

COVID-19 Variant of Concern (VOC) Case Report

October 4, 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 August 30, 2021, B.1.617.2 (Delta) represented approximately 97% of sequenced samples in New Mexico. Sequenced specimens reported from August 30-September 20, 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 97% of sequences reported on 8/30/21. -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.
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.
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 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 7/19/21; 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
B.1.617.2 (Delta)	3194	2382	75%
B.1.1.7 (Alpha)	1830	1556	85%
B.1.351 (Beta)	7	3	43%
P.1 (Gamma)	108	95	88%
B.1.427/B.1.429 (Epsilon)	517	426	82%
B.1.525 (Eta)	4	4	100%
B.1.526 (Iota)	87	73	84%
B.1.617.1 (Kappa)	2	2	100%
P.2 (Zeta)	3	2	67%
B.1.621/B.1.621.1 (Mu)	36	28	78%
Other lineage	4230	3345	79%
Total	10018	7916	79%

*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

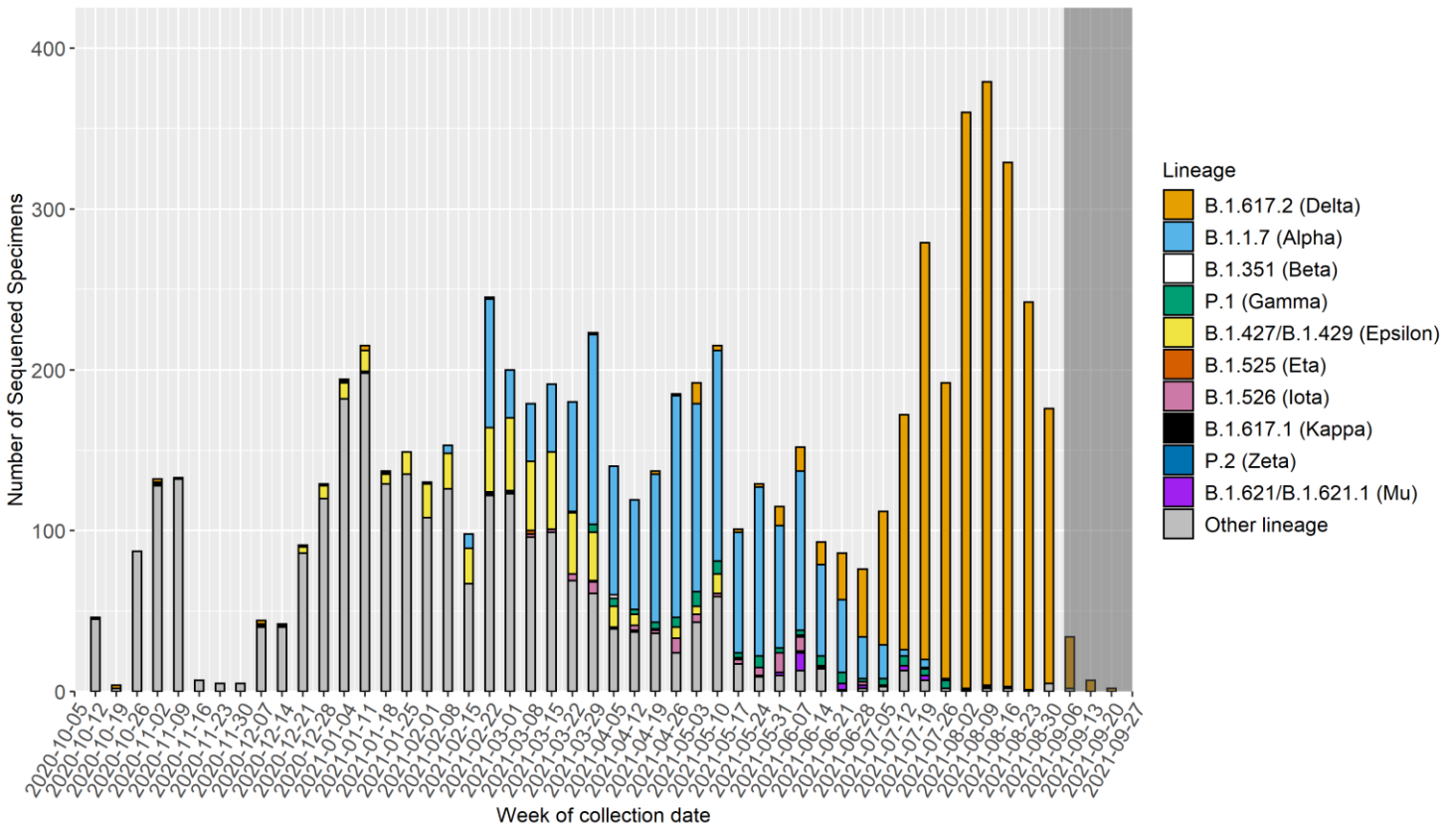
Cumulative number of variant cases, hospitalizations, and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
B.1.617.2 (Delta)	2341	246	11%	57	2%	703
B.1.1.7 (Alpha)	1539	150	10%	20	1%	94
B.1.351 (Beta)	3	0	0%	0	0%	0
P.1 (Gamma)	93	22	24%	2	2%	3
B.1.427/B.1.429 (Epsilon)	415	9	2%	1	0%	0
B.1.525 (Eta)	4	0	0%	0	0%	0
B.1.526 (Iota)	71	3	4%	0	0%	0
B.1.617.1 (Kappa)	2	0	0%	0	0%	0
P.2 (Zeta)	2	0	0%	0	0%	0
B.1.621/B.1.621.1 (Mu)	28	1	4%	0	0%	0
Other lineage	3252	210	6%	66	2%	43

