

COVID-19 Variants Identified in Montana

Updated 7/14/2021

This map includes the counties where variants of concern and variants of interest have been detected in Montana. The tables detail the types of variants detected, the classification of variant, and the counties in which they were detected. This map and table will be updated when additional variants cases are identified, rather than a set schedule. Please note after public health investigation the county of the patient residence may change.

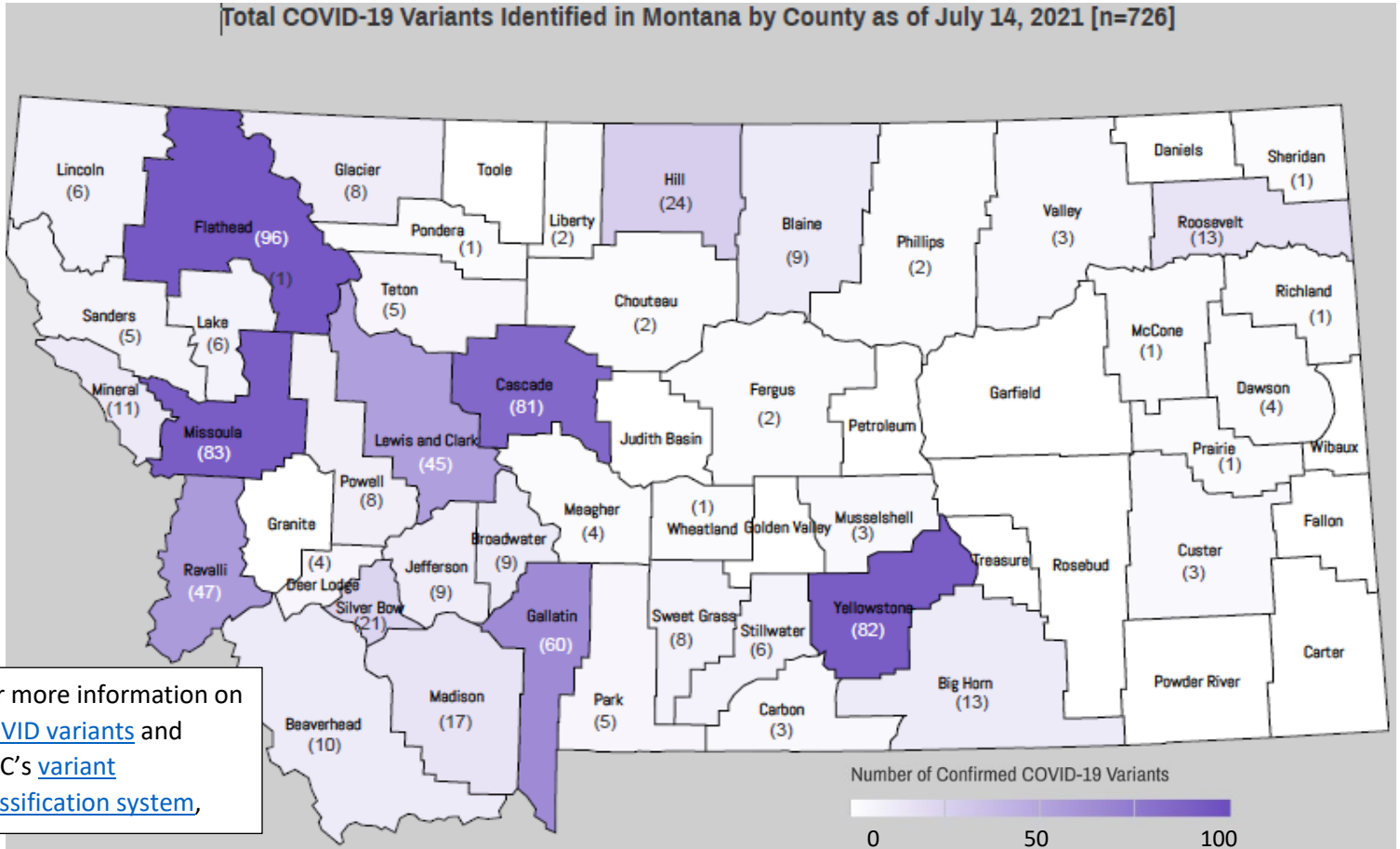


Table 1. Total number of SARS-CoV-2 variants detected in Montana by classification, 7/14/2021

