

SURVEILLANCE OF INFECTIOUS DISEASES IN ANIMALS AND HUMANS IN SWEDEN 2020

Chapter excerpt -
Mink-associated infections with SARS-CoV-2



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Cover: Juvenile mink in hand. Photo: Elina Kähkönen

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Reporting guidelines: Reporting guidelines were introduced in 2018 for those chapters related to purely animal pathogens. The guidelines build on experiences from several EU projects, and have been validated by a team of international experts in animal health surveillance. The aim is to develop these guidelines further in collaboration within the global surveillance community and they have therefore been made available in the form of a wiki on the collaborative platform GitHub (<https://github.com/SVA-SE/AHSURED/wiki>). Feel free to contribute!

Layout: The production of this report continues to be accomplished using a primarily open-source toolset. The method allows the source text, produced by authors, to be edited independently of the template for the layout which can be modified and reused for future reports. Specifically, the chapter texts, tables and captions are authored in Microsoft Word and then converted using pandoc and R to the LaTeX typesetting language. Most figures and maps are produced using the R software for statistical computing and the LaTeX library pgfplots. Development for 2020 has further improved the importing of content from Excel files to automatically build figures in the pgfplots LaTeX library. The tool is available as an R-package on GitHub (<https://github.com/SVA-SE/mill/>). The report generation R-package and process was designed by Thomas Rosendal, Wiktor Gustafsson and Stefan Widgren. In 2020, final typesetting was done primarily by Wiktor Gustafsson with contributions from the report authors.

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Mink-associated infections with SARS-CoV-2

BACKGROUND

Severe Acute Respiratory Syndrome Coronavirus type 2 (SARS-CoV-2) is an emerging zoonotic coronavirus initially described as the causative agent of a cluster of cases of viral pneumonia in the city of Wuhan, China, in December 2019. Since then, SARS-CoV-2 has caused the COVID-19 pandemic in humans, with over 160 million confirmed human cases worldwide and over 3.5 million deaths to date (end of May 2021).

Coronavirus infections are common in both animals and humans, and some are known to be zoonotic. In humans, previously known coronaviruses can cause illness ranging from the common cold to more severe diseases such as Middle East Respiratory Syndrome (caused by MERS-CoV), and SARS (caused by SARS-CoV). SARS-CoV and MERS-CoV as well as SARS-CoV-2 belong to the genus *Betacoronavirus*, and all are believed to have viral ancestors with bats as the original host. Whereas investigations suggest that MERS-CoV and SARS-CoV were transmitted to humans from intermediary animal hosts (dromedary camels and civet cats, respectively), there is not enough scientific evidence to identify a possible intermediate host of SARS-CoV-2 or to explain the original route of transmission to humans, which may or may not have involved an intermediate host.

Susceptibility to SARS-CoV-2 has been demonstrated in several animal species, including, e.g. cats and other felines, ferrets, mink, dogs and non-human primates either through experimental infection or by identification of cases in natural settings after contact with infected humans. With the exception of mink, however, natural infection in animals has been limited to sporadic spill-over events from humans. In farmed mink, on the other hand, SARS-CoV-2 has caused extensive outbreaks with significant between-animal and between-farm spread in several countries with a vast impact on the international mink fur sector. Moreover, cases of mink to human transmission have been reported, including spillovers into society of new SARS-CoV-2 variants associated with mink. Concerns have therefore been raised concerning the risk that mink farms could represent a serious animal reservoir for SARS-CoV-2 resulting in the introduction and circulation of new virus strains in humans potentially with modifications of transmissibility or virulence and decreased treatment and vaccine efficacy and thus with potential future public health impact.

In 2020, before pelting, the Swedish mink fur sector was composed of approximately 35 farms with in-total 600–650,000 animals. Eighteen of these farms were located in the municipality of Sölvesborg, the County of Blekinge, in the south-eastern part of the country.



After pelting in 2020, approximately 900 000 breeding mink remained in the Swedish population and a decision was made to ban mink breeding during 2021. Photo: Svensk Mink.

DISEASE

Animals

Clinical signs of SARS-CoV-2 in mink are often non-specific and present only in a variable proportion of outbreaks. They can include increased mortality, mild respiratory signs, a slight drop in feed intake and occasionally mild gastrointestinal signs.

Humans

In humans according to WHO, infection with SARS-CoV-2 causes COVID-19, a disease characterized by mild to moderate respiratory illness in most people. Among those who develop symptoms, most recover from the disease without needing hospital treatment. About 15% become seriously ill and require oxygen, and 5% become critically ill and need intensive care.

Complications leading to death may include respiratory failure, acute respiratory distress syndrome, sepsis and septic shock, thromboembolism, and/or multiorgan failure, including injury of the heart, liver or kidneys. Older people

and those with underlying medical problems like cardiovascular disease, diabetes, chronic respiratory disease, and cancer are more likely to develop serious illness.

LEGISLATION

Animals

Infection with SARS-CoV-2 in animals is notifiable as an emerging infection in animals (SJVFS 2013:23).

Humans

COVID-19 in humans is notifiable according to the Communicable Disease Act (SFS 2004:168 with amendments, SFS 2013:634)

SURVEILLANCE

Animals

Following the first reports of outbreaks of SARS-CoV-2 in mink in the Netherlands in April and Denmark in June 2020, a dialogue between the competent authority and representatives from the Swedish mink sector was initiated to raise awareness, to ensure enhanced on-farm biosecurity practices and to raise vigilance regarding increased morbidity and mortality. In early October, given the absence of any reports of morbidity/mortality from the Swedish mink farms, an active surveillance scheme was initiated based on sampling up to five dead mink per farm per week. Within the scheme, mink found dead were submitted to the National Veterinary Institute in Uppsala, where they were sampled with swabs from the oral cavity and pharynx and analysed by qRT-PCR. Positive cases were further analysed through whole genome sequencing.