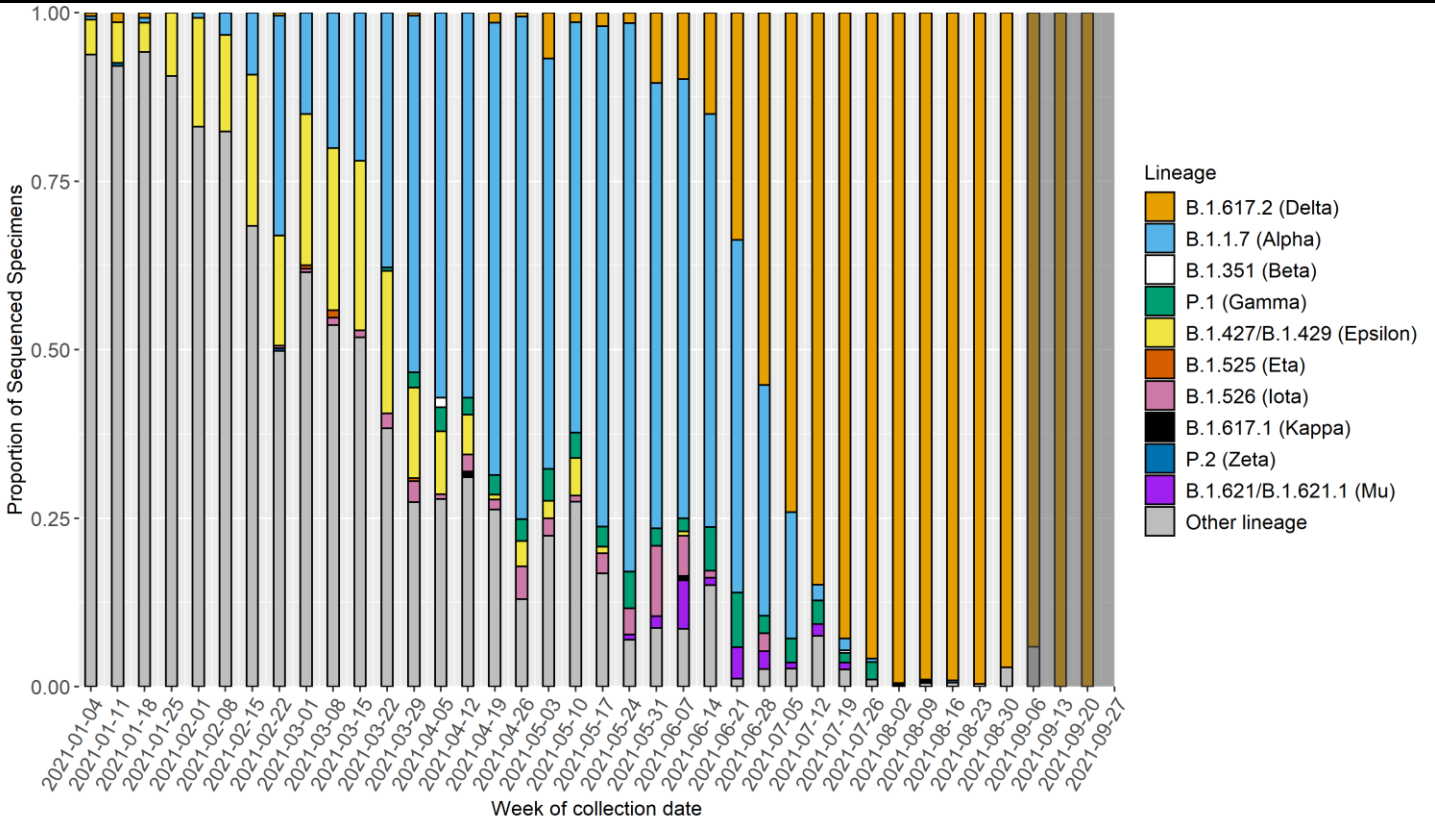
*A vaccine breakthrough (VBT) case is defined as a person who tests positive ≥ 14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. Because samples collected from VBT cases are more frequently sequenced compared to samples from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