| Variant Classification | Classification Explanation | Number |
|-----------------------------|--|------------|
| Variant of Interest (VOI) | A variant with specific genetic markers associated with changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity. | 149 |
| Variant of Concern (VOC) | A variant for which there is evidence of an increase in transmissibility, more severe disease (increased hospitalizations or deaths), significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures. | 577 |
| Variant of High Consequence | A variant of high consequence has clear evidence that prevention measures or medical countermeasures (MCMs) have significantly reduced effectiveness relative to previously circulating variants. | 0 |
| Total | | 726 |

Table 2. SARS-CoV-2 variants detected in Montana by location and lineage, reported to MTDPHHS, 7/14/2021

| County | Variants of Concern | | | Variants of Interest | | | | Total # Cases |
|-------------------|---------------------|-------------------|-------------|----------------------|-------------------|---------------|----------------|---------------|
| | B.1.1.7 (Alpha/UK) | B.1.617.2 (Delta) | P.1 (Gamma) | B.1.427 (Epsilon) | B.1.429 (Epsilon) | B.1.525 (Eta) | B.1.526 (Iota) | |
| Beaverhead | 4 | 4 | | 2 | | | | 10 |
| Big Horn | 4 | 7 | 2 | | | | | 13 |
| Blaine | 9 | | | | | | | 9 |
| Broadwater | 9 | | | | | | | 9 |
| Carbon | 2 | 1 | | | | | | 3 |
| Cascade | 58 | 5 | 3 | 8 | 3 | | 4 | 81 |
| Chouteau | 1 | | | 1 | | | | 2 |
| Custer | 2 | | | | 1 | | | 3 |
| Dawson | 1 | 2 | | | 1 | | | 4 |
| Deer Lodge | 3 | | 1 | | | | | 4 |
| Fergus | 2 | | | | | | | 2 |
| Flathead | 70 | 4 | 4 | 6 | | 2 | 10 | 96 |
| Gallatin | 42 | 2 | 3 | | 8 | 1 | 4 | 60 |
| Glacier | 6 | | 1 | | 1 | | | 8 |
| Hill | 16 | | | 1 | 3 | | 4 | 24 |
| Jefferson | 7 | 1 | | | 1 | | | 9 |
| Lake | 5 | | | | 1 | | | 6 |
| Lewis & Clark | 31 | 3 | | 4 | 1 | | 6 | 45 |
| Liberty | 1 | | | | 1 | | | 2 |
| Lincoln | 1 | | | 2 | 3 | | | 6 |
| Madison | 4 | 2 | 6 | 2 | 3 | | | 17 |
| McCone | 1 | | | | | | | 1 |
| Meagher | | | 2 | 2 | | | | 4 |
| Mineral | 11 | | | | | | | 11 |
| Missoula | 63 | 1 | 2 | 5 | 3 | 2 | 7 | 83 |
| Musselshell | 2 | 1 | | | | | | 3 |
| Park | 4 | | | | | | 1 | 5 |
| Phillips | | | | | 2 | | | 2 |
| Pondera | 1 | | | | | | | 1 |
| Powder River | 1 | | | | | | | 1 |
| Powell | 3 | | | 2 | | | 3 | 8 |
| Prairie | | | | | 1 | | | 1 |
| Ravalli | 43 | | 1 | | | | 3 | 47 |
| Richland | | | | | 1 | | | 1 |
| Roosevelt | 2 | | | | 11 | | | 13 |
| Sanders | 3 | | | | 1 | | 1 | 5 |
| Sheridan | | | | 1 | | | | 1 |
| Silver Bow | 5 | 1 | 1 | 13 | 1 | | | 21 |
| Stillwater | 6 | | | | | | | 6 |
| Sweet Grass | 7 | | | | 1 | | | 8 |
| Teton | 5 | | | | | | | 5 |
| Valley | 2 | | | | 1 | | | 3 |
| Wheatland | 1 | | | | | | | 1 |
| Yellowstone | 62 | 17 | | | 2 | | 1 | 82 |
| Total | 500 | 51 | 26 | 49 | 51 | 5 | 44 | 726 |
| Percentage | 69% | 7% | 4% | 7% | 7% | 1% | 6% | |

Note: The distribution of variants can be influenced by local testing capabilities. As a result, the data in table 2 may not reflect a standardized, statewide sample of variants. Data above are collected in collaboration with partners including, MSU, UM, Fyr Diagnostics, CDC, and other national reference labs.

