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Genomic recombination in primate bocavirus: inconsistency and alternative interpretations

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Abstract Human bocavirus (HBoV) is a single-stranded DNA virus in *Parvoviridae* family, causing respiratory diseases in human. The recent identifications of genomic recombination among the four human bocavirus genotypes and related non-human primate bocaviruses have shed lights into the evolutionary processes underpinning the diversity of primate bocavirus. Among these reports, however, we found inconsistency and possible alternative interpretations of the recombination events. In this study, these recombination events were reviewed, and the related genome sequences were re-analysed, aiming to inform the research community of bocavirus with more consistent knowledge and comprehensive interpretations on the recombination history of primate bocavirus.

Keywords Primate · Bocavirus · Recombination · Evolution

Abbreviations

BoV	Bocavirus
HBoV	Human bocavirus

Main text

Human bocavirus (HBoV) is a single-stranded DNA virus in *Parvoviridae* family, which was first identified in human respiratory tract samples in 2005 [1]. HBoV was then subsequently reported in many respiratory diseases surveillances [2–5], which led to the discovery of four genotypes (HBoV1-4). Later, some non-human primate bocaviruses have been identified, raising the possibility of animal origin for the ancestral bocavirus. Brožová et al. recently reported a new primate bocavirus from chimpanzee and suggested that the genome of this virus (CPZh2-BoV) has a mosaic origin recombining between human bocavirus genotype 3 (HBoV3) and human bocavirus genotype 1 (HBoV1) or a gorilla bocavirus (GBoV) [6]. Indeed, recombination seems to play a major role in the evolution and emergence of new bocavirus variants as a number of research papers have reported inter- and intragenotypic recombinations of bocavirus, for example, suggesting the recombinant origin of HBoV2 and HBoV3 [2, 7, 8]. However, some of these reports have presented conflicting data or have not fully elaborated all the possible interpretations on the data. Here, we reviewed and analysed the published papers and data about recombination among primate bocavirus genotypes, to provide more comprehensive interpretation on the recombination history of these viruses. After preliminary analysis of all complete genome sequences of bocaviruses aligned using MUSCLE v3.5 [9], representative strains were kept (17 HBoV and 2 non-human primate bocaviruses) to produce clear informative

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Yee Ling Chong and Kar Hon Ng have contributed equally to this study.

Availability of data and materials The datasets analysed during the current study are available in the GenBank repository, with the accession numbers indicated before the strain names in the figure.

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