

COVID-19 Variant of Concern (VOC) Case Report

October 18, 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 13, 2021, B.1.617.2 (Delta) represented approximately 99% of sequenced samples in New Mexico. Sequenced specimens reported from September 20-October 11, 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 99% of sequences reported on 9/13/21. -Proportion of deaths is currently 3%.

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 2% of samples collected the week of 7/19/21. -Has not been observed in NM since 8/16/21.
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	-First case sequenced in NM the week of 3/22/21 and has not been observed since 8/9/2021; Gamma peaked at 8% 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.
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 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 10% 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; Mu peaked at 7% of sequenced NM specimens the week of 6/7/21.

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	4491	3113	69%
Alpha	1826	1558	85%
Beta	8	3	38%
Gamma	108	95	88%
Epsilon	517	426	82%
Eta	4	4	100%
Iota	87	73	84%
Kappa	2	2	100%
Zeta	3	2	67%
Mu	37	29	78%
Other lineage	4288	3378	79%
Total	11371	8683	76%

*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

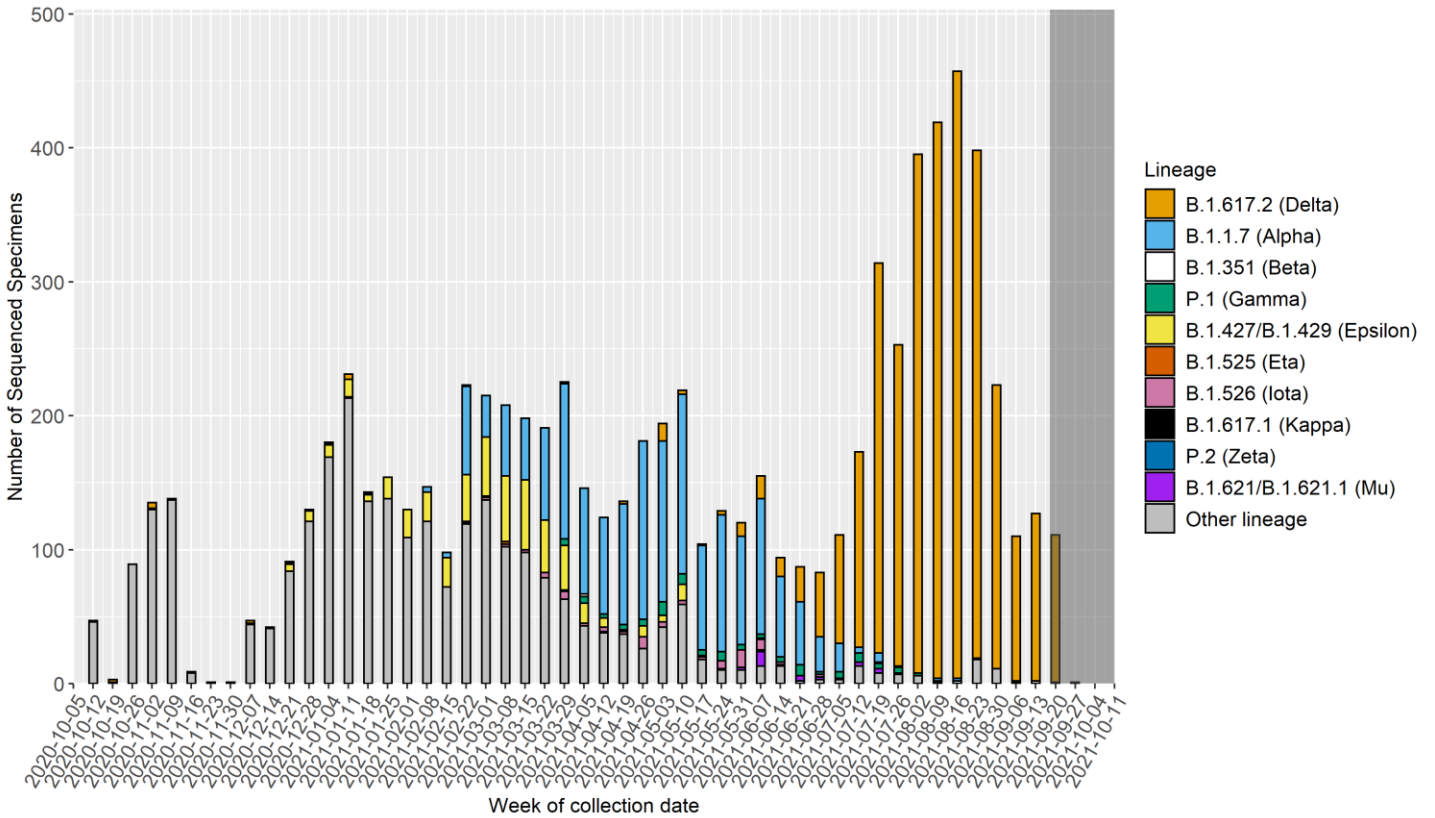
Cumulative number of variant cases, hospitalizations, and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
Delta	3113	355	11%	77	2%	925
Alpha	1558	156	10%	20	1%	94
Beta	3	0	0%	0	0%	0
Gamma	95	24	25%	2	2%	3
Epsilon	426	9	2%	2	0%	8
Eta	4	0	0%	0	0%	0
Iota	73	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	3378	224	7%	67	2%	36

