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CORONAVIRUS DISEASE 2019 UPDATE (08): MONGOLIA (ULAANBAATAR) BEAVER, RESEARCH, 2021

A ProMED-mail post

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<https://www.cidrap.umn.edu/covid-19/researchers-outline-covid-19-outbreak-mongolian-beaver-farm>

Yesterday [19 Jan 2024] in Emerging Infectious Diseases [https://wwwnc.cdc.gov/eid/article/30/2/23-1318_article], scientists describe a 2021 COVID-19 outbreak at a beaver farm in Mongolia.

Located in the Bayanzurkh district in Ulaanbaatar, the farm raised 32 adult beavers and 16 kits in 2021 for conservation purposes. The animals lived in a large indoor area separated by waist-high walls.

On 6 Aug 2021, one of the 7 farm employees tested positive for COVID-19 after experiencing flu-like symptoms. Three days later, the farm reported the death of 2 beavers aged 6 months and 2 years after they exhibited cough, nasal discharge, rasping sounds in the lungs and chest, sluggishness, and food aversion.

On 13 Aug 2021, investigators collected nasal swabs, saliva, and tissue from the 2 dead beavers and obtained nasal samples, saliva, and blood from 7 other beavers exhibiting cough and nasal discharge with pus. Later that week and on 12 Sep 2021, the researchers collected more samples from the same animals and from 2 healthy beavers.

Four unique mutations spark concern

Nearly all (46 of 48) specimens from 9 beavers with clinical signs, including the 2 dead animals, tested positive for COVID-19 on polymerase chain reaction (PCR) testing. Serologic testing of 23 samples revealed the presence of SARS-CoV-2 antibodies in 15. One beaver that didn't show signs of infection also had antibodies.

An alarming aspect of SARS-CoV-2 infection in animals is that host animals can maintain the virus and contribute to the emergence in humans of new variants that have accumulated multiple mutations.

Five random SARS-CoV-2-positive samples were shipped to Austria for whole-genome sequencing, which identified the delta variant. The delta and alpha variants were circulating among people in Mongolia at the time, and the closest related sequences in the beaver samples were from human SARS-CoV-2 in Mongolia, although they contained 4 novel mutations not found in any public databases as of November 2023.

"An alarming aspect of SARS-CoV-2 infection in animals is that host animals can maintain the virus and contribute to the emergence in humans of new variants that have accumulated multiple mutations," the study authors wrote. "Because the emergence of viruses with mutations not targeted by current SARS-CoV-2 vaccines is a credible possibility, more active surveillance of SARS-CoV-2 infection in animals should be encouraged to identify the appearance of mutated viruses."

[Byline: Mary Van Beusekom]

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[The citation, abstract and full text of the article referenced above follow:

Takemura T, Ankhanbaatar U, K Settyapalli TB, et al. SARS-CoV-2 infection in beaver farm, Mongolia, 2021. Emerg Infect Dis. 2024. <https://doi.org/10.3201/eid3002.231318>

Abstract

"We report an outbreak of COVID-19 in a beaver farm in Mongolia in 2021. Genomic characterization revealed a unique combination of mutations in the SARS-CoV-2 of the infected beavers. Based on these findings, increased surveillance of farmed beavers should be encouraged." [References, tables, figures, gray boxes and appendices can be seen at the source URL above]

"The COVID-19 pandemic that began in 2019 remains uncontained, and fatalities and multiple waves of infection continue to occur worldwide (1). The causative agent, SARS-CoV-2, has been detected in humans and several animal species, including domestic, wild, and laboratory animals (2,3). Because SARS-CoV-2 can be transmitted from humans to animals and back to humans, understanding the dynamics of infection in animals can contribute to the creation of more comprehensive response strategies."

"We identified SARS-CoV-2 infection in beavers (_Castor fiber_) farmed for conservation reasons in Mongolia and report on serologic and whole genome sequence data from this outbreak. The beaver farm, located in the Bayanzurkh district in Ulaanbaatar, Mongolia, reared 32 adults and 16 kits in 2021. They were housed indoors in a large area separated by waist-high walls, with space for multiple animals. One of the 7 employees of the farm had influenza-like symptoms for several days and was diagnosed with COVID-19 on 6 Aug 2021. On 9 Aug 2021, the beaver farm reported the death of 2 beavers (one 6 months of age and one 2 years of age) after signs of coughing, nasal discharge, rasping on auscultation of the lungs and chest cavity, sluggish movement, and aversion to food. On 13 Aug 2021 research investigators collected nasal swabs, saliva, and 7 tissue samples (lung, kidney, liver, heart, spleen, larynx, and tongue from the 2 dead animals. Researchers also collected nasal swab specimens, saliva, and blood from 7 other beavers with notable clinical signs of coughing and purulent nasal discharge. Follow-up investigation on 18 or 19 Aug 2021 and on 12 Sep 2021 included collection of additional nasal swab specimens, saliva, and blood samples from the same animals as well as from 2 healthy animals (12 Sep 2021 only)."

