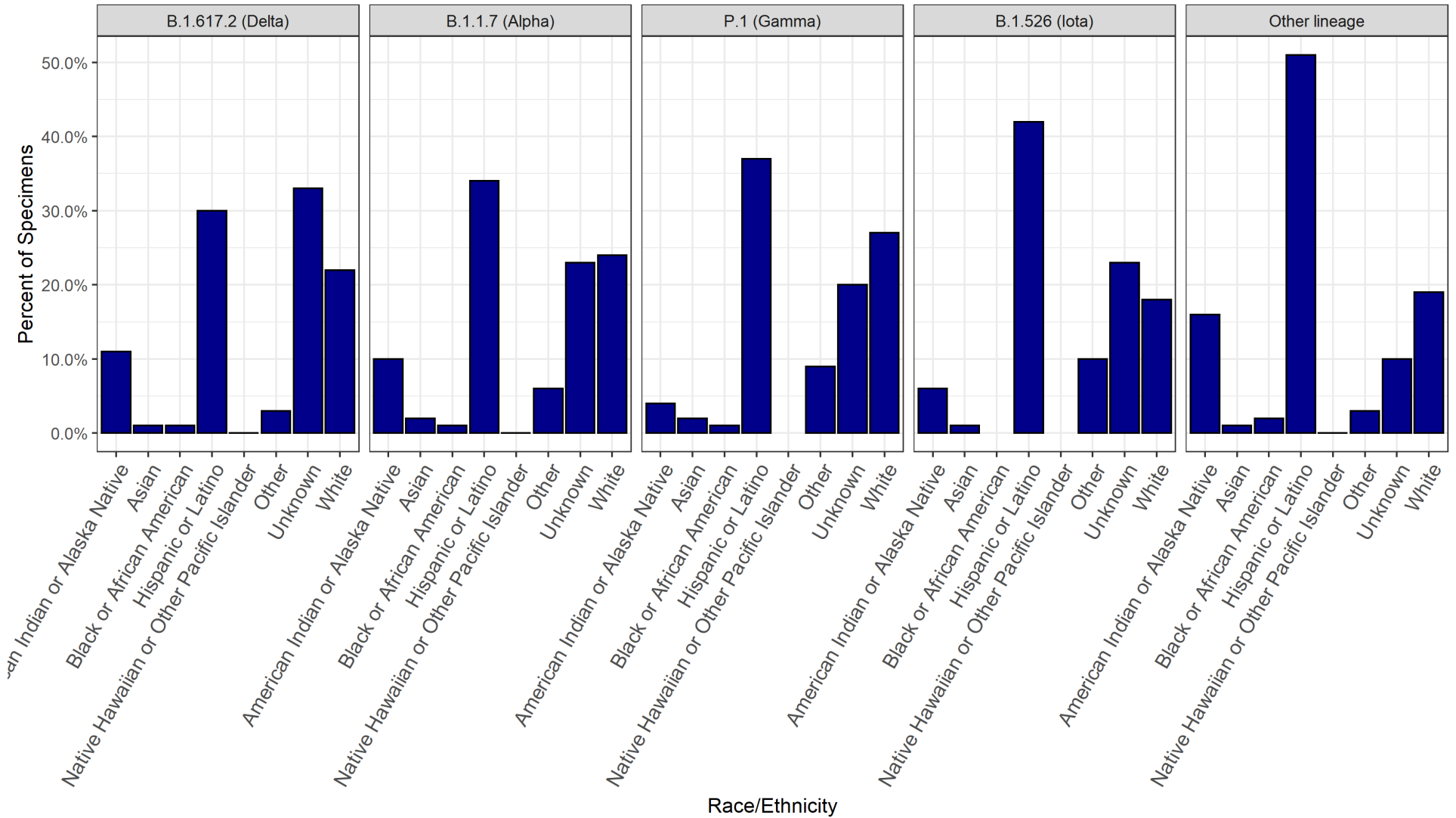


Proportion of identified SARS-CoV-2 lineages by week



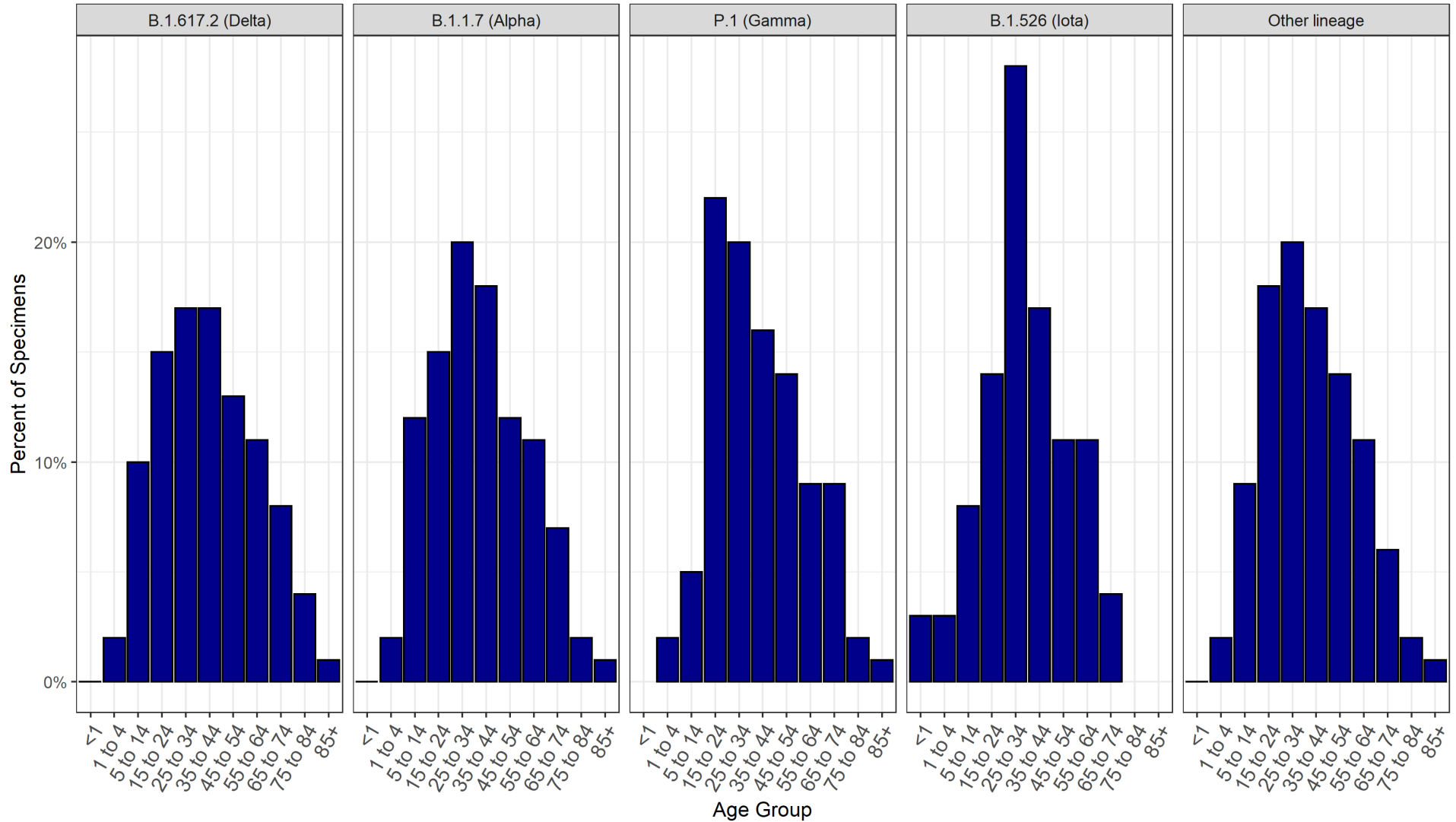
*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

Cumulative proportion of variant cases by Race/Ethnicity



*Only VOCs and VBMs with greater than 50 sequenced specimens in NM are reported and excludes Epsilon due to its diminishing proportion over time.

Cumulative proportion of variant cases by Age Group



*Only VOCs and VBMs with greater than 50 sequenced specimens in NM are reported and excludes Epsilon due to its diminishing proportion over time.

