

# COVID-19 Variant of Concern (VOC) Case Report

September 27, 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 23, 2021, B.1.617.2 (Delta) represented approximately 100% of sequenced samples in New Mexico. Sequenced specimens reported from August 23-September 13, 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 Friday August 20, 2021, NMDOH reinstated wearing masks in all indoor public settings to slow the spread of the highly transmissible Delta variant.

## Cumulative number of Specimens Sequenced and Matched to Case Investigations

| Lineage                  | Sequenced Cases | Matched Cases* | Percent Matched |
|--------------------------|-----------------|----------------|-----------------|
| <b>B.1.1.7 (Alpha)</b>   | 1829            | 1591           | 87%             |
| <b>B.1.351 (Beta)</b>    | 7               | 3              | 43%             |
| <b>P.1 (Gamma)</b>       | 105             | 94             | 90%             |
| <b>B.1.617.2 (Delta)</b> | 2476            | 1981           | 80%             |
| <b>AY.1 (Delta)</b>      | 3               | 3              | 100%            |
| <b>AY.2 (Delta)</b>      | 4               | 3              | 75%             |
| <b>Other lineage</b>     | 4867            | 3916           | 80%             |
| <b>Total</b>             | 9291            | 7591           | 82%             |

\*Cases are matched to NMDOH case investigation data to provide demographic, disease outcome, and other clinical information. This table includes 156 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 Variant Epidemiologic Interpretation

| Name  | First Identified | Attributes <sup>1</sup>   | New Mexico <sup>2</sup>  |
|---|------------------|---|--|
| <b>B.1.1.7 and Q.1-Q.8</b><br>(Alpha/VBM)           | United Kingdom   | -50% more transmissible<br>-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.  |
| <b>B.1.351, B.1.351.2, and B.1.351.3</b> (Beta/VBM) | South Africa     | -50% more transmissible<br>-Reduced effectiveness of antibody treatments<br>-Reduced response of natural and vaccine induced immunity   | - Least reported VOC in NM.  |
| <b>B.1.617.2 and AY.1-AY.26</b><br>(Delta/VOC)      | India            | -Increased transmissibility<br>-May reduce effectiveness of antibody treatments<br>-May cause more severe illness in unvaccinated persons<br>-May reduce natural and vaccine immunity | -Since 6/28/21, Delta has remained the dominant VOC, and represented 100% of sequences reported on 8/23/21.<br>-Proportion of deaths among cases caused by this variant have decreased from 4% to 2%.                                  |
| <b>P.1, P.1.1, and P.1.2</b><br>(Gamma/VBM)         | Japan/Brazil     | -Reduced effectiveness of some antibody treatments<br>-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.<br>-Currently has the highest proportion of hospitalizations (24%); oversampling of severe cases may skew these results. |

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

<sup>2</sup>NM interpretations based on data collected >4 weeks ago to allow for lag in genomic sequencing.