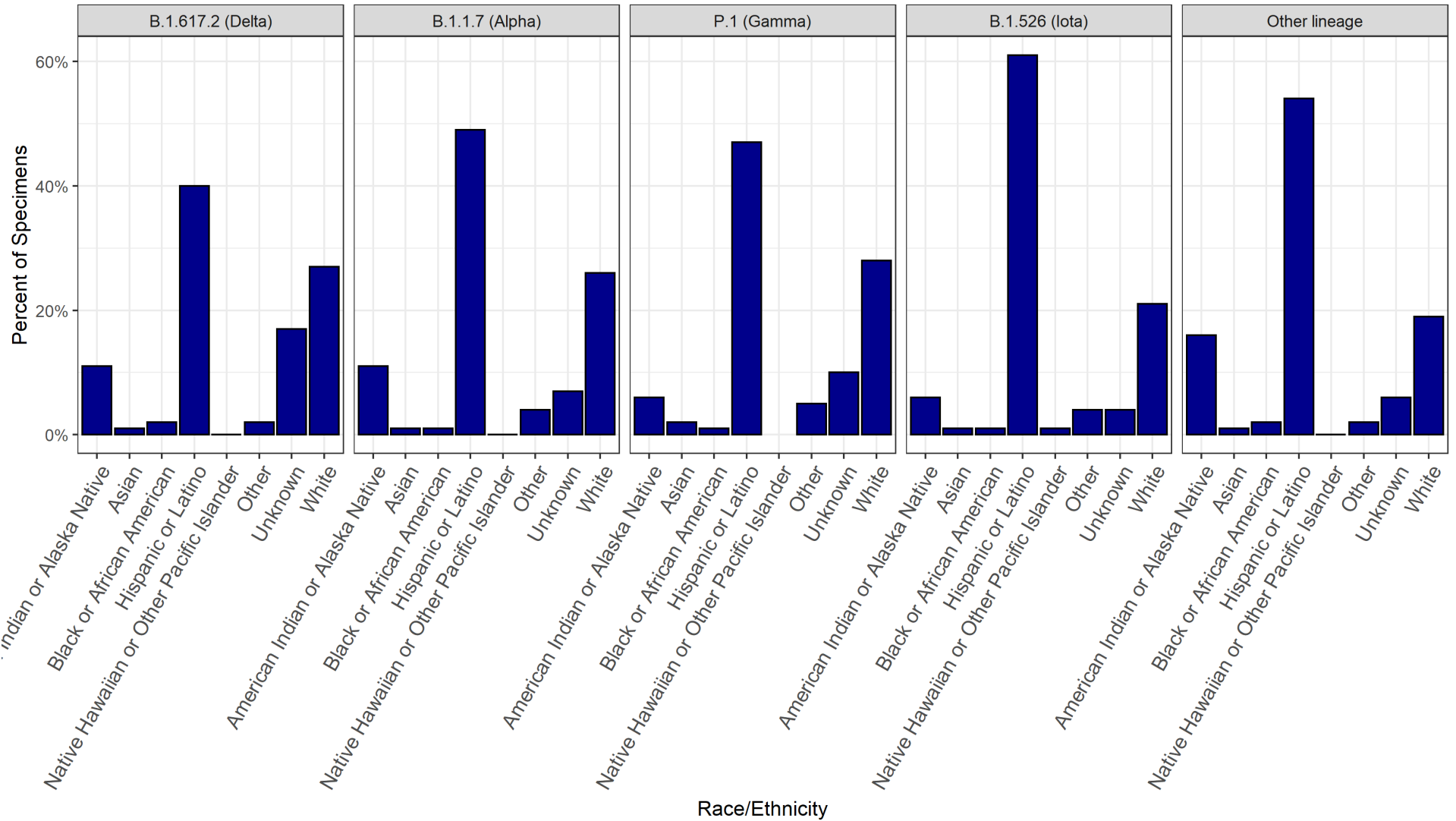


Proportion of identified SARS-CoV-2 lineages by week