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	Delta	Alpha	Gamma	Iota	Other lineage
Bernalillo	772	448	17	18	1096
Chaves	81	13	0	0	60
Cibola	53	13	0	1	115
Colfax	69	24	0	0	31
Curry	55	24	0	10	32
Dona Ana	148	81	6	0	428
Eddy	152	20	0	5	99
Grant	18	13	2	0	35
Guadalupe	47	1	0	0	21
Hidalgo	7	0	0	0	1
Lea	24	15	1	0	113
Lincoln	23	5	3	1	58
Los Alamos	21	9	0	0	24
Luna	7	14	0	0	21
McKinley	48	19	0	0	125
Otero	160	25	2	1	154
Quay	13	3	1	2	0
Rio Arriba	51	91	1	1	39
Roosevelt	4	0	0	0	13
San Juan	201	312	28	2	300
San Miguel	69	10	0	0	55
Sandoval	152	73	6	7	240
Santa Fe	144	96	0	5	300
Sierra	8	5	0	0	6
Socorro	27	9	0	0	30
Taos	24	15	0	0	40
Torrance	24	15	1	15	57
Valencia	80	68	5	3	120

*Only VOCs and VBMs with greater than 50 sequenced specimens in NM are reported and excludes Epsilon due to its diminishing proportion over time.

Percentage of variant cases reporting any symptoms

Lineage	No Symptoms	Unknown Symptoms	Yes Symptoms	Total Cases	Percent Symptomatic
Delta	58	1064	1382	2504	55%
Alpha	101	379	1041	1521	68%
Gamma	10	17	65	92	71%
Iota	4	22	45	71	63%
Other lineage	403	875	2454	3732	66%

Percentage of specific symptoms reported by symptomatic variant cases

The table below includes data ONLY from symptomatic cases.

Symptom	Delta	Alpha	Gamma	Iota	Other lineage
Fever (Measured or Subjective)	56% (767)	47% (479)	50% (32)	51% (23)	43% (1043)
Chills	47% (641)	46% (468)	59% (38)	51% (23)	45% (1085)
Muscle Aches	56% (766)	57% (583)	53% (34)	53% (24)	56% (1348)
Runny Nose	54% (740)	53% (541)	45% (29)	56% (25)	53% (1289)
Sore Throat	46% (625)	45% (459)	45% (29)	44% (20)	43% (1032)
Cough	75% (1025)	74% (757)	83% (53)	69% (31)	64% (1556)
Shortness of Breath	29% (402)	29% (299)	39% (25)	36% (16)	24% (588)
Nausea/Vomiting	27% (366)	27% (275)	34% (22)	38% (17)	23% (550)
Headache	65% (887)	66% (674)	50% (32)	82% (37)	66% (1588)
Abdominal Pain	15% (202)	15% (158)	16% (10)	20% (9)	14% (339)
Diarrhea	29% (399)	29% (293)	23% (15)	36% (16)	27% (642)
Fatigue	68% (925)	70% (719)	69% (44)	87% (39)	66% (1593)
Loss of Appetite	39% (530)	40% (409)	36% (23)	47% (21)	36% (873)
Loss of Taste or Smell	46% (623)	39% (402)	34% (22)	51% (23)	44% (1062)

* Only VOCs and VBM with greater than 50 sequenced specimens in NM are reported and excludes Epsilon due to its diminishing proportion over time.

Percentage of variant cases reporting underlying conditions

Lineage	No	Unknown	Yes	Total Cases	Percent with underlying conditions
Delta	344	1674	486	2504	19%
Alpha	611	393	517	1521	34%
Gamma	40	17	35	92	38%
Iota	25	24	22	71	31%
Other lineage	1676	994	1062	3732	29%

Percentage of specific underlying conditions reported by variant cases

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

Condition	Delta	Alpha	Gamma	Iota	Other lineage
Chronic Lung Disease	27% (120)	25% (128)	27% (8)	14% (3)	27% (256)
Chronic Liver Disease	4% (19)	3% (16)	0% (0)	0% (0)	4% (37)
Chronic Renal Disease	9% (40)	4% (18)	7% (2)	0% (0)	5% (44)
Diabetes Mellitus	28% (126)	19% (95)	13% (4)	9% (2)	22% (209)
Cardiovascular Disease	35% (158)	32% (163)	30% (9)	23% (5)	28% (268)
Autoimmune Disease	6% (29)	7% (38)	7% (2)	5% (1)	5% (45)
Neurological Disability	6% (28)	6% (30)	13% (4)	0% (0)	9% (82)
Current or Former Smoker	44% (197)	54% (273)	73% (22)	64% (14)	50% (482)

* Note: One P.1 variant case reported an underlying condition that is not included on the list above.

** Only VOCs and VBM with greater than 50 sequenced specimens in NM are reported and excludes Epsilon due to its diminishing proportion over time.

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.