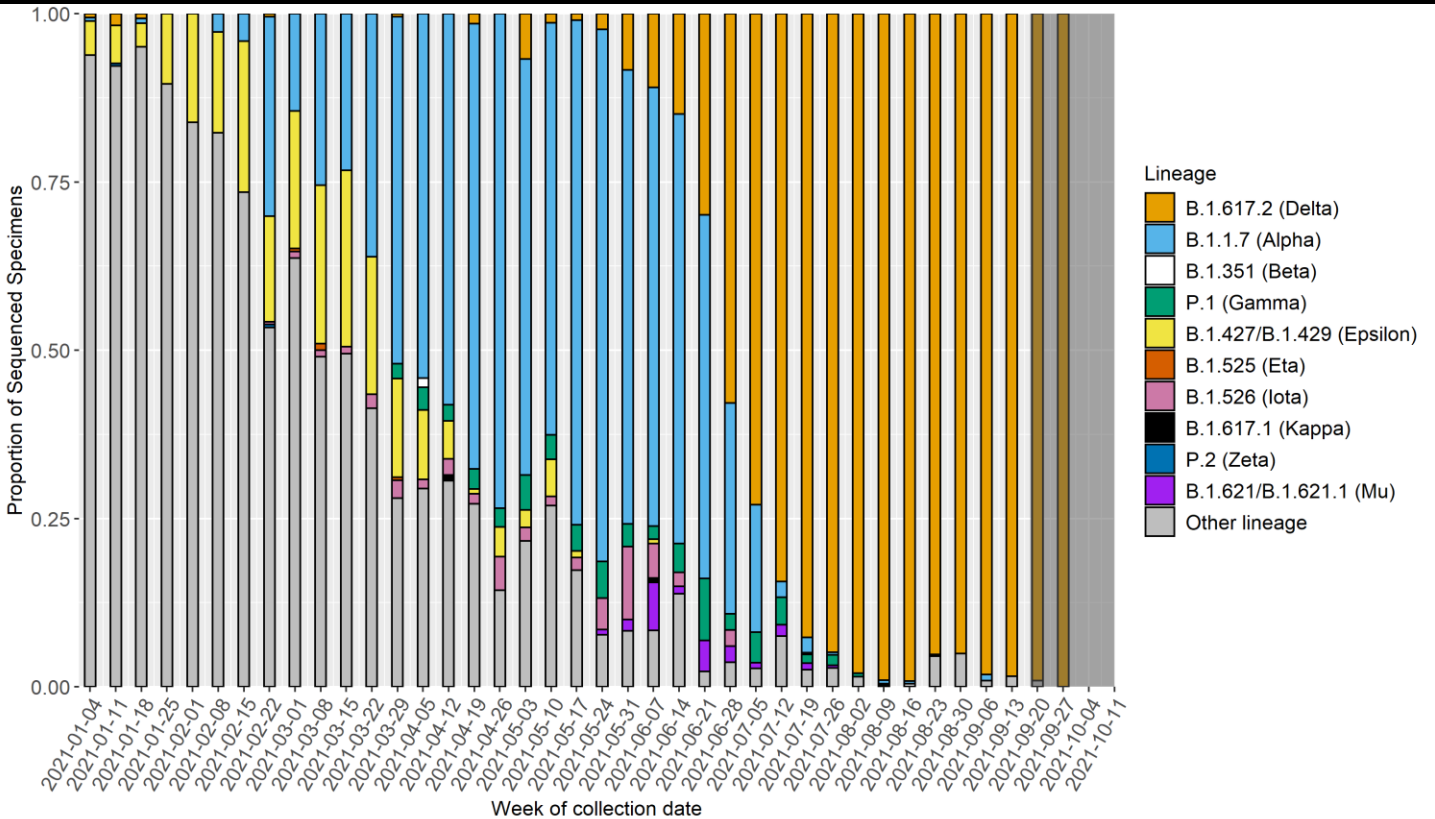
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥ 14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. Because samples collected from VBT cases are more frequently sequenced compared to samples from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