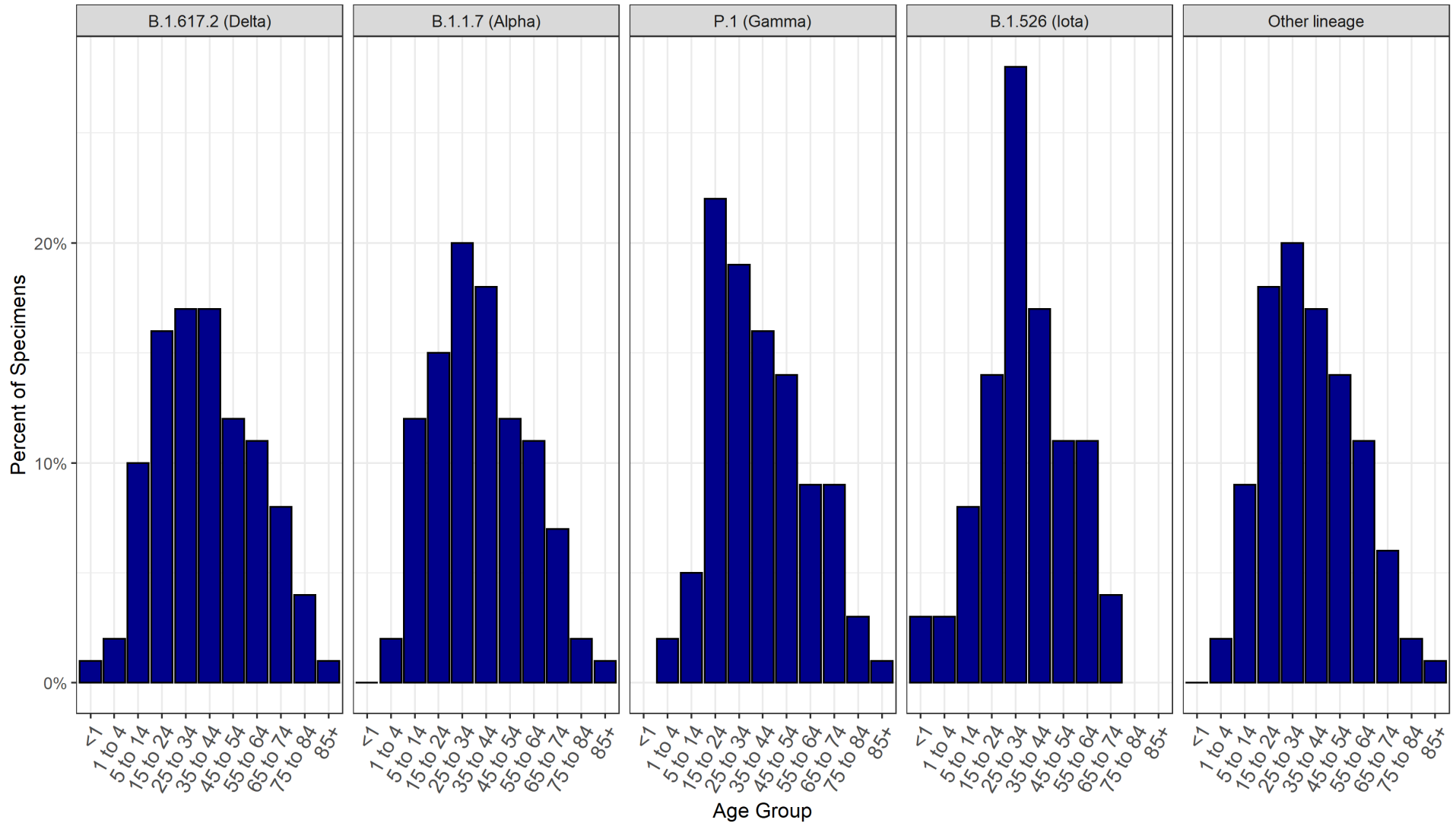
*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