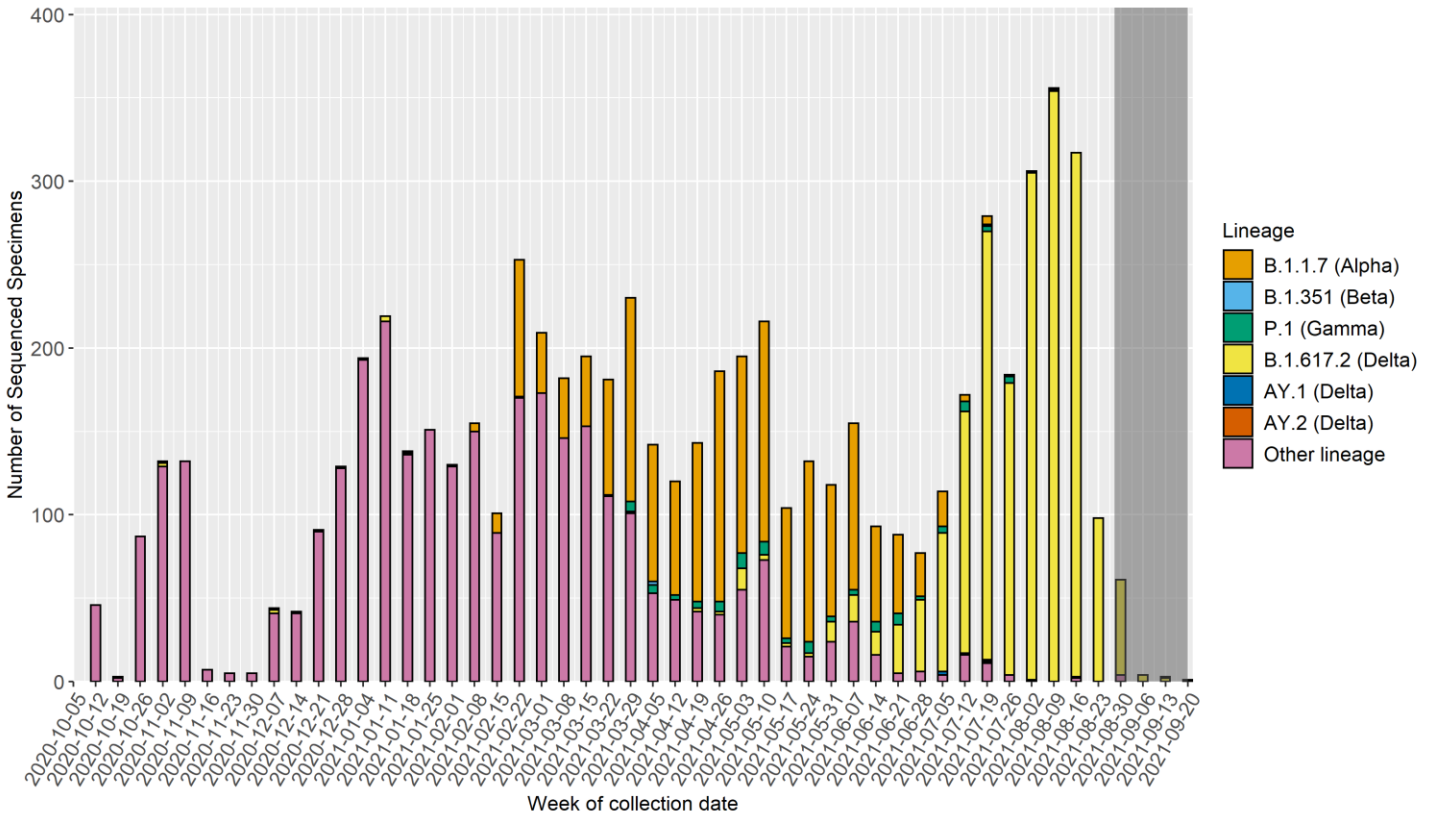
### Cumulative number of variant cases, hospitalizations, and deaths

| Lineage                  | Total Cases | Number Hospitalized | Percent Hospitalized | Number Died | Percent Died | Vaccine Breakthrough Cases* |
|--------------------------|-------------|---------------------|----------------------|-------------|--------------|-----------------------------|
| <b>B.1.1.7 (Alpha)</b>   | 1574        | 162                 | 10%                  | 24          | 2%           | 96                          |
| <b>B.1.351 (Beta)</b>    | 3           | 0                   | 0%                   | 0           | 0%           | 0                           |
| <b>P.1 (Gamma)</b>       | 92          | 22                  | 24%                  | 2           | 2%           | 3                           |
| <b>B.1.617.2 (Delta)</b> | 1949        | 198                 | 10%                  | 45          | 2%           | 617                         |
| <b>AY.1 (Delta)</b>      | 3           | 0                   | 0%                   | 0           | 0%           | 0                           |
| <b>AY.2 (Delta)</b>      | 3           | 0                   | 0%                   | 0           | 0%           | 0                           |
| <b>Other lineage</b>     | 3811        | 226                 | 6%                   | 68          | 2%           | 42                          |

