

COVID-19 Variant of Concern (VOC) Case Report

July 12, 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 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. To date there are no variants that have demonstrated the ability to evade vaccine or natural immunity. Only a small proportion of COVID-19 cases have been sequenced to identify whether they are a VOC since readily available diagnostic tests do not test for specific variant strains and must be sent to a lab for sequencing.

CDC has identified four VOCs in the US. In New Mexico, all four SARS-CoV-2 VOCs have been detected: 1) B.1.1.7 (Alpha), 2) B.1.351 (Beta), 3) B.1.617.2 (Delta), and 4) P.1 (Gamma). While B.1.617.2 (Delta) currently represents a relatively small proportion of sequenced samples in New Mexico, observations from other countries and model projections predict that the proportion will continue to grow and will likely become the dominant variant in the US and New Mexico. On July 6, 2021, the CDC announced that sublineage variants AY.1 and AY.2 will be reported in combination with B.1.617.2 (Delta). Studies indicate that vaccines authorized for use in the US are effective at preventing transmission of COVID-19 VOCs, including B.1.617.2 (Delta), and are the recommended measure to slow the emergence of new variants.

Cumulative number of Specimens Sequenced and Matched to Case Investigations

Lineage	Sequenced Cases	Matched Cases*	Percent Matched
B.1.1.7 (Alpha)	1357	922	68%
B.1.351 (Beta)	3	0	0%
P.1 (Gamma)	52	47	90%
B.1.617.2 (Delta)	58	52	90%
Other lineage	4368	3267	75%
Total	5838	4288	73%

*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 73 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.

NM COVID-19 VOC Epidemiologic Interpretation

Name	First Identified	Attributes ¹	New Mexico ²
B.1.1.7 (Alpha)	United Kingdom	-50% more transmissible -Potential to cause more severe cases and deaths	-Dominant strain in NM but proportionally declining from 77% the week of 5/24/21 to 54% of samples collected the week of 6/7/21.
B.1.351 (Beta)	South Africa	-50% more transmissible -Reduced effectiveness of antibody treatments -Reduced response of natural and vaccine induced immunity	- Least reported VOC in NM.
B.1.617.2 (Delta)	India	-Increased transmissibility -May reduce effectiveness of antibody treatments -May reduce natural and vaccine immunity	-Delta increased to 11% of sequenced specimens as of 6/7/21 suggesting an increasing trend. -Proportion of deaths among cases caused by this variant have decreased from 6% to 4%.
P.1 (Gamma)	Japan/Brazil	-Reduced effectiveness of some antibody treatments -Reduced response of natural and vaccine immunity	-Has been fluctuating between 1% and 7% since the week of 3/29/21. -Currently has the highest proportion of hospitalizations (28%); oversampling of severe cases may skew these results.

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.

