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Short communication

Molecular epidemiology and characterization of picobirnaviruses in small ruminant populations in India

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ABSTRACT

Picobirnavirus (PBV) is recognized as a putative cause of diarrhea and respiratory illnesses. Although PBV has been reported in several mammalian (including humans) and avian host species, data pertaining to its presence in small ruminants are limited. We report, here, PBV infection in small ruminants (ovine and caprine), in India. From January 2015 to December 2017, 400 samples were tested for the presence of PBV, using an RT-PCR assay specific for the genome segment-2. The overall rate of PBV infection was 35.75% (143/400), being higher in caprines (42.35%, 83/196) than in ovines (29.42%, 60/204). Viral genogrouping showed the predominance of PBV genogroup I (GG-I; 53.15%, 76/173), the detection of genogroup II (GG-II; 3.49%, 5/143), a concomitant infection with GG-I and GG-II (38.47%, 55/143), and un-typeable strains (4.9%, 7/143). Of note, these PBV strains exhibit low sequence identity (11.2% to 70.7%) to other reported PBV isolates from humans and other animals. By phylogenetic analysis, camel PBV isolates from the United Arab Emirates (UAE) and the reference human GG-I strain (1-CHN-97) from China were found to be the nearest neighbors of PBV strains. Furthermore, sequence analysis revealed the possible appearance of a new genogroup/genetic cluster and the existence of high genetic heterogeneity in the circulating PBV strains. Although much remains to be understood about the epidemiology and impact of PBV, the present study demonstrates the high prevalence of GG-I, the detection of GG-II, and the possible emergence of new genogroup/genetic cluster in small ruminant populations in India.

1. Introduction

Picobirnavirus (PBV) is an emerging and important member of the double-stranded segmented RNA virus group. The *Picobirnavirus* genus is placed under the order *Diplornavirales* and is identified as the only genus of the *Picobirnaviridae* family (Malik et al., 2014b). PBV is considered an opportunistic pathogen commonly found in patients with diarrhea. Furthermore, reports of its detection in extra-intestinal sites have raised a debate regarding their actual site of infection (Smits et al., 2011). Since the first report on the detection of *Picobirnavirus* in human neonates and rats (*Oryzomis nigripes*), in Brazil in 1988 (Pereira et al., 1988a; Pereira et al., 1988b), these viruses have been reported to be present in different mammalian and avian host species worldwide (Malik et al., 2014b; Kattoor et al., 2016). Apart from the reports of PBV infection in domestic and wild species, data pertaining to small ruminants are still limited, except for a single report in lambs in Spain (Munoz et al., 1996). Hence, we explored the possibility of PBV infection in small ruminant populations from different geographical regions of India. Sampling in this study involved caprine (n = 196) and ovine (n = 204) species from northern regions (plains, hilly, and semi-arid) of India. Samples from caprine species were obtained in the Mathura district (situated alongside the bank of the Yamuna river) of the Uttar Pradesh (UP) state of northern India (n = 106) and from organized farms situated on the foothills of the Himalayan region in the state of Uttarakhand (UK) (n = 90). Similarly, sampling from ovine species was carried out in the Mathura district (UP state; n = 97) and from

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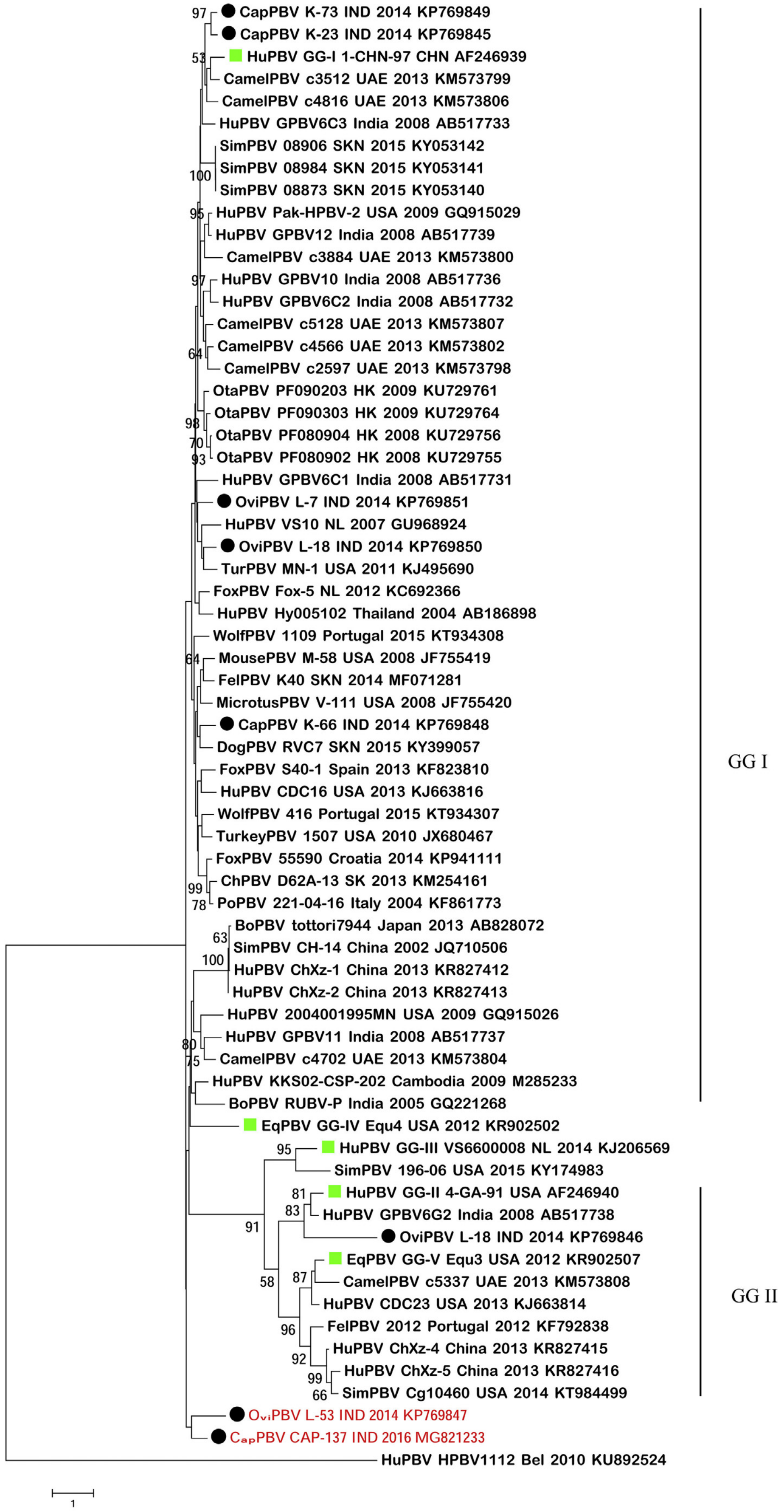

Fig. 1. Nucleotide based phylogenetic analysis of *Picobirnavirus* (PBV). Phylogeny retrieved based on a partial fragment of the RdRp gene (~350 bp) with other mammalian and avian PBVs. The current study PBV sequences obtained are indicated by the dark black circle "●" in the phylogeny. The reference PBV strains used this study are indicated in green square symbol "■". The putative new genogroup strains (L-53 & CAP-137) have been highlighted by the red color. Scale bar indicates nucleotide substitutions per site. Phylogeny was retrieved using the capsid gene sequence of Belgium human PBV strain HPBV1112 (accession number KU892524) as out-group. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)