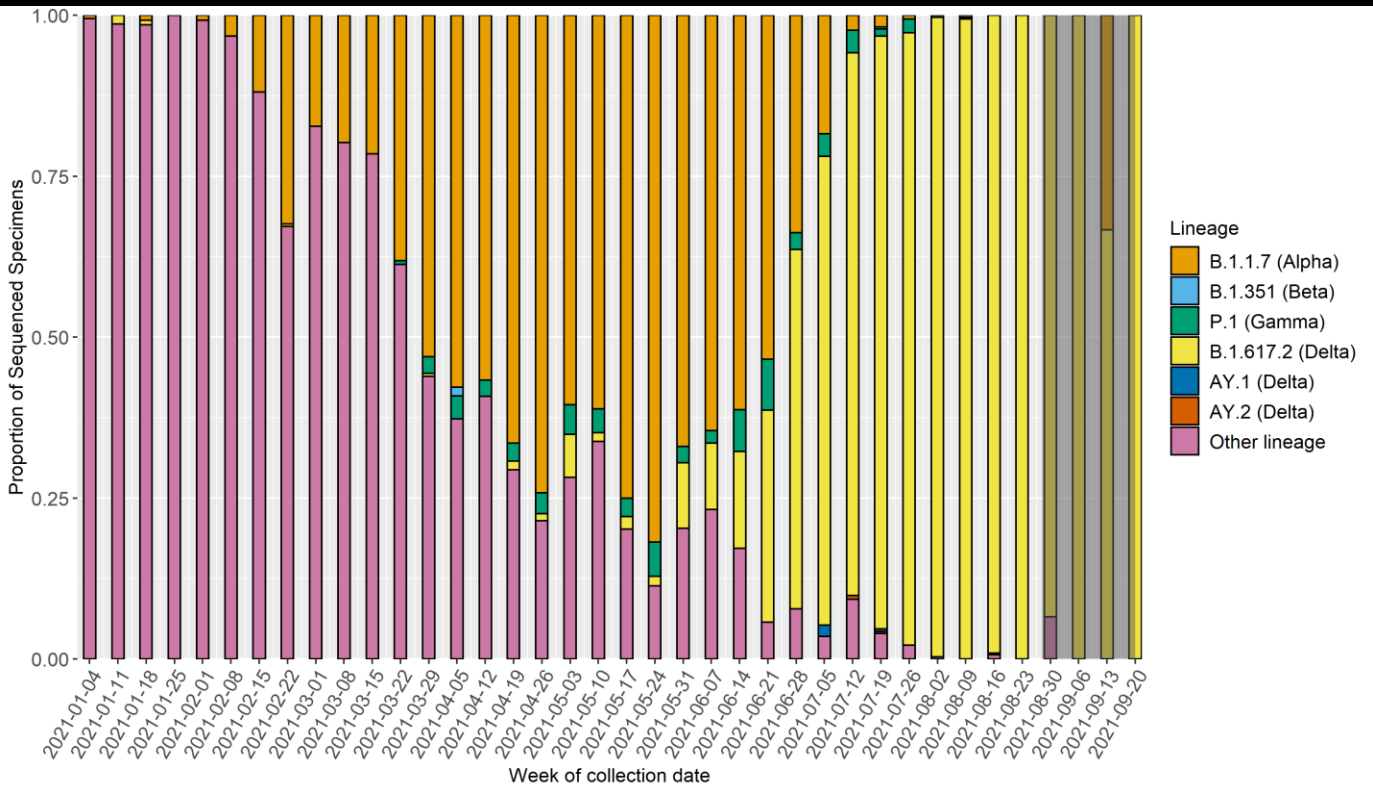
\*A vaccine breakthrough (VBT) case is defined as a person who tests positive  $\geq 14$  days after completing the full series of an FDA-authorized COVID-19 vaccine and has not tested positive the prior 89 days. Because samples collected from VBT cases are more frequently sequenced compared to samples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

