

# Surveillance and molecular characterization of SARS-CoV-2 infection in non-human hosts in Gujarat, India.

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## Abstract

Since December 2019, severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) has been spreading worldwide, triggering one of the most challenging pandemics in human population. In the light of reporting of this virus in domestic and wild animals from several parts of world, a systematic surveillance study was conceptualized to detect the SARS-CoV-2 among species of Veterinary importance. Nasal and/or rectal samples of 413 animals (Dog=195, cattle=64, horse=42, goat=41, buffalo=39, sheep=19, cat=6, camel=6 and monkey=1) were collected from different places of Gujarat state of India. RNA was extracted from samples and subjected to RT-qPCR based amplification of target sequences in viral nucleoprotein (N), spike (S) and ORF1ab genes. A total of 95 (23.79 %) animals were found positive, comprised of 67 (34.35 %) dogs, 15(23.43 %) cattle and 13(33.33 %) buffaloes. Overall, nasal samples (N=80/412, 19.41 %) gave more positive results than rectal samples (N=70/407, 17.19 %) in RT-qPCR. The whole SRAS-CoV-2 genome sequencing was done on one sample (ID-A4N; from dog) where 32 mutations, including 29 single nucleotide variation (SNV) and two deletions, were detected. Among them, 9 mutations were located in the receptor binding domain of the spike (S) protein. The consequent changes in amino acid sequence revealed that T19R, G142D, E156-, F157-, A222V, L452R, T478K, D614G, P681R mutation in S protein and D63G, R203M and D377Y in N protein. The lineage assigned to this SARS-CoV-1 sequence is B.1.617.2. Thus, the present study highlights the importance of SARS-CoV-2 surveillance in non-human host.

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