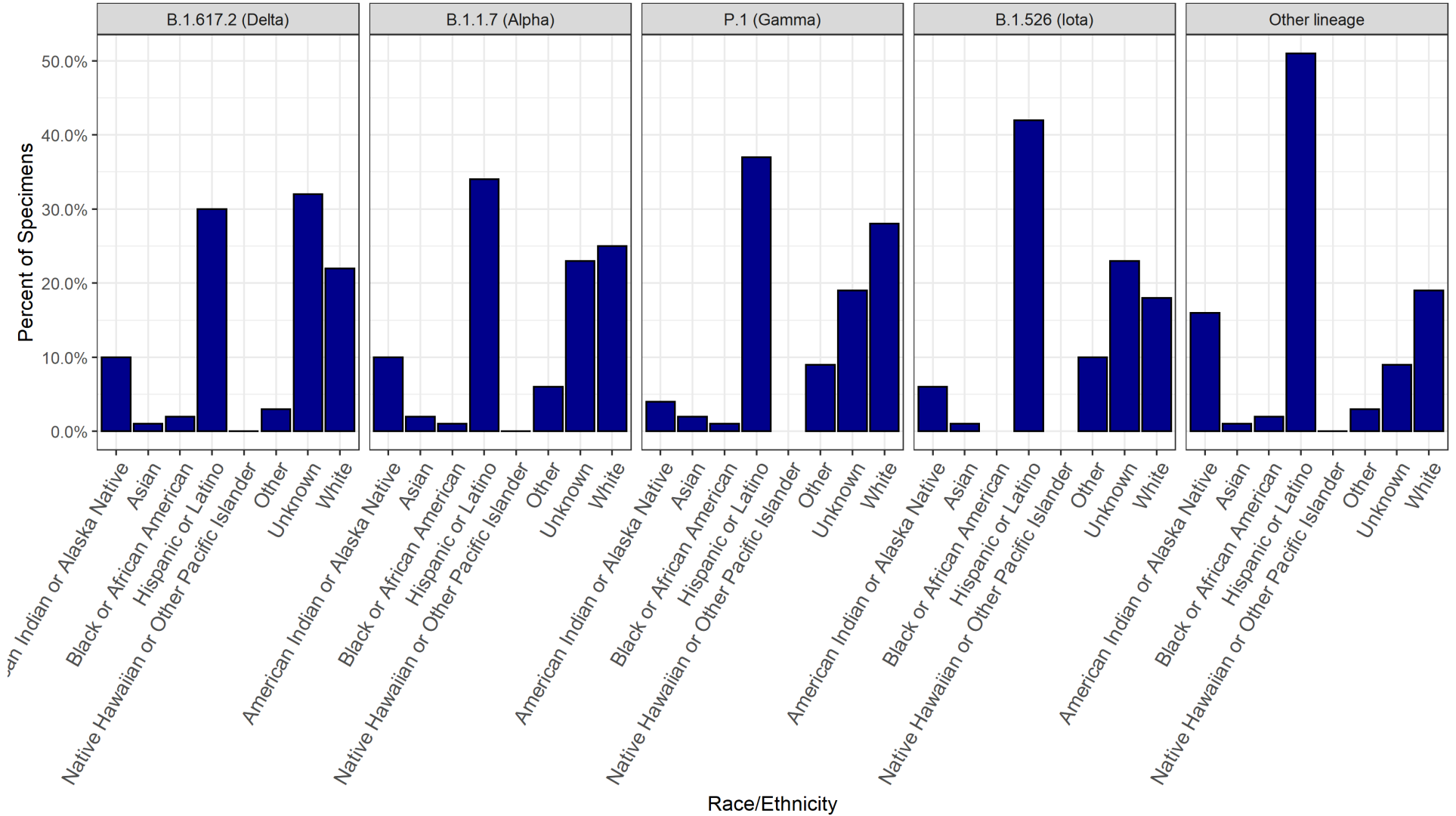


Proportion of identified SARS-CoV-2 lineages by week