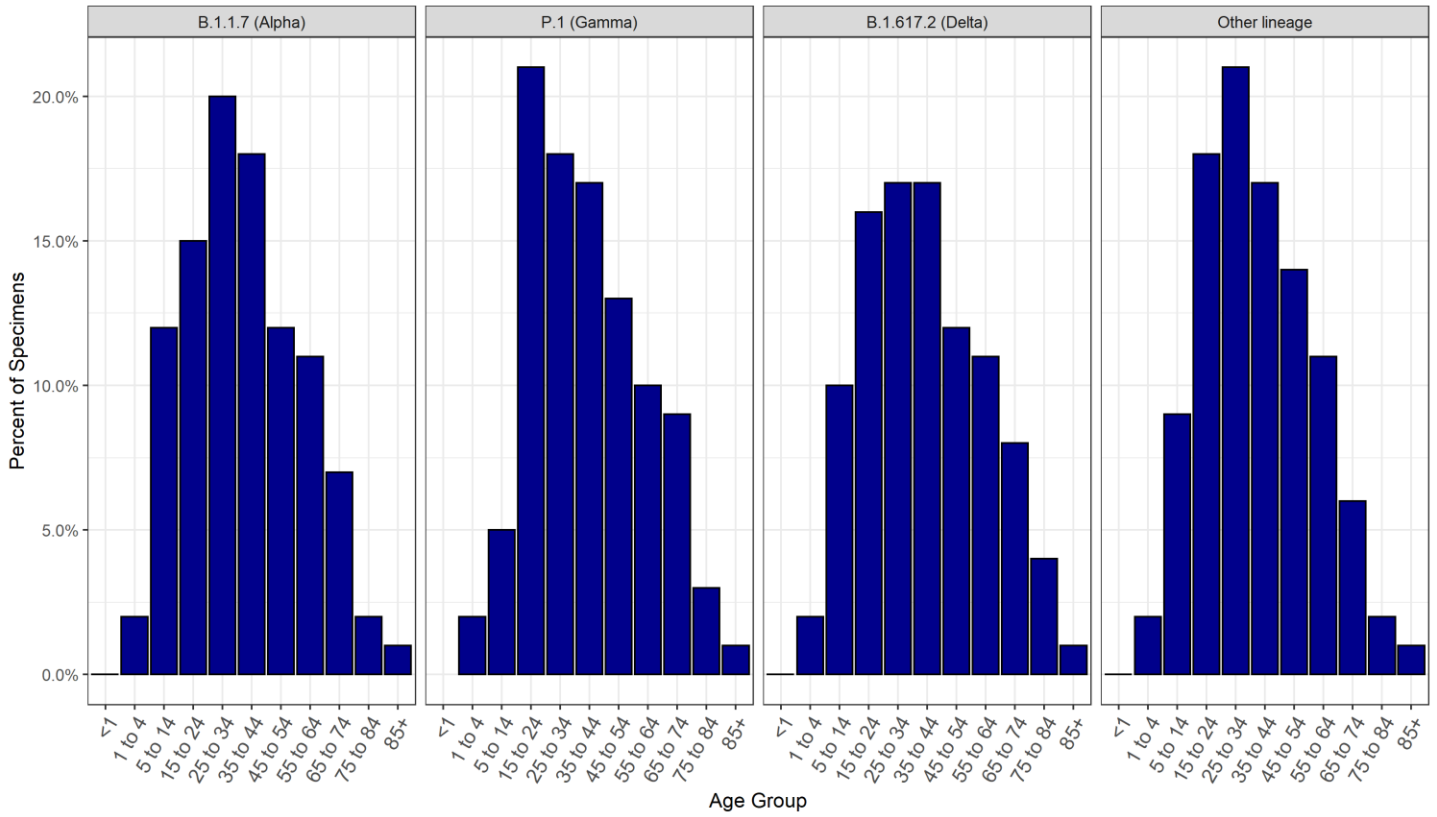


## Proportion of identified SARS-CoV-2 lineages by week\*

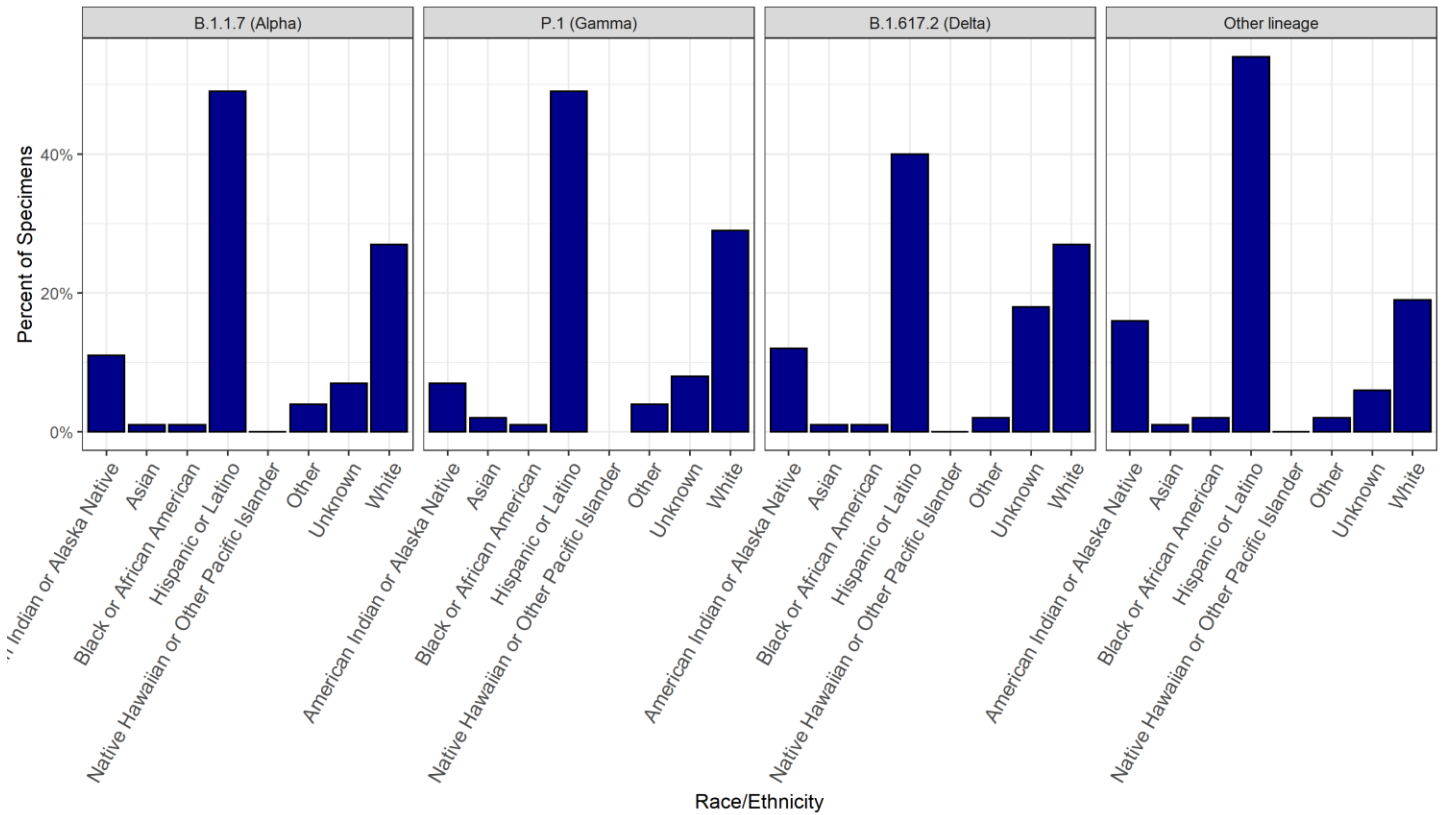


\*The dark grey shaded region in each of the figures on this page represents the lag period between specimen collection and genomic sequencing results such that the results may look different when all specimens available for sequencing have been reported.