"All samples were transported to a Biosafety Level 3 facility in Ulaanbaatar and were screened by quantitative reverse transcription PCR according to the Peiris protocol (4). The results showed that 46 of 48 specimens from 9 animals with clinical signs, including the 2 dead animals, tested positive for SARS-CoV-2 RNA. Serum was separated from the blood samples by centrifugation (2000 x g for 10 min) and stored at -20°C until required. The serum samples were then subjected to antibody screening by using a commercial ELISA kit (ID Screen SARS-CoV-2 Double Antigen Multi-species ELISA; Innovative Diagnostics, <https://www.innovative-diagnostics.com>External Link). Fifteen of 23 samples tested positive and one was intermediate, indicating that all animals became antibody positive within one month of confirmation of SARS-CoV-2 RNA positivity. One clinically unremarkable beaver tested positive for SARS-CoV-2 antibodies, indicating a possible subclinical infection (Table)."

"Phylogenetic tree of SARS-CoV-2 identified from beavers and humans in Mongolia (gray boxes) and reference sequences. The circle size indicates the bootstrap values at the node. The vertical bar shows the genetic distance. SARS-CoV-2 lineages are identified at right. GenBank accession numbers and date identified are shown for reference sequences; the newly obtained sequence data were deposited in GenBank (accession nos. OR389473-7)."

"We shipped 5 randomly selected quantitative reverse transcription PCR-confirmed SARS-CoV-2-positive RNA samples to the Animal Production and Health Laboratory (Seibersdorf, Austria), a joint program of the International Atomic Energy Agency and the Food and Agriculture Organization of the United Nations and subjected them to whole-genome sequencing (Appendix 1; Appendix 2). Based on genotype analysis, all 5 genome sequences were assigned to the B.1.617.2 lineage, commonly referred to as the delta variant. At the time of sampling, alpha and delta variants of SARS-CoV-2 were being identified in humans in Mongolia. The closest related sequences to those we identified in the beavers studied were from human SARS-CoV-2 in Mongolia (GenBank accession nos. ON008302, OM190617, and OM961234) identified during April-September 2021 (Figure). In addition to 4 mutations in the spike region, the sequences shared 7 amino acid substitutions in open reading frame [ORF] 1a, 4 amino acid substitutions in ORF1b, and one amino acid substitution in nucleocapsid genes. In the beaver sequences, 4 amino acid substitutions identified were not in the human isolates from Mongolia: S2500F, A3657V in ORF1a and H604Y, T1404M in ORF1b. Although those substitutions have been identified individually in SARS-CoV-2 sequences in GenBank and the GISAID database (<https://www.gisaid.org>External Link), there are no records of sequences with all 4 mutations."

"Several cases of SARS-CoV-2 transmission between humans and animals have already been reported (5-8). An alarming aspect of SARS-CoV-2 infection in animals is that host animals can maintain the virus and contribute to the emergence in humans of new variants that have accumulated multiple mutations (7-10). Indeed, the specific combination of mutations observed in the beavers we studied has not been found in other SARS-CoV-2 sequences in public databases (as of November 2023). This finding suggests that the mutations might have occurred or accumulated after the introduction of the virus into the beaver population. Because the emergence of viruses with mutations not targeted by current SARS-CoV-2 vaccines is a credible possibility, more active surveillance of SARS-CoV-2 infection in animals should be encouraged to identify the appearance of mutated viruses. In intensively farmed animals, species-species and species-humans contact is more frequent than in animals dwelling in other environments, which might increase the risk for zoonotic pathogen transmission (2). Thus, implementing more active surveillance and infection control strategies is critical to disease prevention and containment."

