
Health, zoonotic pathogens and parasites

SARS-CoV-2 infection in farmed minks from Lithuania

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Lithuania ranks among the ten countries worldwide with established mink farming industries. In 2020, over 1.2 million minks were bred across 57 farms in Lithuania. On November 24, 2020, SARS-CoV-2 infection in minks was detected for the first time in a farm in the Jonava region. Subsequently, nationwide surveillance was conducted across all mink farms in Lithuania. Samples from dead and apparently healthy minks were collected in 15 mink farms located in 12 Lithuanian districts. Genomic sequencing of SARS-CoV-2 strains from these samples was performed to assess viral variants circulating in Lithuanian mink farms and their distribution across various geographic locations. Full-length virus genome sequencing was performed in Illumina MiSeq Sequencer. The genomes were assembled using the Illumina BaseSpace software DRAGEN COVID Lineage. The Fasta format of whole genome sequences was used for clade and lineage assignment using online tools: Nextclade and GISAD.

A total of 276 variable nucleotides were detected among the analysed 47 SARS-CoV-2 genome sequences derived from minks. Phylogenetic analyses and genotype comparisons were made to determine the relationship between mink-associated SARS-CoV-2 strains and those infecting humans. Phylogenetic analysis revealed the circulation of seven GISAID clades or four Nextstrain clades in the minks during the study period. Analysed strains belonged to ten lineages (Nextclade; GISAID). Distribution of CoV-2 variants in minks and humans in Lithuania over clades and locations and phylogenetic relationships between SARS-CoV-2 strains derived from minks in Lithuania and other European countries were analysed. The virus's evolution within an animal reservoir could result in new zoonotic sources, increasing the likelihood of recurrent transmission of emerging SARS-CoV-2 variants from minks to humans and other mammals.