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FIRST CASE OF CANINE DISTEMPER IN GOLDEN JACKALS IN SERBIA

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Introduction:

Canine distemper virus (CDV) is the causative agent of a frequently fatal disease of wild and domesticated carnivores. The virus is a single-stranded RNA virus belonging to the genus *Morbillivirus*, and the family *Paramyxoviridae*. The disease is most common in domestic dogs, although the virus can cross species boundaries, and thus poses a threat to endangered wildlife.

Material and methods:

In the study, we examined 52 brain samples from legally hunted 43 golden jackals, four red foxes, three badgers, and two wild cats. Brain tissue was homogenised with a mortar and pestle and mixed with PBS at a ratio of 1:10 ratio. It was then centrifuged at 4000 rpm, and the supernatant was decanted and stored at -20 °C until further use. Viral RNA was extracted using a commercial IndiSpin Pathogen Kit (IndiSpin Pathogen Kit, Indical, Germany), and PCR products were amplified using primers previously published protocols. The products were visualised on a 1.5% agarose gel by electrophoresis. The expected length of the PCR product was 290bp. Samples found to be positive were further purified using the GeneJET PCR purification kit (ThermoFisher Scientific, Waltham, MA, USA), and sequenced at LGC, Biosearch Technologies, Germany, using the Sanger sequencing method. Consensus sequences were generated using Geneious Prime (Geneious Prime, Dotmatics, Boston, MA, USA), and a phylogenetic study was performed using MEGA X software.

Results:

Of the 52 tested samples, two were positive (3.8%). Good-quality sequences were deposited in NCBI under accession numbers OQ565284 and OQ565285. The sequences tested in this study were compared with 100 sequences from NCBI. The highest identity detected was 98.4% with 100% coverage with strains from Iran (JN941243.1, JN941241.1, JN941240.1, MZ802994), China (EU716315.1, EU489475.1). Phylogenetic analysis revealed a separate clade with Serbian variants and the previously mentioned strains from Iran and China, as well as strains from Russia (KX774415, MN267063), and one strain from Germany (AF166268).

Conclusion:

Three branches can be identified within the group, with the Serbian variants splitting into their own branch. The strains in this group are from different species, including dogs (JN941243, MZ802994, AF166268) jackals (JN941241, JN941240), tigers (KX774415), seals (MN267063), racoon dogs (EU716315), and foxes (EU489475), and from different time periods. The oldest sample AF166268 was collected in 1999, while the most recent sample MN267063, was collected in 2020, with few differences. Because the virus has a variety of hosts, different strains of the virus can be present in isolated populations of wild carnivore species and still retain the ability to infect different species, posing a high risk for possible cross-transmission to/from domestic dogs and wildlife. Golden jackals live in groups and are scavengers, so they are often found near settlements where they come into contact with domestic dogs. Because golden jackals are very numerous, they can be classified as a high-risk category for CDV transmission and thus can be a significant source of infection for other (endangered) species.