An image of beaver can be seen at <https://www.cidrap.umn.edu/sites/default/files/Beaver.jpg>

The FAO's "SARS-CoV-2 in animals situation update (5 Dec 2023)" is available at <https://www.fao.org/animal-health/situation-updates/sars-cov-2-in-animals>.

"As the COVID-19 pandemic continues, the number of mammal species that are susceptible to infection with SARS-CoV-2 increases. We are at the beginning of a macrocycle that may become the 1st documented case of a viral infection with exceptional characteristics in terms of host-range susceptibility. Coronavirus infections in humans find their origins in viruses circulating in wildlife -- in particular, bats -- through cross-species transmission that often includes intermediate hosts, such as alpacas, palm civets, rodents, cattle, and dromedary camels. Overall, the transmission of pathogens is not unidirectional; ecosystem disruptions and alterations to the human-wildlife interface also create opportunities for circulating infectious agents to undergo reverse zoonotic transmission, or spillback, into domestic and wild animal species." (<https://academic.oup.com/bioscience/article/73/11/814/7478069>) - Mod.TTM

ProMED map:
Mongolia: <https://promedmail.org/promed-post?place=8714374,1>

See Also

- COVID-19 update (07): Bangladesh, JN.1, variant of interest 20240120.8714357
- COVID-19 update (06): India, decrease in cases 20240117.8714284
- COVID-19 update (05): Pakistan, JN.1, variant of interest 20240111.8714166
- COVID-19 update (04): selected locations, JN.1 virology, severity, omicron BA.4.1 in dogs 20240111.8714155
- COVID-19 update (03): Israel, JN.1, new variant 20240104.8714055
- COVID-19 update (02): India 20240103.8714052
- COVID-19 update (01): Cambodia, new JN.1 variant detection 20240101.8714020
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- COVID-19 update (39): Saudi Arabia, JN.1 variant, MOH 20231222.8713858
- COVID-19 update (38): WHO classifies JN.1 coronavirus strain as 'variant of interest' 20231220.8713808
- COVID-19 update (37): vaccine comp., selected regions, circ. variants, research 20231219.8713789
- COVID-19 update (36): selected countries/regions, vaccines 20231212.8713666
- COVID-19 update (35): Singapore, increase 20231209.8713618
- COVID-19 update (34): selected country/region updates, variants, WHO 20231130.8713398
- COVID-19 update (33): country updates, vaccines, vaccine refusal, WHO update 20231105.8713000
- COVID-19 update (32): updates, variants, vaccines, antivirals, scientific literature 20231026.8712809
- COVID-19 update (31): BA.2.86 & EG.5, selected regions, vaccines, WHO, global 20231009.8712522
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COVID-19 update (22): trends, immunity, children, metformin, WHO 20230612.8710546

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COVID-19 update (04): PHEIC, China, susp outbreaks, responses, vaccines, global 20230130.8708043

COVID-19 update (03): China, guidelines, vacc, immunity, sequelae, WHO 20230122.8707910

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COVID-19 update (01): China, Hong Kong, XBB.1.5, PAHO, treatment, testing, WHO 20230107.8707667

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COVID-19 update (181): Africa vacc hesitancy, pre-eclampsia, boosters, nasal vacc, WHO, global 20221014.8706143

COVID-19 update (180): long COVID, neuropsych. illness, Paxlovid, subvariants, WHO 20221007.8706007

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COVID-19 update (160): vaccine rollout disparities, smell & taste, WHO, global 20220731.8704776

COVID-19 update (150): France, omicron 2nd gen variant, paxlovid, WHO, global 20220705.8704255

COVID-19 update (140): Thailand, human to cat to human transmission 20220612.8703819

COVID-19 update (130): surveill., cardiac eff., long COVID subtypes, WHO, global 20220601.8703606

COVID-19 update (120): N Korea, pandemic exit, youth vaccine, US deaths, WHO 20220518.8703327

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COVID-19 update (60): animal, China, origin, research 20220227.8701690

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COVID-19 update (40): Denmark, rosemary, pregnancy, stroke, WHO 20220205.8701276

COVID-19 update (30): variants in immuno-comp., stability, endemic, WHO 20220126.8701074

COVID-19 update (20): Africa vacc., Taiwan, waning immunity, persistence, global 20220117.8700915

COVID-19 update (10): animal, omicron origin statement, OIE 20220110.8700763

COVID-19 update (01): omicron severity & changes, Germany, T-cell reactivity 20220101.8700616

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