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Identification and cross-species transmission of a novel ichthyic parvovirus in marine species in Hainan Island, China

Jiang Du^{1,2,3#}, Wen-qi Wang^{1,2#}, Jasper Fuk-Woo Chan^{1,4,5,6#}, Gao-yu Wang^{1,2}, Yi Huang^{1,2}, Yu-fang Yi^{1,2}, Zheng Zhu^{1,4,5,6#}, Ruo-yan Peng^{1,2}, Xiao-yuan Hu^{1,2}, Yue Wu^{1,2}, Ji-feng Zeng^{7,8}, Ji-ping Zheng⁹, Xiu-ji Cui^{1,2,3}, Li-na Niu^{1,2,3}, Wei Zhao^{1,2,3}, Gang Lu^{1,2,3}, Kwok-Yung Yuen^{1,4,5,6}, Fei-fei Yin^{1,2,3✉}

¹Hainan Medical University–The University of Hong Kong Joint Laboratory of Tropical Infectious Diseases, Hainan Medical University, Haikou, Hainan, China; and The University of Hong Kong, Pokfulam, Hong Kong

²Key Laboratory of Tropical Translational Medicine of Ministry of Education, Hainan Medical University, Haikou, Hainan, China

³Department of Pathogen Biology, Hainan Medical University, Haikou, Hainan, China

⁴State Key Laboratory of Emerging Infectious Diseases, The University of Hong Kong, Pokfulam, Hong Kong

⁵Department of Microbiology, The University of Hong Kong, Pokfulam, Hong Kong

⁶Carol Yu Centre for Infection, The University of Hong Kong, Pokfulam, Hong Kong

⁷Key Laboratory of Tropical Animal Breeding and Epidemic Disease Research of Hainan Province, Hainan University, Haikou, Hainan, China

⁸Key Laboratory of Tropical Biological Resources of Ministry of Education, Haikou, Hainan, China

⁹Hainan Key Laboratory for Sustainable Utilization of Tropical Bioresources, Hainan University, Haikou, China

Parvoviruses are a diverse group of viruses that are capable of infecting a wide range of animals. In this study, we report the discovery of a novel parvovirus, tilapia parvovirus HMU-HKU, in the fecal samples of crocodiles and intestines of tilapia in Hainan province, China. The novel parvovirus was firstly identified from crocodiles fed with tilapia using next-generation sequencing. Screening studies revealed that the prevalence of the novel parvovirus in crocodile feces samples fed on tilapia (75%-86%) was apparently higher than that in crocodiles fed with chicken (4%). Further studies revealed that the prevalence of the novel parvovirus in tilapia feces samples collected at four areas in Hainan province was between 40% and 90%. Four stains of the novel parvovirus were identified in this study based on sequence analyses of *NS1* and all the four strains were found in tilapia in contrast only two of them were detected in crocodile feces. These findings proposed a possibility of cross-species transmission of the novel parvovirus from tilapia to crocodile. The nearly full-length genome sequence of the tilapia parvovirus HMU-HKU was determined and showed less than 28.3% and 25% amino acid identity with other members of *Parvoviridae* in *NS1* and *VP1* genes respectively. Phylogenetic analysis based on the *NS1* and *VP1* amino acid sequences showed that it was most closely related to members of the novel genus *Chapparvovirus* which did not belong to subfamily *Parvovirinae* nor *Densovirinae*. Tilapia parvovirus HMU-HKU formed an independent branch with *Chapparvovirus* and separated from it in the deep root of the phylogenetic tree. This indicated that the tilapia parvovirus HMU-HKU and *Chapparvovirus* viruses may have had a common ancestor and they independently evolved in their natural hosts. The identification of tilapia parvovirus HMU-HKU provides further insight into the viral and genetic diversity of parvoviruses and its infections in tilapia populations need to be evaluated in terms of pathogenicity and production losses in tilapia farming.

Keywords: Parvovirus; Cross-species transmission; Crocodile, Tilapia; Hainan

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[#]These authors contributed equally to this work.

[✉]Corresponding author: Fei-fei Yin, Hainan Medical University–The University of Hong Kong Joint Laboratory of Tropical Infectious Diseases, Hainan Medical University, Haikou, Hainan, China.

E-mail: yinfeifeiff@163.com

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