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	B.1.617.2 (Delta)	B.1.1.7 (Alpha)	P.1 (Gamma)	B.1.526 (Iota)	Other lineage
Bernalillo	735	450	17	18	1087
Chaves	56	13	0	0	60
Cibola	53	13	0	1	115
Colfax	69	24	0	0	30
Curry	59	24	0	10	29
Dona Ana	134	82	6	0	425
Eddy	131	20	0	5	98
Grant	17	13	2	0	35
Guadalupe	42	1	0	0	19
Lea	33	16	1	0	113
Lincoln	20	5	4	1	58
Los Alamos	21	9	0	0	24
Luna	8	14	0	0	20
McKinley	45	18	0	0	126
Otero	130	25	2	1	151
Quay	14	3	1	2	0
Rio Arriba	47	92	1	1	39
Roosevelt	3	0	0	0	12
San Juan	190	321	28	2	299
San Miguel	70	10	0	0	55
Sandoval	138	75	6	7	239
Santa Fe	133	97	0	5	296
Sierra	8	5	0	0	5
Socorro	25	9	0	0	32
Taos	24	15	0	0	40
Torrance	28	16	1	15	57
Valencia	82	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
B.1.617.2 (Delta)	62	985	1294	2341	55%
B.1.1.7 (Alpha)	101	383	1055	1539	69%
P.1 (Gamma)	10	17	66	93	71%
B.1.526 (Iota)	4	22	45	71	63%
Other lineage	400	866	2440	3706	66%

Percentage of specific symptoms reported by symptomatic variant cases*

The table below includes data ONLY from symptomatic cases.

Symptom	B.1.617.2 (Delta)	B.1.1.7 (Alpha)	P.1 (Gamma)	B.1.526 (Iota)	Other lineage
Fever (Measured or Subjective)	56% (713)	47% (483)	49% (32)	51% (23)	43% (1033)
Chills	47% (603)	46% (479)	58% (38)	51% (23)	45% (1078)
Muscle Aches	56% (718)	57% (594)	54% (35)	53% (24)	56% (1342)
Runny Nose	54% (690)	53% (550)	46% (30)	56% (25)	53% (1280)
Sore Throat	46% (585)	45% (465)	46% (30)	44% (20)	43% (1024)
Cough	75% (961)	74% (767)	83% (54)	69% (31)	64% (1542)
Shortness of Breath	28% (356)	29% (305)	40% (26)	36% (16)	24% (581)
Nausea/Vomiting	26% (331)	27% (284)	34% (22)	38% (17)	23% (546)
Headache	65% (834)	66% (683)	51% (33)	82% (37)	65% (1575)
Abdominal Pain	15% (190)	16% (163)	15% (10)	20% (9)	14% (339)
Diarrhea	29% (367)	29% (300)	25% (16)	36% (16)	26% (637)
Fatigue	67% (859)	70% (731)	69% (45)	87% (39)	66% (1586)
Loss of Appetite	38% (486)	41% (420)	35% (23)	47% (21)	36% (869)
Loss of Taste or Smell	46% (588)	39% (408)	34% (22)	51% (23)	44% (1055)

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Percentage of variant cases reporting underlying conditions**

Lineage	No	Unknown	Yes	Total Cases	Percent with underlying conditions
B.1.617.2 (Delta)	353	1535	453	2341	19%
B.1.1.7 (Alpha)	618	396	525	1539	34%
P.1 (Gamma)	40	17	36	93	39%
B.1.526 (Iota)	25	24	22	71	31%
Other lineage	1674	972	1060	3706	29%

Percentage of specific underlying conditions reported by variant cases**

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

Condition	B.1.617.2 (Delta)	B.1.1.7 (Alpha)	P.1 (Gamma)	B.1.526 (Iota)	Other lineage
Chronic Lung Disease	26% (108)	26% (132)	26% (8)	14% (3)	27% (255)
Chronic Liver Disease	4% (19)	3% (16)	0% (0)	0% (0)	4% (38)
Chronic Renal Disease	8% (35)	4% (20)	6% (2)	0% (0)	5% (44)
Diabetes Mellitus	27% (116)	19% (98)	13% (4)	9% (2)	22% (209)
Cardiovascular Disease	35% (150)	32% (166)	29% (9)	23% (5)	28% (269)
Autoimmune Disease	6% (27)	8% (39)	6% (2)	5% (1)	5% (45)
Neurological Disability	6% (27)	6% (31)	13% (4)	0% (0)	9% (82)
Current or Former Smoker	44% (187)	54% (279)	74% (23)	64% (14)	50% (480)

* 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.