In December, after pelting, a serological screening was conducted targeting breeding animals. Blood was collected on filter papers from 24 animals per farm and sent to the National Veterinary Institute for the detection of SARS-CoV-2 specific antibodies using a commercially available ELISA (ID Screen SARS-CoV-2 double antigen multiple species ELISA).

The surveillance scheme was voluntary and organised in close collaboration with the industry.

Humans

In parallel to the surveillance of mink, an active surveillance program was launched for mink farmworkers in Sölvesborg and Skara municipalities at the end of November. The surveillance program encompassed 21 of the mink farms in Sweden. The program included voluntary screening of ongoing infection, where samples from farmworkers were screened by PCR weekly. The purpose of the program was to identify infected workers to prevent transmission from workers to mink. Moreover, the system provided early warning of mutations of concern that could arise within the animal population and subsequently be introduced to the human community. The surveillance of virus variants was achieved by performing whole-genome sequencing of SARS-CoV-2 PCR-positive samples. In addition to the screening for ongoing infection, voluntary serological surveys of the participating mink farmworkers were conducted.

RESULTS

Animals

Between mid-October and mid-November, the National Veterinary Institute received 74 submissions of between 3–5 dead mink, representing between 1 and 4 submissions per farm. Thirteen farms gave positive results for SARS-CoV-2 nucleic acids using qRT-PCR. All positive farms were located in Sölvesborg, the County of Blekinge, in the south-eastern part of the country. None of the positive farms had reported increased morbidity or mortality before testing positive but, retrospectively, a slight increase in daily mortalities could be observed in the records from several of the farms. All sequences from mink belonged to sub-lineage B.1.1.39, a sub-lineage only seen once in Sweden before the outbreak.

From the serological screening, 24 samples per farm were received from 26 out of the 28 mink farms that remained after the pelting. Specific SARS-CoV-2 antibodies were detected in the vast majority of samples from 23 farms, including in all farms that previously had been tested positive for SARS-CoV-2 nucleic acids. In the remaining three farms, all samples tested negative.

Humans

A total of 100 persons have been registered in the program, but due to the seasonal mode of work, and changes in the workforce, the number of participants has varied. The 317 samples that have been taken and analysed for ongoing viral infection within the surveillance program have resulted in 8 positive persons. In addition to samples from these persons another 14 samples from mink farmworkers that was tested positive before the surveillance was launched were collected. All 22 samples were whole-genome sequenced (WGS). In the serological survey, 78 persons participated, among whom 27 tested positive.

The resulting sequences from WGS were analysed using pangolin. Generally, two main groups were seen, one representing sequences with a pangolin classification similar to that of sequences recovered from WGS of samples from minks (B.1.1.39) and the second group representing sequences with a pangolin classification identical to those circulating in Sweden at the time. The sequences were further analysed by aligning them towards the reference sequence NC_045512. A phylogenetic tree was calculated, and the subtree representing sequences with the pangolin classification B.1.1.39 was studied separately as new sequences were added. A majority of sequences from human cases had clear phylogenetic relationships to sequences recovered from mink samples. Sequences from humans and mink from the same mink farms clustered closely together, suggesting within-farm human-to-mink and/or mink-to-human transmission. In sequences from two human samples from one of the negative mink farms the mutation Y453F, considered as an adaptation to mink, was observed.

DISCUSSION

Whereas a number of animal species have been shown to be susceptible to infection with SARS-CoV-2, and have the capacity to transmit the virus, extensive outbreaks in animals have only been seen in farmed mink. Once introduced into a farm, SARS-CoV-2 appears to spread efficiently among the animals. The high animal density that is typically present in a mink farm, provides ideal conditions for viral replication and transmission, also increasing the risk of virus evolution. Furthermore, experience from e.g. the Netherlands and Denmark demonstrates that once SARS-CoV-2 has been introduced into an area with high density of mink farms, farm-to-farm transmission is likely to occur, with potential spill over to people associated to the farms and to human communities close to the farms. Also, in Sweden extensive spread within and between farms occurred in spite of implemented biosecurity measures, as shown by the results from the surveillance carried out. A clear association was also observed between presence of SARS-CoV-2 among the mink and COVID-19 in people associated to mink, supported by the results of the whole genome sequencing. In contrast to e.g. Denmark, however, no community spread within the communities close to the affected farms was observed.

In Sweden, none of the affected farms was culled. The Swedish outbreak coincided with the annual pelting, when approximately 80% of the mink are killed as part of the production cycle. According to the assessment made, culling of affected farms as part of disease control measures would

not speed up the process of reducing the number of susceptible animals compared with the annual pelting and killing, and would therefore not contribute to any significant reduction in the risk of further spread of the disease. Pelting was carried out from mid-November to early December, under strict biosecurity recommendations, to prevent mink-to-human SARS-CoV-2 transmission. After pelting, approximately 90 000 breeding animals remained in Sweden.

Given the extensive spread of SARS-CoV-2 among Swedish mink experienced during the fall, with spill-over to people associated to the affected farms, a concern was raised regarding the potential public health risk of allowing breeding to occur during the following season (i.e. spring 2021). With this in mind, and based on a risk assessment, a decision was taken to ban mink breeding during 2021.

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