## Cumulative proportion of variant cases by age group



## Cumulative proportion of variant cases by race/ethnicity



## 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.1.1.7 (Alpha) | B.1.351 (Beta) | P.1 (Gamma) | B.1.617.2 (Delta) | Other lineage |
|-------------------|-----------------|----------------|-------------|-------------------|---------------|
| <b>Bernalillo</b> | 456             | 3              | 17          | 621               | 1112          |
| <b>Catron</b>     | 0               | 0              | 1           | 0                 | 0             |
| <b>Chaves</b>     | 13              | 0              | 0           | 46                | 60            |
| <b>Cibola</b>     | 13              | 0              | 0           | 40                | 118           |
| <b>Colfax</b>     | 25              | 0              | 0           | 31                | 30            |
| <b>Curry</b>      | 25              | 0              | 0           | 35                | 39            |
| <b>Dona Ana</b>   | 83              | 0              | 7           | 114               | 431           |
| <b>Eddy</b>       | 20              | 0              | 0           | 116               | 104           |
| <b>Grant</b>      | 13              | 0              | 2           | 13                | 36            |
| <b>Guadalupe</b>  | 1               | 0              | 0           | 41                | 19            |
| <b>Hidalgo</b>    | 0               | 0              | 0           | 4                 | 1             |
| <b>Lea</b>        | 16              | 0              | 1           | 32                | 113           |
| <b>Lincoln</b>    | 5               | 0              | 4           | 15                | 58            |
| <b>Los Alamos</b> | 12              | 0              | 0           | 19                | 25            |
| <b>Luna</b>       | 14              | 0              | 0           | 6                 | 20            |
| <b>McKinley</b>   | 18              | 0              | 0           | 44                | 127           |
| <b>Mora</b>       | 0               | 0              | 0           | 0                 | 2             |
| <b>Otero</b>      | 25              | 0              | 3           | 124               | 154           |
| <b>Quay</b>       | 3               | 0              | 1           | 8                 | 2             |
| <b>Rio Arriba</b> | 94              | 0              | 1           | 40                | 40            |
| <b>Roosevelt</b>  | 0               | 0              | 0           | 2                 | 12            |
| <b>San Juan</b>   | 328             | 0              | 28          | 189               | 302           |
| <b>San Miguel</b> | 10              | 0              | 0           | 47                | 56            |
| <b>Sandoval</b>   | 75              | 0              | 6           | 112               | 247           |
| <b>Santa Fe</b>   | 101             | 0              | 0           | 102               | 305           |
| <b>Sierra</b>     | 5               | 0              | 0           | 6                 | 5             |
| <b>Socorro</b>    | 9               | 0              | 0           | 18                | 33            |
| <b>Taos</b>       | 14              | 0              | 0           | 20                | 40            |
| <b>Torrance</b>   | 17              | 0              | 1           | 22                | 73            |
| <b>Union</b>      | 1               | 0              | 0           | 1                 | 0             |
| <b>Valencia</b>   | 71              | 0              | 3           | 68                | 126           |

## Percentage of variant cases reporting any symptoms

| Lineage                  | No Symptoms | Unknown Symptoms | Yes Symptoms | Total Cases | Percent Symptomatic |
|--------------------------|-------------|------------------|--------------|-------------|---------------------|
| <b>B.1.1.7 (Alpha)</b>   | 103         | 398              | 1073         | 1574        | 68%                 |
| <b>B.1.351 (Beta)</b>    | 0           | 2                | 1            | 3           | 33%                 |
| <b>P.1 (Gamma)</b>       | 9           | 18               | 65           | 92          | 71%                 |
| <b>B.1.617.2 (Delta)</b> | 50          | 787              | 1118         | 1955        | 57%                 |
| <b>Other lineage</b>     | 406         | 887              | 2518         | 3811        | 66%                 |