Table 3. Outcome of patients infected with SARS-CoV-2 variants in Montana, by lineage, 7/14/2021

| | Variant lineage | Not Hospitalized | Hospitalized | Percentage Hospitalized | Deceased |
|----------------------|--------------------|------------------|--------------|-------------------------|----------|
| Variants of Concern | B.1.1.7 (Alpha/UK) | 379 | 36 | 8.7% | 5 |
| | B.1.617.2 (Delta) | 31 | 10 | 24.4% | 1 |
| | P.1 (Gamma) | 18 | 2 | 10.0% | 1 |
| Variants of Interest | B.1.427 (Epsilon) | 42 | 3 | 6.7% | 0 |
| | B.1.429 (Epsilon) | 43 | 2 | 4.4% | 1 |
| | B.1.525 (Eta) | 3 | 0 | 0.0% | 0 |
| | B.1.526 (Iota) | 34 | 3 | 8.1% | 0 |

Data in table 3 show the hospitalization and death status for cases where that information is recorded in Montana’s communicable disease database (n=641). We continue to see approximately 1/4 of cases infected with the Delta variant (B.1.617.2) were hospitalized, 1 died.

SARS-CoV-2 sequencing results are also reported to GISAID, which promotes the rapid sharing of data from all influenza viruses and the coronavirus causing COVID-19. These results do not contain county-level geography for all specimens, so the data in table 2 are the subset of the results reported to GISAID captured in table 4. A summary table of all the sequencing performed on SARS-CoV-2 specimens from Montana and reported to GISAID is below. More information about GISAID is available here:

<https://www.gisaid.org/>

Table 4. SARS-CoV-2 specimens sequenced in Montana by lineage, reported to GISAID, 7/14/2021

| Sequences not of concern or interest | Variants of Concern | | | Variants of Interest | | | | | Total # Sequenced |
|--------------------------------------|---------------------|-------------------|-------------|----------------------|-------------------|---------------|----------------|--------------|-------------------|
| | B.1.1.7 (Alpha/UK) | B.1.617.2 (Delta) | P.1 (Gamma) | B.1.427 (Epsilon) | B.1.429 (Epsilon) | B.1.525 (Eta) | B.1.526 (Iota) | P.2 (Brazil) | |
| 479 | 670 | 85 | 34 | 74 | 68 | 6 | 71 | 1 | 1488 |
| 32% | 45% | 6% | 2% | 5% | 5% | <1% | 5% | <1% | |

Viruses constantly change through mutation. A variant has one or more mutations that differentiate it from other variants in circulation. As expected, multiple variants of SARS-CoV-2 have been documented in the US and globally throughout this pandemic.

COVID Breakthrough Cases

Breakthrough infection surveillance began in Montana on February 15, 2021. A breakthrough COVID-19 infection is defined as a positive SARS-CoV-2 RNA or antigen detection in a respiratory specimen that is collected ≥14 days after completing the primary COVID-19 vaccine series of an FDA-authorized COVID-19 vaccine. Depending on the specific vaccine administered, completion of series could be one or two doses of vaccine.

As of 7/14/21, Montana reports 437 cases of confirmed breakthrough disease, this includes 47 hospitalizations and 8 deaths, 93/101 with subtyping performed are known to be infected with variants of concern or interest. These cases occurred in 38 different jurisdictions across the state.

Table 5. SARS-CoV-2 variants detected in Montana breakthrough cases by lineage, 7/14/2021

| Breakthrough Cases | Variants of Concern | | | Variants of Interest | | | | Total # Variants |
|--------------------|---------------------|-------------------|-------------|----------------------|-------------------|---------------|----------------|------------------|
| | B.1.1.7 (Alpha/UK) | B.1.617.2 (Delta) | P.1 (Gamma) | B.1.427 (Epsilon) | B.1.429 (Epsilon) | B.1.525 (Eta) | B.1.526 (Iota) | |
| | 61 | 9 | 5 | 5 | 6 | 2 | 5 | 93 |