

# Weird SARS-CoV-2 outbreak in mink suggests hidden source of virus in the wild

The lineage had not been seen in the area for over two years.

Beth Mole - Apr 21, 2023 8:19 pm UTC



[Enlarge](#) / Minks are seen at a farm in Gjol, northern Denmark, on October 9, 2020.

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Between September to January of this year, mink in three Polish farms tested positive for the pandemic coronavirus, SARS-CoV-2— presenting a concerning mystery as to how the animals became infected.

SARS-CoV-2 infections in mink aren't particularly noteworthy or concerning on their own; it's well established that mink are susceptible to the virus. The realization early in the pandemic resulted in extensive [culls in Denmark](#) and the Netherlands during 2020 and led to intensive monitoring and regulation of remaining mink herds in many places, including Poland.

But [the recent cases in Polish mink](#), reported this week in the journal *Eurosurveillance*, are unusual. While previous mink outbreaks have linked to infected farmworkers and local circulation of the virus—indicating human-to-mink spread—none of the farm workers or families in the recently affected farms tested positive for the virus. In fact, health investigators found that the infected mink carried a strain of SARS-CoV-2 that has not been seen in humans in the region in more than two years (B.1.1.307).

The finding suggests that humans were not responsible for infecting the mink—at least not directly. Rather, it suggests that another unknown species may have been stealthily harboring and spreading the otherwise bygone strain for some time and managed to carry it onto the mink farms.

The suggestion raises more concern over viral "spillover." The term relates to the more recognized "spillover," when a virus jumps from a host population—a reservoir—to a new population, such as humans. SARS-CoV-2 is thought to have originated in a reservoir of horseshoe bats before it reached humans. Since then, it is clear that it can also infect a broad range of animals, including rodents, cats, dogs, white-tail deer, non-human primates, as well as ferrets and mink. Researchers fear that the virus could spill back to an animal population that could become a new reservoir from which the virus could periodically move back to humans.

This fear gained attention when the omicron variant abruptly emerged with its strikingly large suite of genetic changes. Some researchers speculated that omicron might have cryptically spread and evolved in mice before re-infecting humans. Other researchers, however, hypothesize that the variant evolved in an immunocompromised person.

## Cryptic cases

The farmed mink in Poland again highlight the risk of spillbacks by suggesting an unknown reservoir of SARS-CoV-2 in wild animals. In an investigation, researchers at National Veterinary Research Institute and Erasmus University Medical Centre looked into cases at three farms within 8 km (about 5 miles) of each other. The first farm reported two infected mink (out of 15 tested and about 8,650 animals total) on September 19, but they subsequently tested negative and were pelted as scheduled. On November 16, a second farm with 4,000 mink reported six infected animals out of 15 tested, and they were pelted with precautions. The third farm, with 1,100 mink, found 15 infected animals out of 15 tested on January 18, but they subsequently tested negative in two rounds of testing within 50 days. All of the infected animals on the three farms were asymptomatic.

The researchers obtained eight whole genome sequences—four each from the second and third farms; there wasn't enough genetic material in samples from the first farm. The genome sequences showed they were nearly identical and most closely matched the lineage B.1.1.307, which hadn't been seen in humans in Poland in over two years. The viruses also had 40 small genetic mutations, some of which have previously been associated with circulation in mink, and could have been acquired quickly. None of the farm families or workers tested positive for SARS-CoV-2 at any of the three farms.

The researchers noted that all three farms had concrete fences 1.8 meters (6 feet) high and about 30–40 cm (around a foot) deep. There was no evidence of animals burrowing under the fences, but the researchers noted overhanging tree branches that could have created a route for wild animals. Interviews with owners and staff revealed that the farms were occasionally visited by wild martens, weasel-like carnivores. And there were also feral cats around. The researchers tested feral cat droppings around the farms but found they were negative for SARS-CoV-2.

The researchers concluded that a wild animal—possibly the martens, feral cats, or even escaped mink—could have cryptically spread the SARS-CoV-2 lineage and introduced it to the three neighboring farms on separate occasions. They called for more surveillance, not just on mink farms but also of wild animal populations, such as martens, polecats, and foxes.

"The animals on the SARS-CoV-2-positive mink farms did not show signs of disease, which creates a possibility of independent viral evolution and may establish a source for future outbreaks with novel strains," they wrote.



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