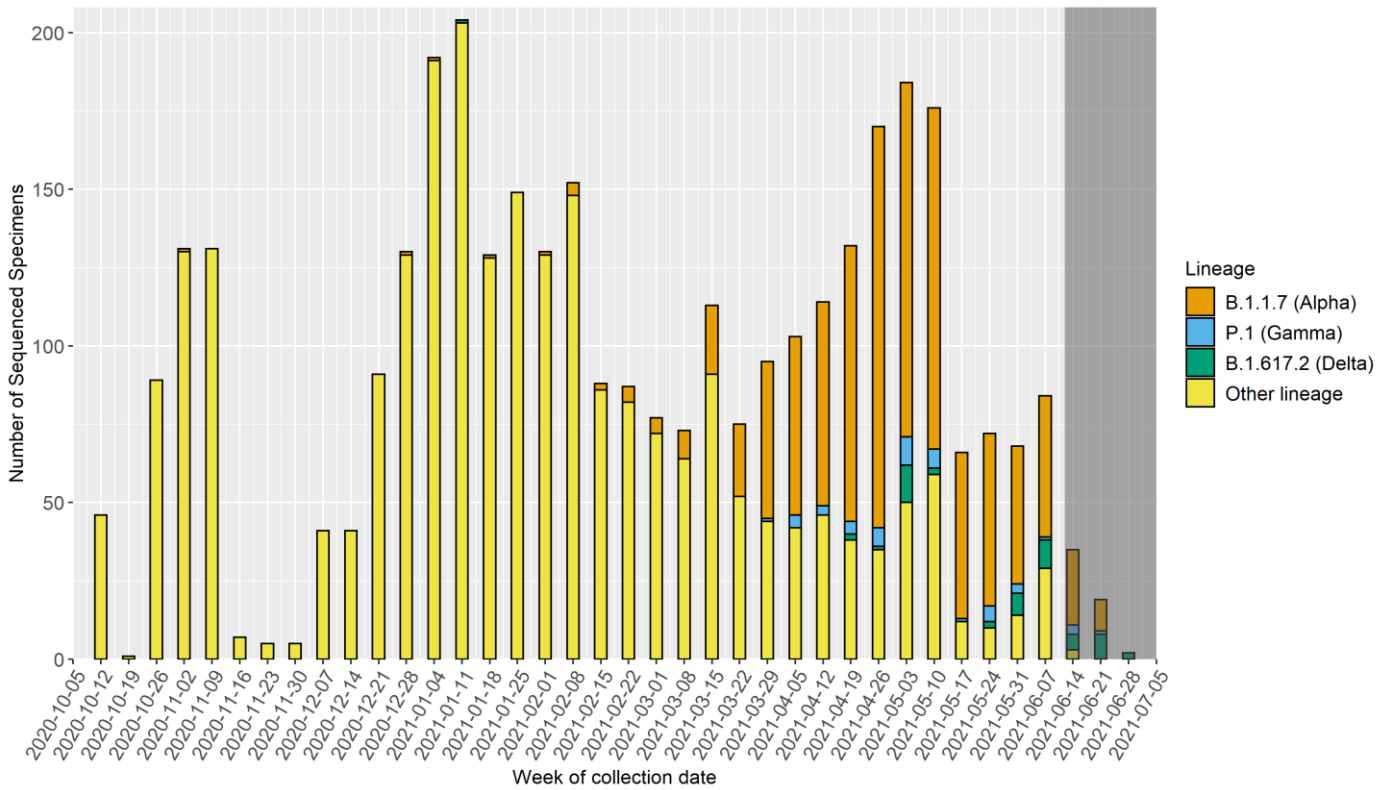
Cumulative number of VOC cases, hospitalizations and deaths

Lineage	Total Cases	Number Hospitalized	Percent Hospitalized	Number Died	Percent Died	Vaccine Breakthrough Cases*
B.1.1.7 (Alpha)	918	88	10%	9	1%	53
P.1 (Gamma)**	47	13	28%	2	4%	2
B.1.617.2 (Delta)	51	2	4%	2	4%	5
Other lineage	3199	178	6%	60	2%	30

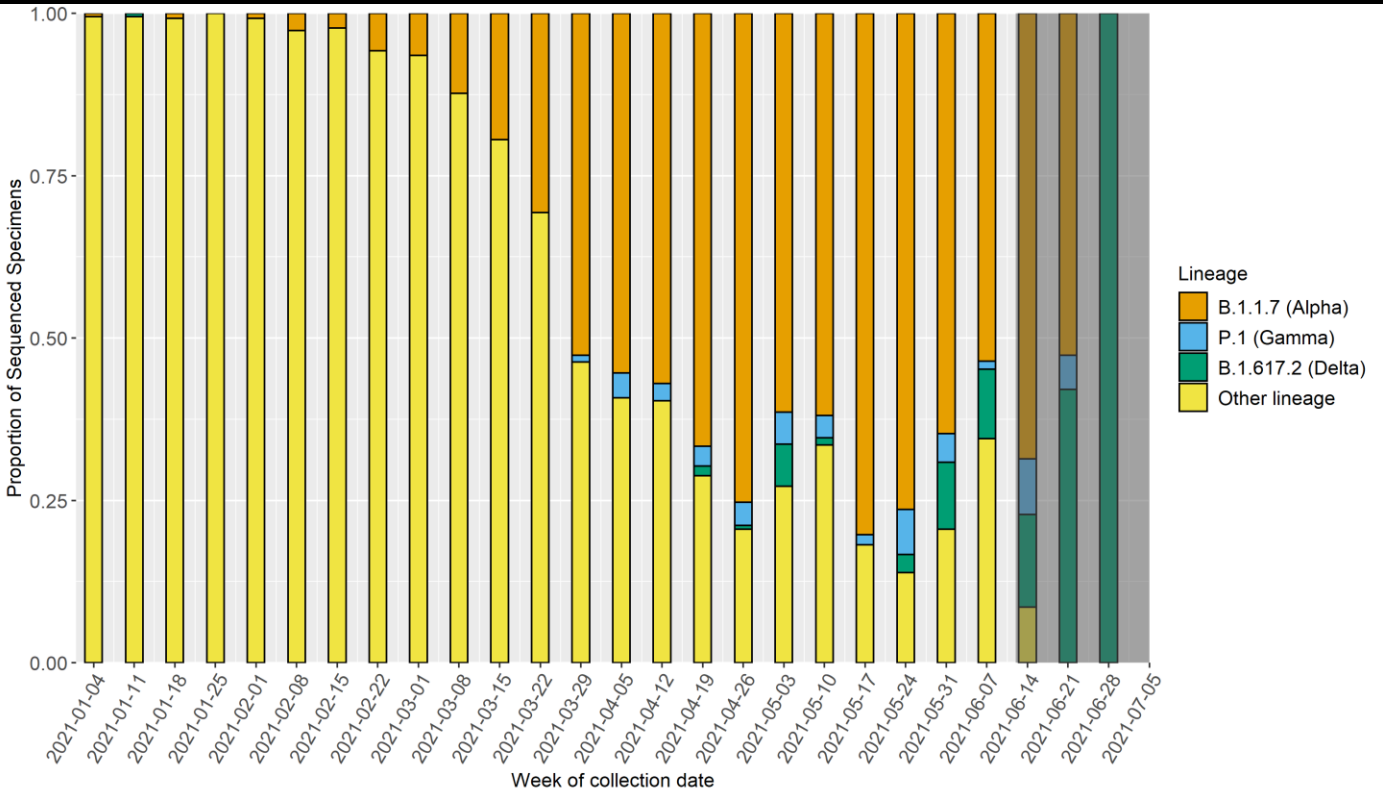
*A Vaccine Breakthrough Case is defined as a person who tests positive ≥ 14 days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. Percentages are not a reliable representation of VBTs in the community since VBTs are sequenced for variants more frequently for surveillance.