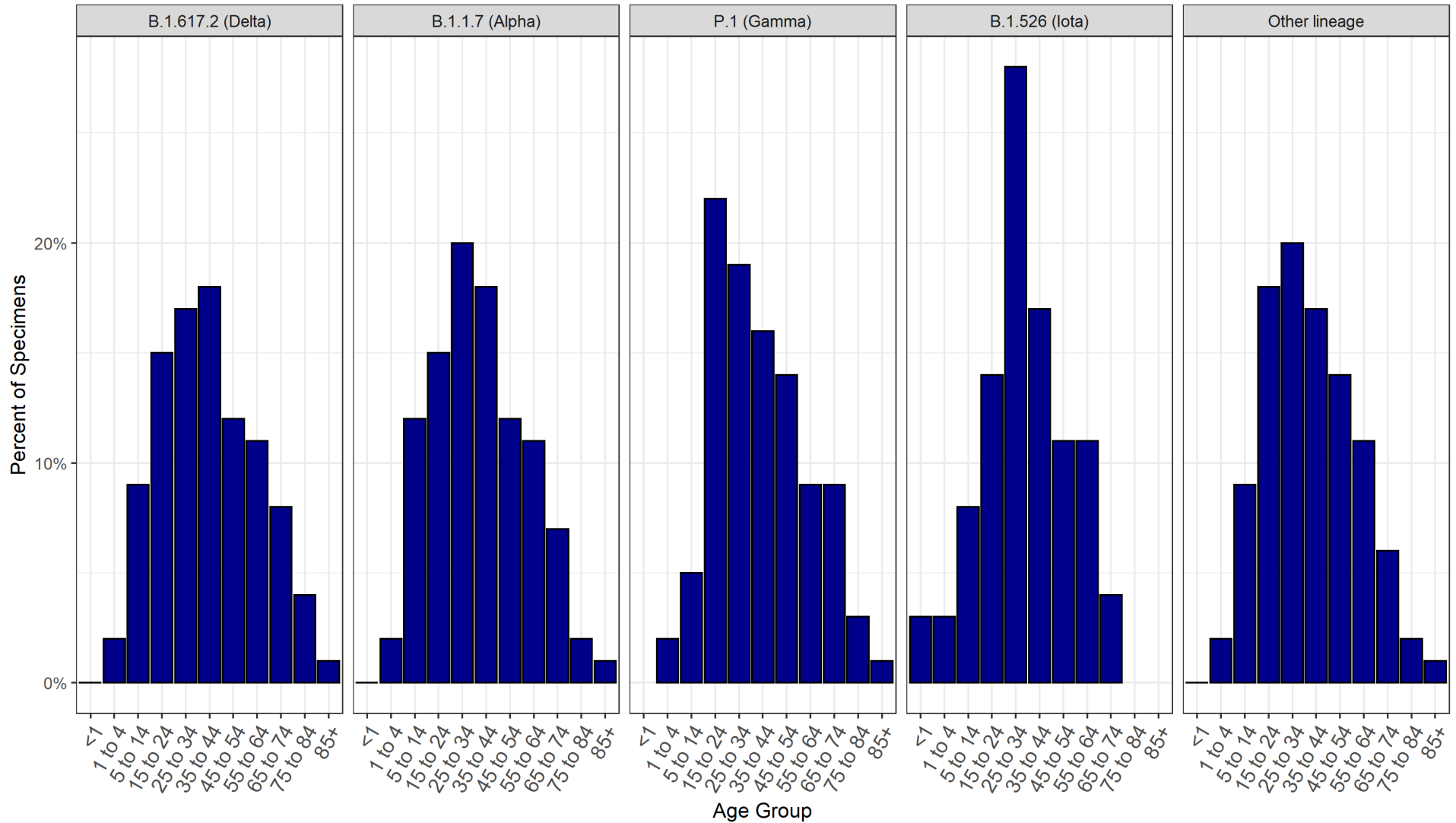
*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