## Percentage of specific symptoms reported by symptomatic variant 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 |
|---------------------------------------|-----------------|-------------|-------------------|---------------|
| <b>Fever (Measured or Subjective)</b> | 47% (493)       | 50% (32)    | 56% (614)         | 43% (1064)    |
| <b>Chills</b>                         | 46% (487)       | 61% (39)    | 47% (520)         | 45% (1114)    |
| <b>Muscle Aches</b>                   | 57% (602)       | 55% (35)    | 57% (632)         | 56% (1382)    |
| <b>Runny Nose</b>                     | 53% (557)       | 47% (30)    | 55% (606)         | 53% (1322)    |
| <b>Sore Throat</b>                    | 45% (471)       | 47% (30)    | 47% (516)         | 43% (1062)    |
| <b>Cough</b>                          | 74% (782)       | 83% (53)    | 77% (847)         | 64% (1592)    |
| <b>Shortness of Breath</b>            | 30% (314)       | 42% (27)    | 27% (303)         | 24% (603)     |
| <b>Nausea/Vomiting</b>                | 27% (286)       | 34% (22)    | 26% (285)         | 23% (571)     |
| <b>Headache</b>                       | 65% (690)       | 53% (34)    | 66% (729)         | 66% (1632)    |
| <b>Abdominal Pain</b>                 | 16% (166)       | 16% (10)    | 15% (166)         | 14% (353)     |
| <b>Diarrhea</b>                       | 29% (308)       | 25% (16)    | 29% (318)         | 27% (661)     |
| <b>Fatigue</b>                        | 71% (747)       | 70% (45)    | 68% (757)         | 66% (1643)    |
| <b>Loss of Appetite</b>               | 41% (428)       | 36% (23)    | 38% (421)         | 36% (897)     |
| <b>Loss of Taste or Smell</b>         | 39% (413)       | 34% (22)    | 47% (516)         | 44% (1087)    |

## Percentage of variant cases reporting underlying conditions

| Lineage                  | No   | Unknown | Yes  | Total Cases | Percent with underlying conditions |
|--------------------------|------|---------|------|-------------|------------------------------------|
| <b>B.1.1.7 (Alpha)</b>   | 625  | 408     | 541  | 1574        | 34%                                |
| <b>B.1.351 (Beta)</b>    | 1    | 2       | 0    | 3           | 0%                                 |
| <b>P.1 (Gamma)</b>       | 38   | 18      | 36   | 92          | 39%                                |
| <b>B.1.617.2 (Delta)</b> | 336  | 1204    | 415  | 1955        | 21%                                |
| <b>Other lineage</b>     | 1720 | 993     | 1098 | 3811        | 29%                                |

## Percentage of specific underlying conditions reported by variant cases

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

| Condition                       | B.1.1.7 (Alpha) | P.1 (Gamma) | B.1.617.2 (Delta) | Other lineage |
|---------------------------------|-----------------|-------------|-------------------|---------------|
| <b>Chronic Lung Disease</b>     | 25% (135)       | 25% (8)     | 26% (101)         | 26% (258)     |
| <b>Chronic Liver Disease</b>    | 4% (20)         | 0% (0)      | 3% (12)           | 4% (39)       |
| <b>Chronic Renal Disease</b>    | 4% (22)         | 6% (2)      | 8% (32)           | 4% (44)       |
| <b>Diabetes Mellitus</b>        | 20% (104)       | 12% (4)     | 27% (105)         | 22% (215)     |
| <b>Cardiovascular Disease</b>   | 32% (170)       | 28% (9)     | 36% (143)         | 28% (278)     |
| <b>Autoimmune Disease</b>       | 8% (41)         | 6% (2)      | 6% (24)           | 5% (46)       |
| <b>Neurological Disability</b>  | 7% (35)         | 12% (4)     | 7% (26)           | 8% (83)       |
| <b>Current or Former Smoker</b> | 54% (289)       | 75% (24)    | 45% (176)         | 50% (498)     |

\* 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 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.