**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

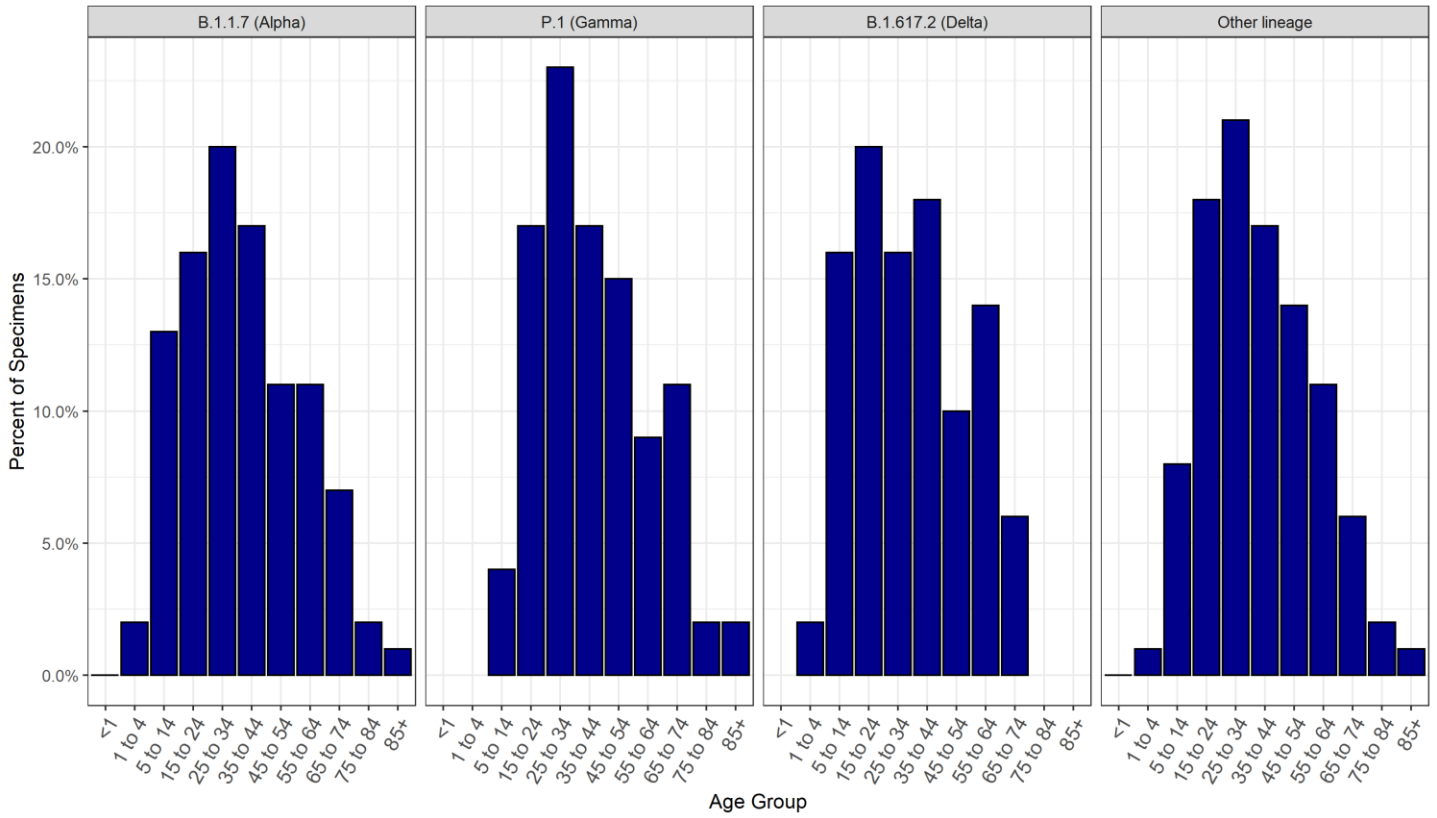


Proportion of identified SARS-CoV-2 lineages by week

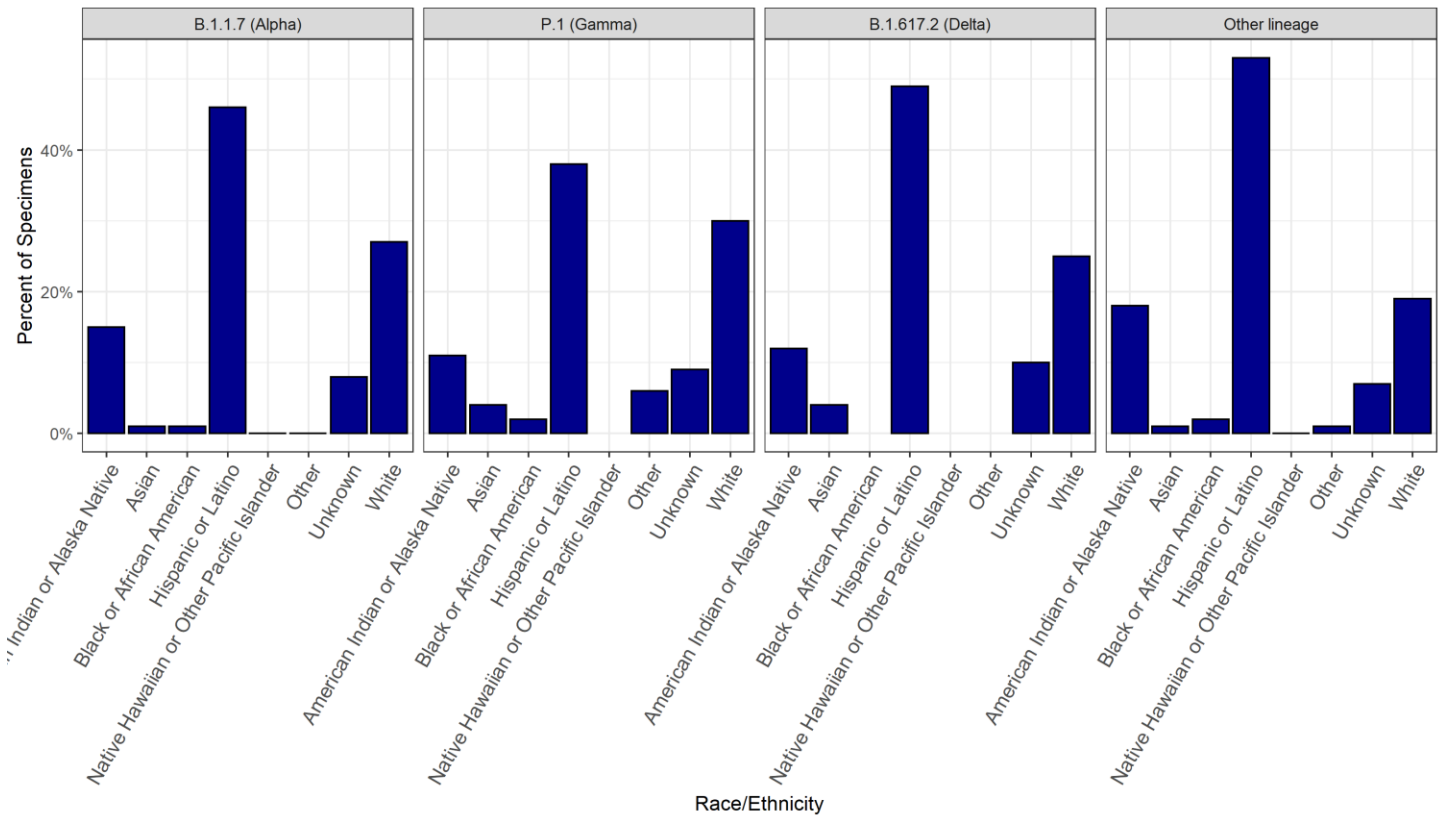


*The dark grey shaded region represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported. Only 2 specimens from the week of June 28, 2021 have been sequenced, both of which were Delta variants.

