

First Report of Canine Bufavirus and its Whole genome Sequence in India

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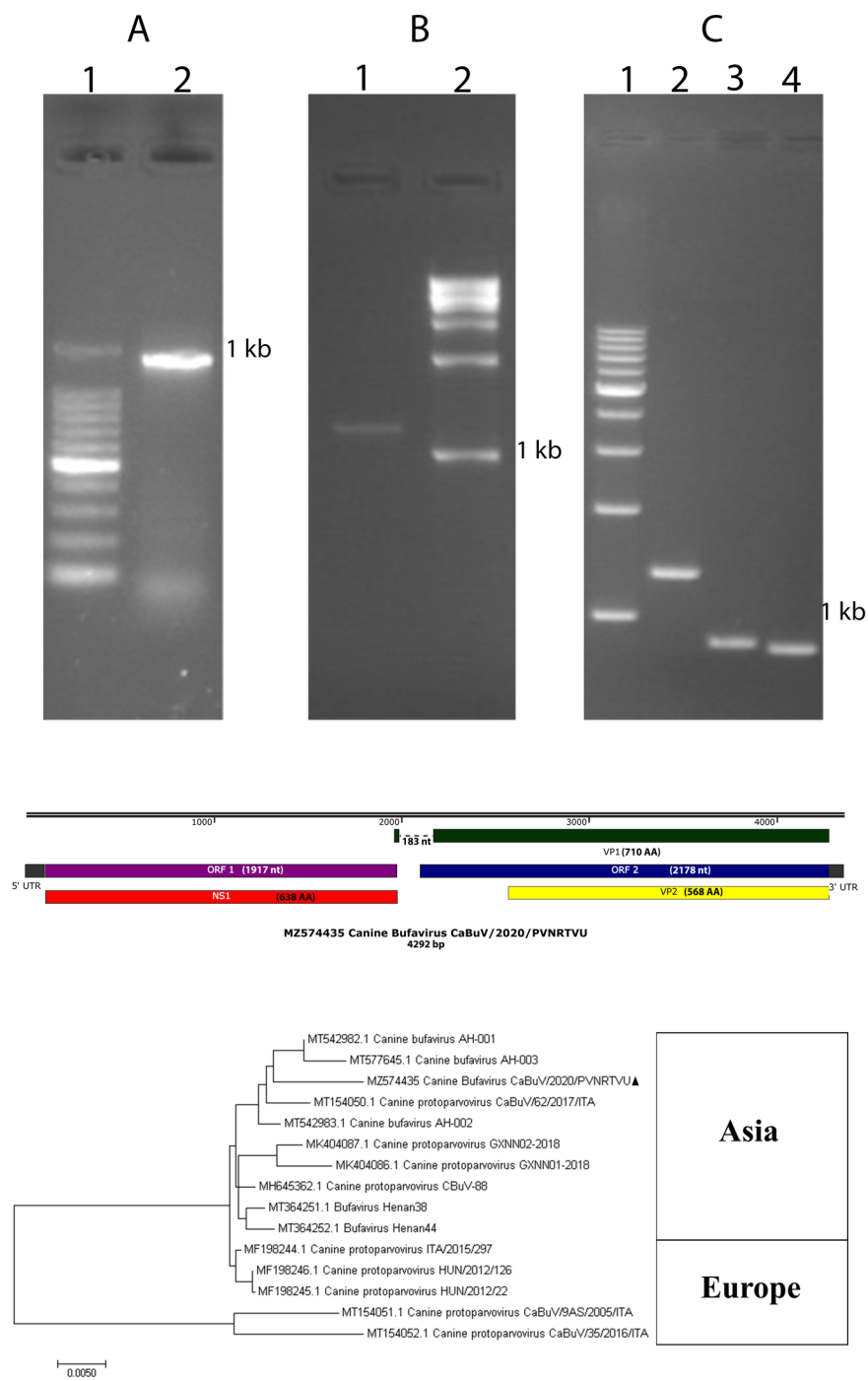
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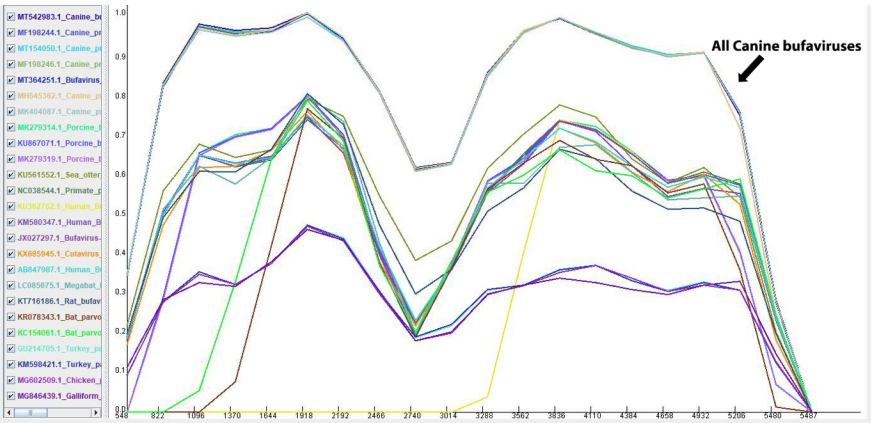
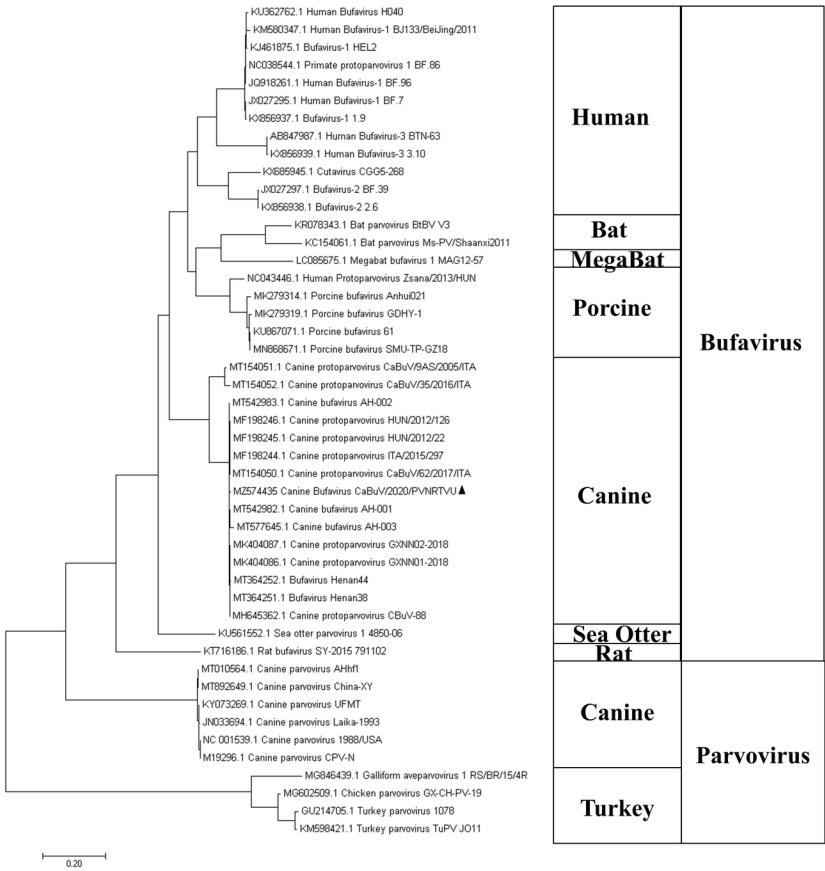
Abstract

Canine bufavirus (CaBuV), a novel protoparvovirus of dogs was reported only in Italy and China, till date. It was detected from dogs with enteric and respiratory symptoms and is distantly related to the human bufavirus. To explore the enteric prevalence of CaBuV in India, 186 diarrheic faecal samples were collected in Telangana State between 2019 and 2020. Among the samples, 4.3% (8/186) were positive for CaBuV by PCR. Co-infection with canine parvovirus CPV-2 was seen in 75% (6/8) of CaBuV positive samples. The near complete genome (4292 bp) of CaBuV was amplified and reconstructed for one isolate 407/PVNRTVU/2020. Sequence alignment indicated 93.42–98.81% homology with the other available CaBuV sequences; 70.88–73.39%, and 54.4–54.8% identity with human bufavirus, and CPV-2, respectively. Phylogenetic analysis showed that CaBuV 407/PVNRTVU/2020 was most closely related to CaBuV Chinese strains, together separated as Asian lineage. All Bufaviruses clustered together in one clade; however, the bat and sea otter parvoviruses also showed close relation with Bufaviruses. This first report of prevalence of CaBuV in India provides a good reference, emphasizes the need for further epidemiological surveillance of CaBuV in India and its role in canine enteritis.

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