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	893	450	17	18	1098
Chaves	108	13	0	0	62
Cibola	75	13	0	1	115
Colfax	78	24	0	0	31
Curry	86	26	0	10	32
Dona Ana	173	82	6	0	428
Eddy	197	20	0	5	99
Grant	21	13	2	0	35
Guadalupe	46	1	0	0	21
Hidalgo	8	0	0	0	1
Lea	73	16	1	0	113
Lincoln	26	5	4	1	58
Los Alamos	22	9	0	0	24
Luna	8	14	0	0	21
McKinley	53	19	0	0	128
Otero	201	25	2	1	154
Quay	16	3	1	2	0
Rio Arriba	55	92	1	1	40
Roosevelt	4	0	0	0	13
San Juan	222	322	28	2	300
San Miguel	89	10	0	0	55
Sandoval	176	75	6	7	239
Santa Fe	189	97	0	5	300
Sierra	8	5	0	0	6
Socorro	34	9	0	0	30
Taos	29	16	0	0	40
Torrance	41	16	1	15	57
Valencia	106	69	5	3	120

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Percentage of variant cases reporting any symptoms

Lineage	No Symptoms	Unknown Symptoms	Yes Symptoms	Total Cases	Percent Symptomatic
Delta	82	1388	1643	3113	53%
Alpha	107	386	1065	1558	68%
Gamma	10	17	68	95	72%
Iota	4	24	45	73	62%
Other lineage	413	941	2490	3844	65%

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% (902)	47% (490)	51% (34)	51% (23)	43% (1061)
Chills	47% (756)	46% (485)	60% (40)	51% (23)	45% (1100)
Muscle Aches	55% (901)	57% (598)	57% (38)	53% (24)	56% (1369)
Runny Nose	54% (869)	53% (554)	46% (31)	56% (25)	53% (1304)
Sore Throat	45% (732)	45% (468)	49% (33)	44% (20)	43% (1045)
Cough	75% (1221)	74% (775)	85% (57)	69% (31)	64% (1572)
Shortness of Breath	30% (481)	30% (310)	42% (28)	36% (16)	24% (593)
Nausea/Vomiting	26% (427)	28% (289)	34% (23)	38% (17)	23% (554)
Headache	65% (1060)	66% (688)	52% (35)	82% (37)	66% (1613)
Abdominal Pain	14% (232)	16% (163)	16% (11)	20% (9)	14% (343)
Diarrhea	30% (481)	29% (301)	27% (18)	36% (16)	26% (649)
Fatigue	68% (1099)	70% (736)	70% (47)	87% (39)	66% (1617)
Loss of Appetite	39% (636)	41% (425)	37% (25)	47% (21)	36% (883)
Loss of Taste or Smell	47% (759)	39% (409)	34% (23)	51% (23)	44% (1074)

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Percentage of variant cases reporting underlying conditions

Lineage	No	Unknown	Yes	Total Cases	Percent with underlying conditions
Delta	388	2176	549	3113	18%
Alpha	625	401	532	1558	34%
Gamma	41	17	37	95	39%
Iota	25	26	22	73	30%
Other lineage	1699	1062	1083	3844	28%

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	26% (130)	25% (132)	29% (9)	14% (3)	26% (257)
Chronic Liver Disease	4% (22)	3% (16)	0% (0)	0% (0)	4% (38)
Chronic Renal Disease	9% (44)	4% (21)	6% (2)	0% (0)	5% (44)
Diabetes Mellitus	28% (142)	19% (100)	13% (4)	9% (2)	22% (214)
Cardiovascular Disease	35% (176)	32% (167)	29% (9)	23% (5)	28% (272)
Autoimmune Disease	7% (34)	8% (40)	6% (2)	5% (1)	5% (45)
Neurological Disability	6% (31)	6% (32)	13% (4)	0% (0)	8% (82)
Current or Former Smoker	43% (218)	54% (283)	74% (23)	64% (14)	50% (488)

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

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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.