Cumulative proportion of VOC cases by age group



Cumulative proportion of VOC cases by race/ethnicity



Cumulative number of VOC cases by county of residence

Counties with less than 5 matched sequenced cases are not included in the table below.

County	B.1.1.7 (Alpha)	P.1 (Gamma)	B.1.617.2 (Delta)	Other lineage
Bernalillo	229	8	2	920
Chaves	11	0	1	58
Cibola	9	0	5	128
Colfax	19	0	0	27
Curry	7	0	1	30
Dona Ana	55	2	0	316
Eddy	16	0	0	83
Grant	11	1	0	30
Guadalupe	1	0	15	19
Lea	5	1	1	99
Lincoln	3	0	0	30
Los Alamos	8	0	2	19
Luna	9	0	0	13
McKinley	14	0	0	123
Otero	25	5	0	197
Rio Arriba	45	0	1	35
Roosevelt	0	0	0	11
San Juan	285	28	17	286
San Miguel	4	0	1	48
Sandoval	31	2	0	182
Santa Fe	64	0	1	294
Sierra	3	0	0	4
Socorro	3	0	0	27
Taos	10	0	1	36
Torrance	11	0	0	78
Valencia	37	0	3	92

Percentage of VOC cases reporting any symptoms

Lineage	No Symptoms	Unknown Symptoms	Yes Symptoms	Total Cases	Percent Symptomatic
B.1.1.7 (Alpha)	58	185	675	918	74%
P.1 (Gamma)	5	10	32	47	68%
B.1.617.2 (Delta)	1	13	37	51	73%
Other lineage	342	795	2062	3199	65%

Percentage of specific symptoms reported by symptomatic VOC cases

The table below includes data ONLY from symptomatic cases

Symptom	B.1.1.7 (Alpha)	P.1 (Gamma)	B.1.617.2 (Delta)	Other lineage
Fever (Measured or Subjective)	47% (312)	55% (17)	41% (15)	44% (900)
Chills	47% (309)	77% (24)	43% (16)	45% (912)
Muscle Aches	58% (381)	68% (21)	65% (24)	56% (1141)
Runny Nose	56% (371)	45% (14)	46% (17)	54% (1090)
Sore Throat	46% (303)	45% (14)	41% (15)	42% (864)
Cough	75% (494)	84% (26)	59% (22)	65% (1312)
Shortness of Breath	31% (203)	45% (14)	14% (5)	25% (511)
Nausea/Vomiting	27% (180)	39% (12)	19% (7)	23% (469)
Headache	66% (438)	55% (17)	59% (22)	65% (1324)
Abdominal Pain	16% (107)	10% (3)	24% (9)	15% (295)
Diarrhea	29% (191)	26% (8)	30% (11)	27% (542)
Fatigue	71% (468)	84% (26)	65% (24)	66% (1339)
Loss of Appetite	39% (257)	42% (13)	46% (17)	37% (752)
Loss of Taste or Smell	38% (253)	42% (13)	38% (14)	45% (910)

Percentage of VOC cases reporting underlying conditions

Lineage	No	Unknown	Yes	Total Cases	Percent with underlying conditions
B.1.1.7 (Alpha)	397	201	320	918	35%
P.1 (Gamma)	17	10	20	47	43%
B.1.617.2 (Delta)	17	15	19	51	37%
Other lineage	1065	1276	858	3199	27%

Percentage of specific underlying conditions reported by VOC cases

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

Condition	B.1.1.7 (Alpha)	P.1 (Gamma)	B.1.617.2 (Delta)	Other lineage
Chronic Lung Disease	25% (79)	22% (4)	24% (4)	27% (216)
Chronic Liver Disease	3% (8)	0% (0)	0% (0)	4% (33)
Chronic Renal Disease	3% (10)	11% (2)	6% (1)	4% (34)
Diabetes Mellitus	19% (59)	22% (4)	6% (1)	22% (181)
Cardiovascular Disease	33% (105)	33% (6)	29% (5)	27% (217)
Autoimmune Disease	6% (18)	11% (2)	6% (1)	5% (38)
Neurological Disability	7% (21)	17% (3)	0% (0)	9% (75)
Current or Former Smoker	56% (176)	67% (12)	47% (8)	49% (397)

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

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.